SOUTHEASTERN BIOLOGY

Volume 72 January-December, 2025 Number 1

THE 86TH ANNUAL MEETING OF THE ASSOCIATION OF SOUTHEASTERN BIOLOGISTS

Myrtle Beach, SC, March 12-15, 2025

T-shirt designed by Rebecca Lewis, Jacksonville University

The Official Publication of the Association of Southeastern Biologists, Inc.
http://www.sebiologists.org

SOUTHEASTERN BIOLOGY
(ISSN 1533-8436)

SOUTHEASTERN BIOLOGY (ISSN 1533-8436) is published online annually by the Association of Southeastern Biologists, Inc. All contributions, inquiries about missing back numbers and other matters should be addressed to info@sebiologists.org.

TABLE OF CONTENTS

ASB Leadership and Purpose 2
The View From Here 4
Featured Institutions 6
ASB 2025 R.H. Martin Plenary Session 7
ASB Patrons and Affiliate Organizations 8
ASB 2025 Exhibitors 9
ASB Career Award Winners 10
ASB Support Award Winners 11
ASB Research Grant Winners 12
ASB Presentation Awards 13
ASB Affiliate Presentation Awards 14
ASB Symposia 16
ASB Workshops 27
ASB Presentations 28
ASB Posters 81
ASB Lightening Talks 186
Tri-Beta Presentations 193
Tri-Beta Posters 201
Index of Authors 215

Holly Boettger-Tong
President
Wesleyan College

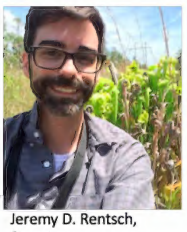
Heather Joesting
President-elect
GA Southern Univ

Lyndsay Rhodes
Vice President
Florida Gulf Coast Univ

Chris Brown
Past President
GA Gwinnett College

Charles Horn
Treasurer
Newberry College

Sahar Hasim
Associate Treasurer
Alabama State Univ


Jeremy D. Rentsch,
Secretary
Francis Marion Univ

Members At Large

Matt C. Estep,
Appalachian State Univ

Julie Ballenger
Columbus State Univ

Jennifer Mandel
Univ of Memphis

Dennis Haney
Furman Univ

Natasha Vanderhoff
Jacksonville Univ

Andrea L. Moore,
Savannah State Univ

ASB Officers

President	Holly Boettger-Tong, Wesleyan College, Macon, GA, hboettger-tong@wesleyancollege.edu
President-Elect	Heather Joesting, Georgia Southern University, Savannah, GA, hjoesting@georgiasouthern.edu
Vice President	Lynday Rhodes, Florida Gulf Coast University, Fort Meyers, FL, lrhodes@fgcu.edu
Past-President	Christopher G. Brown, Georgia Gwinnett College, Lawrenceville, GA, cbrown37@gmail.com
Secretary	Jeremy D. Rentsch, Francis Marion University, Florence, SC, JRentsch@fmarion.edu
Treasurer	Charles Horn, Newberry College, Newberry, SC, charles.horn@newberry.edu
Assoc. Treasurer	Sahar Hasim, Alabama State University, Montgomery, AL, shasim@alasu.edu
Meeting Planner	Shannon Oliphant-Gordon, Experient, Shannon.oliphant-gordon@experientselect.com

Executive Committee Members-at-Large

Class of 2025	Jennifer Mandel, University of Memphis, Memphis, TN, jmandel@memphis.edu Natasha Vanderhoff, Jacksonville University Jacksonville, FL, nvander4@ju.edu
Class of 2026	Julie Ballenger, Columbus State University, Columbus, GA, ballenger_julie@columbusstate.edu Dennis Haney, Furman University, Greenville, SC, dennis.Haney@furman.edu
Class of 2027	Matt Estep, Applachian State University, Boone, NC, estepmc@appstate.edu Andrea Moore, Savannah State University, Savannah, GA, moorean@savannahstate.edu

Outgoing Executive Officers at the 2025 Meeting

Thank you for your service

President:	Holly Boettger-Tong, Wesleyan College, Macon, GA, hboettger-tong@wesleyancollege.edu
Vice President:	Lynday Rhodes, Florida Gulf Coast University, Fort Meyers, FL, lrhodes@fgcu.edu
Past President:	Christopher G. Brown, Georgia Gwinnett College, Lawrenceville, GA, cbrown37@gmail.com
Members-at-Large:	Jennifer Mandel, University of Memphis, Memphis, TN, jmandel@memphis.edu
	Natasha Vanderhoff, Jacksonville University Jacksonville, FL, nvander4@ju.edu
	Julie Ballenger, Columbus State University, Columbus, GA, ballenger_julie@columbusstate.edu

ASB Officers for 2025-2026

PRESIDENT
Heather Joesting
Georgia Southern University
Savannah, GA

VICE PRESIDENT
Natasha Vanderhoff,
Jacksonville University

Past-President
Holly Boettger-Tong
Wesleyan College
Macon, GA

SECRETARY
Jeremy D. Rentsch,
Francis Marion University,
Florence, SC

TREASURER
Charles Horn
Newberry College
Newberry, SC

ASSOCIATE TREASURER
Sahar Hasim
Alabama State University
Montgomery, AL

MEMBERS-AT-LARGE

Class of 2028

Joydeep Bhattacharjee
University of LA, Monroe

Megan Gibbons,
University of AL at Birmingham

Class of 2027

Andrea L. Moore,
Savannah State University,
Savannah, GA

Matt C. Estep,
Appalachian State University,
Boone, NC

Class of 2026

Dennis Haney
Furman University
Greenville, SC

Jennifer Hurst-Kennedy,
Agnes Scott College

Purpose

The purpose of this association shall be to promote the advancement of biology as a science by encouraging research, the imparting of knowledge, the application of knowledge to the solution of biological problems, and the preservation of biological resources. The ASB has representation in Section G Committee of the AAAS. Varying types of membership are available to individuals and institutions. See inside back cover.

Time and Place of Future Meetings

2026 Mobile, Alabama

March 25-28, 2026

The View from Here: A Message from the President

It is truly my honor to serve as the President of ASB, and I am grateful for the opportunity to report on the activities of ASB. We continue to hold our Annual Meeting, which provides a venue for student and professionals from across the Southeastern United States to present their research. This year we held the 86th Annual Meeting of the Association of Southeastern Biologists at the Myrtle Beach Convention Center in Myrtle Beach, South Carolina, March 12 – 15, 2025. The meeting kicked off with the R.H. Martin Plenary Address. This year our address was given by Dr. Erica Woolsey, who took us on an underwater adventure with her presentation "Diving the Great Barrier Reef". During Dr. Woolsey's presentation, meeting attendees were introduced to the diversity of life that calls coral reefs home as well as some of the technical aspects of diving. Dr. Woolsey also shared some of her research on coral conservation and how future climate change will affect life on the reef. This highly engaging presentation was made possible through the generous support of the R.H. Martin family and ASB general meeting funding.

The 2025 ASB meeting continued to provide a venue for both undergraduate and graduate students and professionals to present their research. A large proportion of our attendees are undergraduate and graduate students, and for many of these students, this was their first scientific conference. To help defray the costs of attending the meeting, ASB offers several Student Support Awards. The funding for these awards come from a variety of sources, including the "Silent Auction", which was held in honor of Dr. Rebecca Cook this year in thanks for her longstanding commitment to this fundraiser. We are committed to increasing our support mechanisms for students to attend ASB, so please consider donating, either through providing items to the Silent Auction at 2026 ASB meeting or monetary donations to our Support Fund any time. Preparing students for a career in biology is an important part of the mission of ASB – thank you in advance for your support!

Our annual meetings are enhanced by our Featured Institutions and Affiliate Organizations. In Myrtle Beach, we were fortunate to have the Coastal Carolina University Gupta College of Science and Francis Marion University as Featured Institutions. Their participation was integral to making the 2025 ASB meeting a success, and we deeply appreciate their support. The 2025 ASB meeting also benefited from the participation of our Affiliate Organizations – the National Association of Biology Teachers (NABT), Tri-Beta ($\beta\beta\beta$) Districts I and II, Spring Wildflower Pilgrimage, Southeast Section of the Botanical Society of America (BSA), Southern Appalachian Botanical Society (SABS), Southeast Chapter of the Ecological Society of America (ESA), and Southeastern United States Chapter of the Society of Herbarium Curators (SHC-SEUSA). Our affiliates expand opportunities for meeting attendees through student travel support awards, student presentation awards, and networking events.

Executing an ASB meeting is a complex process that takes months of planning. Of course, our meetings would not be possible without our fantastic meeting planner Shannon Oliphant-Gordon. With Shannon, a group of dedicated individuals who serve on the ASB Executive Committee (EC) work with our collaborators to plan our annual meetings. It has been my privilege to work with the members of the EC, who volunteer hours to preparing our annual meeting, including reviewing Workshop, Symposium, and Field Trip proposals, engaging our Featured Institutions and exhibitors, researching and selecting Plenary speakers, considering and organizing presentation abstracts into

a meeting program, recruiting and assigning presentations to volunteer judges for student presentation awards, and so much more! The work of ASB is fueled by committed volunteers, and I hope you will consider serving on an ASB Committee or even the Executive Committee. A new, diverse viewpoint is always welcome!

Occasionally, ASB will choose to comment on a current issue that is of importance to our organization. In January 2025, the White House issued an Executive Order to end funding for programs related to Diversity, Equity, and Inclusion (DEI) initiatives. To reemphasize the Association's support and dedication to facilitating diversity in the biological sciences, the following statement was released:

As biologists, we acknowledge the vital role that diversity plays in enriching the ecosystems we study. The Association of Southeastern Biologists affirms, embraces and intends to continue to grow the diversity of our professional ecosystem and is unequivocal in our position that all are welcome in our society, regardless of sexual orientation, gender expression, ethnicity or race. The study of Biology deserves nothing less than the equal participation of those who choose to pursue this field, and ASB will continue to fulfill our mission to, "promote the advancement of biology as a science by supporting research and education, using knowledge to solve biological problems, and preserving biological resources." Membership in ASB is a valuable resource and during these challenging times, we pledge as a Society to remain, "a welcoming place for serious science."

As the summer winds down, the EC is focusing their efforts on preparing for 2026 ASB in Mobile, Alabama March 25 – 28. We are excited to offer our meeting in a new venue and experience the southern coastal charm of Mobile. I encourage you to submit an abstract, apply for research and support awards, and nominate a worthy colleague or mentor for a career award. You can find out more about the 2026 ASB meeting as well as access the calendar for deadlines at sebiogists.org, and we will also communicate important dates via email. We are looking forward to another awesome meeting, and we thank you for being a valuable member of ASB.

I look forward to seeing you in Mobile in 2026!

Heather M. Joesting, ASB President

Featured Institutions at ASB 2025

Thank You for Your Support!

ASB 2025 R.H. Martin Plenary Session
Dr. Erika Woolsey

Erika Woolsey is a marine biologist and chief scientist of The Hydrous, a nonprofit that uses emerging technologies like virtual reality to improve the public's engagement with the ocean. Originally from the San Francisco Bay area, she conducted her Ph.D. research on the Great Barrier Reef in Australia with James Cook University. As an undergraduate student at Duke University, she studied biology and art history. Woolsey was an Ocean Design Fellow and lecturer at Stanford University's d.school and the Center for Ocean Solutions and is currently a Visiting Scholar at Stanford's Virtual Human Interaction Lab. She was honored by the Explorers Club in 2023 as one of 50 people changing the world.

About the R.H. Martin Plenary

Robert H. Martin, founder and owner of Martin Microscope Company from 1946 until his death in 2006, was an avid supporter of ASB and of the sciences in general. He supported ASB for decades as a Patron member and sponsor of the ASB Student Research Award, and, with his passing, his family established what has become the Robert H. Martin Plenary Address fund to help cover the costs of bringing in highly qualified speakers for the ASB annual meeting.

ASB 2025 Patrons and Sponsors

Martin Microscope .com

There are many ways to support ASB's mission to provide high-quality opportunities for biologists across the southeast to present their work, network with peers, and develop professionally.

Find out more on our website:

https://www.sebiologists.org/sponsors--exhibitors.html

2025 Affiliate Organizations

NABT
National Association of Biology Teachers

Connecting the public, experts, and nature through nonprofit educational hikes since 1951
SPRING WILD FLOWER PILGRIMAGE 2024
Wildflowerpilgrimage.org

Southern Appalachian Botanical Society
Publishing Castanea since 1936

Botanical Society Of America
Southeast section

Society of Herbarium Curators
Southeast chapter

ECOLOGICAL SOCIETY OF AMERICA
esa
Southeast chapter

Βλέπειν βασιν βιον
Districts I and II

ASB 2025 Exhibitors

AWARDS PRESENTED AT THE 2025 ANNUAL MEETING IN MYRTLE BEACH

CAREER AWARDS

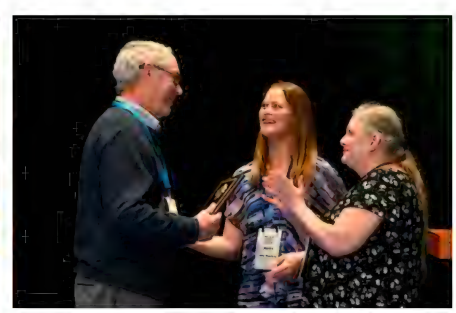
ASB JOHN HERR LIFETIME ACHEIVEMENT AWARD

This prestigious award recognizes unusually significant contributions by its members to the life of the Association and to biology in the southeastern US. The award is given in honor of Distinguished Professor Emeritus John Herr (Department of Biological Sciences, University of South Carolina).

Dr. Zack Murrell
Professor of Biology
Appalachian State University

ASB MERITORIOUS TEACHING AWARD

The Association of Southeastern Biologists Meritorious Teaching Award honors excellence in biology teaching at the undergraduate and/or graduate level. The Meritorious Teaching Award Committee reviews nomination packages from the ASB membership and selects the winner.



Dr. Charles Horn
Professor of Biology
Newberry College

ASB SUPPORT AWARDS

THE LAFAYETTE FREDERICK UNDEREPRESTENED MINORITIES SCHOLARSHIP	**Thalia Paiz**	Mary Baldwin University
SUPPORT AWARDS FOR FIRST-GENERATION UNDERGRADUATE STUDENT MEMBERS OF ASB	**Amaiya McDowell**	Lander University
	April Wooten	Francis Marion University
	Elyssa Ghazali	Applachian State University
	Emily Parrish	Univesity of South Alabama
	Giselle Ponce-Bautista	Moravian University
	Kiberly Sipanela	Lander University
	Lily Ridgell	Frostburg Stare University
	Nicholas Allen Bates	Georgia Gwinnett College
	Tara Maurano-Castrejon	Georgia Southern University
SUPPORT AWARD FOR GRADUATE STUDENT MEMBERS OF ASB	**Sarah Durham**	Old Dominion University
	Syndey Hermann	Marshall University
	Jpahet Senyo	Alabama State University
	Gavriel Burger	Florida Gulf Coast University
	Brogin Van Skoik	Tuskegee University
	Kayla Quincy	Agnes Scott College
	Olufemi Ebenezer Fatunsin	Alabama A&M University
	Julia Prins	University of Tennessee at Chattanooga
	Zak Bartholomew	Marshall University
	Katalina Cunningham	University of South Alabama

ASB RESEARCH AWARDS

ASB STUDENT RESEARCH AWARD

Sponsored by Martin Microscope

Olufemi Fatunsin

Alabama A&M University

ASB PROFESSIONAL RESEARCH AWARD

Alexander Orfinger

Dalton State University

Larval Taxonomy of the *Caddisfly Cernotina truncona Ross, 1947 (Trichoptera: Polycentropodidae)*

ASB PRESENTATION AWARDS

ASB STUDENT POSTER PRESENTATION AWARD – ANIMAL BIOLOGY

Evelyn Page, James Madison University
Temporal and geographic genetic dynamics of the invasive Kudzu Bug (Megacopta cribaria) across the Southeastern United States

ASB STUDENT POSTER PRESENTATION AWARD – AQAUTIC BIOLOGY

Jonathan Daniel, Furman University
The effects of cobalt on the symbiotic relationship between Exaiptasia diaphana sea anemoes and Beviolum minutum algae

ASB STUDENT POSTER PRESENTATION AWARD – CELL AND MOLECULAR BIOLOGY

Cassidy Lawrence, Florida Gulf Coast University
The effects of Eastern Diamondback rattlesnake (Crotalus adamenteus) venom on human triple-negative breast cancer

ASB STUDENT POSTER PRESTNATION AWARD - MICROBIOLOGY

William Johnson, Furman University
Abundance of fecal indicator bacteria and genetic diversity of Escherichia coli in streams draining residential areas of varying socioeconomic status

ASB STUDENT ORAL PRESENTATION AWARD – ANIMAL BIOLOGY

Mel Lhuillier, Old Dominion University
Swimming behavior of the longfin squid Doryteuthis pealeii paralarvae

ASB STUDENT ORAL PRESENTATION AWARD – AQUATIC BIOLOGY

Sally Sir, Georgia College and State University
Diversity of Panamanian amphipods (Crustacea) with the parvorder Caprellidira

ASB STUDENT ORAL PRESENTATION AWARD – CELL AND MOLECULAR BIOLOGY

Gavriel Burger, Florida Gulf Coast University
The effects of stilbene compounds on triple-negative breast cancer 3D cell culture model

ASB STUDENT ORAL PRESENTATION AWARD – MICROBIOLOGY

Hannah Blanton, Berry College
Streptococcus equi subspecies equi biofilm formation and role in environmental and host persistence

ASB DR. FLOYD SCOTT AWARD FOR THE BEST ORAL PRESENTATION IN HERPETOLOGY

Peyton Kinavey, Coastal Carolina University
eDNA: A powerful tool for Pine Snake (Pituophis melanoleucus) conservation

ASB AFFILIATE AWARDS

BOTANICAL SOCIETY OF AMERICA SOUTHEAST SECTION – STUDENT POSTER AWARD IN PLANT SCIENCE

Annabelle Mayes, Georgia Southern University
Spartina super seeders: Linking seedling production to plant and soil characteristics in coastal Georgia salt marshes

BOTANICAL SOCIETY OF AMERICA SOUTHEAST SECTION – STUDENT PAPER AWARD IN PLANT SCIENCE

Daniel Stanton, University of Florida IFAS Citrus Research and Education Center
Detection and prevalence of citrus blight infection in Florida varieties of citrus

ECOLOGICAL SOCIETY OF AMERICA SOUTHEAST SECTION – EUGENE P. ODUM AWARD

Grant Bowers, New Jersey Institute of Technology
Area-limited versus isolation-limited species: testing whether land vertebrates' differing responses to island area and isolation produce non-nested island communities in the Gulf of Maine

ECOLOGICAL SOCIETY OF AMERICA SOUTHEASTE SECTION – ELSIE QUARTERMAN-CATHERINE KEEVER AWARD

Garrett Timmons, Mississippi State University
Investigating patterns in breast cancer metastasis using invasion ecology frameworks

NORTH CAROLINA BOTANICAL GARDEN AWARD

Julia Prins, University of Tennessee at Chattanooga
Modeling NatureServ subnational conservation status ranks for Tennessee vascular plants

SOUTHERN APPALACHIAN BOTANICAL SOCIETY – CONFERENCE SUPPORT AWARDS

Rebekah Davis
Elyssa Ghazali
Lauren Gray
Kate Loughran
Ethan Smith
Salem Fleming
Lily Ridgell
Zak Bartholomew
Emma Crouch
Erica Edinger
Rebecca Foy
Clara Minnich
Jorge Vera
Kira Lindelof
Jake Thompson
Benjamin Warfield
Sara Durham
Anna Wyngaarden
Noah Williamson
Clair Epling
Aster Ayer
Nicholas Stalford

SOUTHERN APPLACHIAN BOTANICAL SOCIETY – EARL CORE STUDENT RESEARCH AWARD

Luke Sparreo, New York Botanical Garden and City University of New York
Systematics of the North American pitcher plants Sarracenia, their symbiotic mites Sarraceniopus, and cophylogenetic analysis

SOUTHERN APPLACHIAN BOTANICAL SOCIETY – RICHARD AND MINNIE WINDLER AWARD FOR BEST ECOLOGY PAPER IN *CASTANEA*	**David L. Phillips and Justin L. Hart** *Twenty years of strucrtual change, including tornado damage, in southern disjunct eastern hemlock stands*
SOUTHERN APPLACHIAN BOTANICAL SOCIETY – RICHARD AND MINNIE WINDLER AWARD FOR BEST SYSTEMATICS PAPER IN *CASTENEA*	**Edward E. Schilling, Aaron Floden, Jordan Reed, Cory Hale, Todd Crabtree, and Caitlin Elam** *Molecular barcoding the rare plants of Tennessee*
SOUTHERN APPLACHIAN BOTANICAL SOCIETY – ELIZABETH ANN BARTHOLEMEW AWARD	**Carol Baskin,** University of Kentucky
SOUTHERN APPLACHIAN BOTANICAL SOCIETY – BEST POSTER PRESENTATION	**Anna Wyngaarden,** University of Georgia *Snorkelwort occupancy in granite outcrop pools is driven by soil depths: A comprehensive approach incorporating detection rates*
SOUTHERN APPLACHIAN BOTANICAL SOCIETY – BEST ORAL PRESENTATION	**Sarah Durham,** Old Dominion University *Climate growth relationships among longleaf and associated pines in Southeastern Virginia*

ASB Symposia

SYMPOSIUM: Biodiversity in Peril

LaRoy Brandt, Lincoln Memorial University, Harrogate, TN

10582 - Introductory Remarks

10400 - Loss of Biodiversity in Protected Lands Due to Removal of Natural Disturbances

Noel Cawley

Lincoln Memorial University, Harrogate, TN

Many of our protected lands are being encroached upon by people, particularly by the growth of housing into areas that were once considered to be too far away from town. These locations are now thought to be desirable locations to reside in. Protected lands such as state parks, wildlife refuges, nature preserves, etc. . . that were once surrounded by natural areas now are surrounded by housing and infrastructure. Many ecosystems require periodic disturbances to maintain their integrity. Removal of these disturbances may result in the demise of an ecosystem. Management plans for these areas typically include activities to mimic natural disturbances such as prescribed burn. The challenge now is that people are so close to these protected areas that these activities may need to be restricted or altered to prevent injury to people. I will present several examples of protected lands that require disturbances and which may need to utilize different management techniques to maintain the integrity of these protected lands and prevent loss of biodiversity. Conversely, failing to maintain these protected lands can result in risks to people and property, particularly in regard to fire and flooding.

10557 - Evaluating spatial errors in Global Biodiversity Information Facility Data and its impacts on biodiversity assessments

Kayla Stan

University of Southern Mississippi, Hattiesburg, MS

The Global Biodiversity Information Facility is one of the largest open-source biology digitization and data communication platforms with over 3 billion records. These data have been used in hundreds of research papers with applications in conservation, species distribution modelling, and biodiversity monitoring. While some work has been done to assess the representativeness of species in the GBIF database and the impact that data errors may have on species distribution modelling, limited work has been done on quantifying the local and regional spatial biases in the data and their impact on potential biodiversity outcomes. Here we use the GBIF data from the southeast along with census, terrain, land cover and infrastructural data to determine which geographic variables influence the local bias of species. Additionally, we use the estimates error metrics to assess the impact including spatial error estimates have on resulting biodiversity indies. Overall, we find heavy spatial bias based on population, infrastructure and landcover, with marshes, forests, grasslands, and rural areas having fewer overall responses. These results vary across different taxonomic classes. Additionally, when geographic error is included as part of estimates in biodiversity, many counties significantly change in their assessed diversity indices both in total diversity and in evenness. Overall, our findings highlight the important aspect of addressing spatial bias and measure uncertainties when using open-source biological sighting data, even if the data is considered research grade. Solely using open-source databases like GBIF is often insufficient, particularly when considering conservation and management policies and strategies.

10562 - Biodiversity and Habitat Loss in a Lowland Caribbean Forest of Costa Rica

LaRoy Brandt

Lincoln Memorial University, Harrogate, TN

Habitat loss is widely recognized as one of the greatest threats facing biodiversity around the world. In the tropics of Latin America, biodiversity has seen an estimated 94% loss of biodiversity since 1970. Habitat losses include destruction of grasslands, forests, and wetlands to make room for large-scale farming. The Caribbean lowlands of Costa Rica are no exception where large-scale, corporate, monoculture agricultural practices continue to destroy and degrade habitats that would typically support considerable levels of

biodiversity. For example, since 2015, Costa Rica has lost ~110 Kha (~271K acres) of forest habitat; in the Caribbean lowlands natural habitats have been replaced primarily by pineapple and banana plantations. The loss of biodiversity is immeasurable. But, what happens to the remaining biodiversity and any remaining habitat. The research presented here represents over 15 years of monitoring the biodiversity at the La Suerte Biological Field Station (LBFS) in the Northeast region of Costa Rica. Although the abundance for a few species has declined, and had remained stable for other species, the abundance for a number of species has increased. Additionally, during this 15yr time period overall biodiversity has increased as we have regularly observed a number species become permanent residents at LBFS in recent years that were not residents previously. On the surface, the increase in species abundance and biodiversity at LBFS may seem to a positive outcome, however, it may represent a more negative consequence as greater amounts of habitat are lost, the existing animals may be seeking refuge in the only place of suitable habitat available.

10583 – Discussion

SYMPOSIUM: Tree-ring Science for Ecosystem Management

Thomas Saladyga, Concord University, Athens, WV and Clay Tucker, University of Southern Mississippi, Baton Rouge, LA

10584 - Introductory Remarks

10044 - Spatial Clustering of Fire Activity in Central Appalachian Pine-Oak Forests Since the Coal Boom Era

Thomas Saladyga[1], Stockton Maxwell[2]

[1]Concord University, Athens, WV, [2]Radford University, Radford, VA

Fire has played a critical role in shaping forest ecosystems across Central Appalachia, influencing species composition and landscape dynamics for millennia. Spatiotemporal variability of historical fire regimes, however, has not been examined at the regional scale. In this study, we used dendrochronological fire-scar records from 15 sites in Virginia and West Virginia to analyze fire frequency dynamics from 1800 to 2020. Data were sourced from both previously published studies and newly developed fire-scar chronologies, using samples collected from 873 fire-scarred pine trees. Our results reveal a pattern of spatial contraction and clustering of fire activity over time. Early in the record, fire occurrence was more evenly distributed across the region, but by the early 20th century, sites with higher fire frequency became increasingly clustered in the southern and western portions of the study area. This pattern intensified during the Coal Boom Era (1920s–1950s), when industrial-scale mining and associated deforestation reshaped the landscape. Across the broader region, fire frequency declined significantly during this time due to widespread fire suppression policies, development, and forest fragmentation, leading to the spatial isolation of fire activity in the West Virginia coalfields. These findings provide new insights into the historical spatial contraction and clustering of fire activity in Central Appalachia and serve as a framework for developing forest management strategies that address the uneven legacy of fire activity across the region.

10305 - Temporal and Spatial Patterns of Tree Invasion in a Shale Barren, Ouachita Mountains, Arkansas, USA

William Flatley

Department of Geography, University of Central Arkansas, Conway, AR

Ouachita shale barrens can be described as “habitat islands” within a broader matrix of pine-oak forests in the Ouachita Mountains of Arkansas. A key attribute of barrens is the absence of a woody tree canopy allowing light to reach the ground surface, supporting a suite of endemic and rare species. However, many barrens are being invaded by woody species which is shifting species composition and ecosystem structure. Therefore, we conducted a case study in a shale barren at Alum Fork State Natural Area to examine the following questions: (1) Does the timing of tree invasion align with the timing of disturbance regime changes? (2) How are fine scale edaphic conditions influencing tree invasion? We found that the majority of trees established following cessation of grazing at the site in 1970, with juniper dominating a mix of other species. Generalized linear modeling found that juniper presence (versus other tree species) was associated with reduced soil depth and that higher solar radiation intensity delayed the establishment of all species. Our results support the current model of glade and barren invasion, in which a shift in the disturbance regimes is the primary driver/input that has altered the system conditions. However, changes are mediated through the other system inputs – i.e. solar radiation and soil depth. This understanding can offer several insights to managers. First, the least dry sites are likely to be the first sites that are invaded by woody plants and converted from the glade habitat to forest. After 50 years of altered tree establishment, juniper is currently invading

the most marginal sites and degrading the last of the open habitat within the glade complex at AFNA. Our results could help inform managers in their identification, maintenance, restoration, and creation of these habitats at AFNA and other glade-woodland complexes within this landscape.

10361 - Tree-ring and sediment analyses reveal processes of bald cypress ghost forest formation from dredging in the Cape Fear River, North Carolina, USA

Monica Rother[1], Kendra Devereux[2], Andrea Hawkes[3], Philip Bresnahan[3]

[1]Department of Environmental Sciences, University of North Carolina Wilmington, Wilmington, NC, [2]University of North Carolina Wilmington, Wilmington, NC, [3]Department of Earth & Ocean Sciences, University of North Carolina Wilmington, Wilmington, NC

Forested freshwater tidal wetlands in the southeastern US are dominated by bald cypress (*Taxodium distichum*), which tolerate low levels of salinity. However, the response of old-growth bald cypress to prolonged increases in salinity remains uncertain. Bald cypress ghost forests occur along Smith Creek, a tributary of the Cape Fear River, NC which has been dredged multiple times since 1871. Atop relative sea-level rise, dredging may be accelerating saltwater intrusion and ghost forest formation. We used a paired proxy approach and sampled trees and sediments along a salinity gradient in Smith Creek. We developed tree-ring chronologies for a high salinity (8–12 ppt) and a low salinity (< 5 ppt) site. Agglutinated benthic foraminifera and thecamoebians found in sediment samples were used to examine increasing salinity over time. At the high salinity site, foraminifera began to appear at 25 cm depth in the sediment profile (indicating elevated salinity since *c.*1950). The low salinity site has yet to have foraminifera appear (no major salinity increase). We identified five growth suppression events in bald cypress at the high salinity site (1859–1860, 1877–1887, 1946–1960, 1971–1983, and 1985–2022), three of which are consistent with stress following years of dredging in the Cape Fear River (1946, 1970, and 2000). Tree stress in response to dredging was not observed at the low salinity site. The length and severity of the most recent suppression event at the high salinity site suggests that those bald cypress are experiencing permanently stressful conditions. Additionally, we found that these trees have increased sensitivity to climate variability. Bald cypress forests support diverse wetland ecosystems and provide flood protection, improved water quality, carbon storage, and pollution and sediment control. These services could be impaired or lost across the southeastern US as saltwater intrusion converts forested wetlands into ghost forests.

10165 - Presentation Withdrawn

9857 - Post Oak Response to Hydrologic Change at the Western Extent of Eastern Redcedar

Clay Tucker[1], Audrey Heichelbech[2]

[1]University of Southern Mississippi, Baton Rouge, LA, [2]University of Southern Mississippi, Hattiesburg, MS

Annual growth rings of *Quercus stellata* (i.e., post oak) can be used as a proxy for hydroclimatic changes. At the western extent of its range, it grows along uplands and rocky outcrops with well-drained soils and little herbaceous ground cover. Moisture-limited sites like these create environments in which secondary tree growth recorded in annual growth rings is sensitive enough to environmental parameters such that tree-ring width patterns can be matched to climatic factors. This research indicates that *Q. stellata* tree-ring width data from the Elk Lake Reservoir in eastern Kansas has responded to various hydroclimatic parameters (e.g., precipitation, temperature, drought indices). Additionally, long-term decline in growth rates beginning in the mid-20th century correspond with creation of the reservoir for water retention and flood mitigation at a similar time. Decline in growth through these decades has also anecdotally seen an increase in recruitment through time of *Juniperus virginiana* (i.e., eastern redcedar). These results indicate a distinct sensitivity of *Q. stellata* to its environment to the region, and results also suggest that modifications of the landscape have led to changes in tree growth and recruitment at the site.

10585 - Discussion

SYMPOSIUM: Inclusive Teaching Practices Through the HHMI IE3 Program

Kim Hays[1], Clay Runck[2], Alison Roark[3] and Tricia Brown[4], [1]Dalton State College, Dalton, GA[2]Georgia Gwinnett College, Lawrenceville, GA[3]Furman University, Greenville, SC[4]Georgia Southern University, Savannah, GA

10578 - Introductory Remarks

9831 - HHMI Inclusive Excellence at Dalton State College

Kim Hays

Dalton State College, Dalton, GA

In 2022, Dalton State College was one of 104 institutions receiving a Howard Hughes Medical Institute Inclusive Excellence 3 grant. This six-year program "challenges US colleges and universities to substantially and sustainably build capacity for student belonging, especially for those who have been historically excluded from the sciences." Dalton State College has partnered with 14 other institutions in a learning community cluster to focus on inclusive excellence in three areas: faculty development, student engagement and belonging, and curricular development. During the first two years of this process, Dalton State has focused heavily on faculty development by utilizing a world cafe symposium model which allowed all faculty the opportunity to strategically engage in the planning and development of inclusive programming in STEM departments. Additionally, faculty had the opportunity to participate in the STEM Inclusive Teaching Project, an NSF sponsored program, and associated on campus learning communities and communities of practice. In this presentation, we will discuss the highs and lows of the HHMI IE3 experience at Dalton State and share the faculty development models used at our institution.

10075 - Review and Reflections on Georgia Gwinnett College's Participation and Progress in the HHMI Inclusive Excellence 3 Project

Clay Runck, Allison D'Costa, Latanya Hammonds-Odie, Yi Ding, Omar Villanueva

Georgia Gwinnett College, Lawrenceville, GA

Ranked as the most ethnically diverse Southern regional college, faculty members at GGC are committed to employing effective and inclusive teaching practices to support the learning of such a diverse student body. However, GGC's existing faculty evaluation system lacks clear policies, guidance, and sources of evidence to help instructors effectively document their inclusive teaching practices. As part of IE3, GGC is a member of Learning Community Cluster 4 (LCC4), along with fifteen other institutions across the United States, whose challenge is "the meaningful evaluation of effective and inclusive teaching". Focusing on the School of Science and Technology (SST) as a campus model for inclusive excellence, our first success was the drafting and adoption of a shared definition of inclusive teaching. This presentation will review GGC's progress to date, as well as successes and challenges, in the three areas of focus: 1) professional development on inclusive teaching practices and self-refection of teaching; 2) surveys to gauge student sense of belonging, and faculty awareness of inclusive teaching and its value; and 3) alignment of our annual teaching evaluation with promotion policies. We will also share our experiences working with other institutions of our LCC4.

10237 - Building capacity for inclusive excellence in STEM through faculty development, student agency and engagement, and curricular change

Alison Roark

Furman University, Greenville, SC

In 2022, the Howard Hughes Medical Institute awarded an Inclusive Excellence 3 (IE3) grant to a Learning Community Cluster (LCC1) comprising Furman and 14 other institutions. Collectively, these 15 institutions range geographically from California to Puerto Rico and run the gamut from small and private to large and public. Despite vast differences in institutional type, geopolitical context, and demographic composition, the members of LCC1 all recognize the need to build institutional capacity for inclusive excellence in STEM on their campuses and are committed to doing so by focusing on faculty development, student agency and engagement, and curricular change. At Furman, IE3 funds are being used to support the following initiatives: an inclusive pedagogy learning community called the STEM Equity Fellows Program, a near-peer learning assistance framework called the STEM Consultants Program, a STEM DEI Curriculum Mapping Program, a Faculty STEM Ambassadors Program and a Student STEM Ambassadors Program, inclusivity reading circles, student surveys, longitudinal interviews of students in STEM courses, and analysis of institutional data. These initiatives have been developed and facilitated by a diverse and highly collaborative institutional leadership team characterized by both individual autonomy and shared decision-making and responsibility. The work of the team has also benefitted from the sharing of ideas and resources among LCC1 institutions. Preliminary findings from these initiatives support the use of data-informed decision-making and suggest that change is possible (but slow), that distributed leadership is both effective and sustainable, and that collaboration and consistent communication are key components of institutional change.

10104 - An Inclusive Teacher Training Program for Peer-Teachers

Sara Gremillion[1], Tricia Brown[1], Karelle Aiken[2], Regina McCurdy[2]

[1]Georgia Southern University, Savannah, GA, [2]Georgia Southern University, Statesboro, GA

A peer-teacher is any student who teaches other students in a formal or informal setting. The advantages of peer-teachers in the health professions have been well documented, specifically showing benefits to the peer-teachers in terms of subject matter knowledge and communication skills and benefits to the students through social congruence with their teacher. Studies investigating the impact of the training itself document improvements in understanding and confidence. We have developed a peer-teacher training for instructors in the Georgia Southern (GS) University College of Science and Mathematics (COSM) with the goal to improve COSM's peer-teachers' knowledge of and motivation to use inclusive teaching strategies.

During the training, participants define inclusive teaching, are exposed to demographic data from the institution, and learn about key principles and categories of inclusive excellence in teaching and language. The training concludes with a discussion on bias and stereotypes. Each portion of the training is sourced from validated literature from university teaching and learning centers or other national institutions.

Peer-teachers were assessed with pre- and post-surveys and with a follow-up survey. The surveys included Likert scale questions in the categories of knowledge of inclusive teaching, motivation to use inclusive teaching, and likelihood of asking for support. There is also an open-ended question to gather inclusive teaching techniques used by the time of the follow-up survey. Results show an increase in all areas immediately after the training, with some decline in the follow-up survey. The impacts to GS's training due to the involvement with the Learning Community Cluster associated with the grant and the ripple effects to other institutions are explored.

This work is sponsored by a Howard Hughes Medical Institute Inclusive Excellence 3 Learning Community (IE3 LC) Grant, GT15193 & GT16021.

10579 - Discussion

SYMPOSIUM: Old Growth Communities in the Southeastern US: What have we learned and how do we find them?

Margaret Woodbridge[1], Neil Pederson[2] and Christine Martens[3], [1]USDA Forest Service Southern Research Station[2]Harvard University[3]Southern Research Station, Asheville, NC

10048 - The Struggle to Define Old Growth

Christine Martens

Southern Research Station, Asheville, NC

Everyone has a picture in their minds when asked to imagine an old-growth forest. We often envision towering, large trees and huge downed logs and primeval ferns. However, old growth can look very different depending on where you are on the landscape. Old growth looks drastically different depending on community type, adaptations to different disturbance regimes, and variable structure. Coming up with a definition for old growth has been a struggle for decades, and there is still no single widely accepted definition. If you start looking, you may find dozens of different definitions by different organizations and agencies. So why is it so difficult? To evaluate that question, consider all the things that could possibly have happened to an ecosystem over time. Many of us have learned that old growth forests are "climax communities," when a system has reached a steady state in terms of its growth, but that view glosses over the role of disturbances in an ecosystem. Every ecosystem is subject to disturbances of some kind or another, whether that's fire, hurricanes, wind events, or anthropogenic fire regimes. This talk will address some of the complex questions surrounding defining old-growth forests, including: How do disturbances play a role in defining old-growth forests? Should we look more at how the ecosystem functions than at the age of the trees? Humans have left their mark on every corner of the globe, through invasive species, fire, logging, and climate change. What baring does this have on our definitions of old growth? If a forest has been logged, when will the forest that grows back be considered old growth? This talk will provide opportunities to think critically about the questions, many of which are unanswered, while outlining the nature of the struggle to define old growth.

10432 - Classifying, inventorying, and mapping mature and old-growth forests in the United States

Kevin Barnett

Silvx Labs, Duluth, MN

Conservation of old-growth forests in the U.S. has been an issue of management concern since at least the 1970s when discovery of their habitat value coincided with realization of their imminent disappearance. However, no national inventory of the old-growth forest estate has precluded our understanding of their distribution, abundance, and vulnerabilities. We proposed a functional definition of mature and old growth based on rates and patterns of forest carbon accumulation over time using national forest inventory data. Sample design-based estimates of the mature and old-growth forest estate revealed significant variation among forest types-groups throughout the United States. Here, we discuss the strengths and limitations of our modeling approach as compared to complementary classifications that use forest structure to characterize old growth. We posit that continued improvements to modeling the dynamic process of forest development and integration with structural definitions of old growth will be needed to ensure targets for old-growth forest retention and recruitment are achieved.

10285 - Vertical Grasslands at the Gap: Exploring Old-Growth Cliffside Grasslands at Cumberland Gap National Historical Park, Lee County, Virginia

Alaina Krakowiak[1], Laura M Boggess[2]

[1]Southeastern Grasslands Institute, Roanoke, VA, [2]Mars Hill University, Mars Hill, NC

In the Southeastern United States, grasslands are often not recognized as having the potential to represent old-growth plant communities. Areas of grassland vegetation found on cliffs, or "vertical grasslands," are particularly under-recognized and under-surveyed. We surveyed a calcareous cliff line at Cumberland Gap National Historical Park in Lee County, Virginia via rappel to search for rare species and diverse plant communities indicative of old-growth grassland habitat. We documented at least 10 state-rare plant species (ranked S1 to S3), including *Houstonia canadensis*, *Liatris aspera*, *Myriopteris alabamensis*, *Sisyrinchium albidum*, and *Solidago rigida* var. *rigida*, along with numerous other conservative grassland species. Additionally, core samples taken from cliffside eastern red cedars (Juniperus virginiana) displaying old-growth characteristics such as bark-stripping and strongly tapered stems revealed individual ages of 250 years or more. However, despite the inaccessibility of these vertical grasslands, we observed severe habitat degradation in some areas. Through this research, we demonstrate that cliffs can serve as refugia for grassland vegetation in areas where the majority of grasslands have otherwise been lost, but that these remote vertical grasslands are not immune to degradation, and warrant further inventory and conservation efforts.

10408 - Knee-deep in the Ecology of Old-Growth Bottomland Hardwood Forests

Loretta Battaglia

Texas A & M University Corpus Christi, Corpus Christi, TX

Bottomland hardwood forests occupy river floodplains throughout the southeastern US. Coverage of these forests on the modern landscape is greatly diminished relative to their historical distribution due to timber extraction, hydrologic alterations, conversion to agriculture and urban expansion. Old-growth examples are particularly rare. The focus of this presentation is the Congaree Swamp National Park in South Carolina, which contains the largest area of old-growth bottomland forest today. The objective of this study is to explore key (deep) ecological concepts of old-growth, through the lens of this grand forest ecosystem. Long-term vegetation monitoring plots established in 1989, following Hurricane Hugo, provide the basis for conventional ecological analyses. This disturbance toppled and snapped trees and left the “cathedral-like” forest full of canopy gaps and piles of woody debris. Some areas, however, remained intact with little sign of disturbance. While the forest was heavily disturbed in places, the condition of old-growth remains. Hugo is one of many tropical storms that continue to impact this area - they are part of the fabric of the forest. Community composition shifted slightly with reorganization, but recovery was rapid and within ~10 years, canopies had reformed. Fast growth rates in this forest mean that big trees are not always old ones. Unexpected insights into features that create wonder when a forest is shaped and connected through time by natural forces were made possible through closely bearing witness to the process of disassembly and reassembly. Deep connections exist with humans too, manifested as superstition, awe, fear, memories, and personal spirituality. At all levels, links are continually forged between the ancient and the new.

10143 - Techniques for Identifying Old-Growth Forest in the Southern Blue Ridge Mountains

Josh Kelly

MountainTrue, Asheville, NC

The Southern Blue Ridge Mountains have experienced industrial logging since the mid-1800s. However, rugged topography, conservation efforts, and stochastic events have preserved diverse examples of temperate old-growth forests there. Despite having globally significant quantities of old-growth forest, the extent and location of old growth in the region was poorly known prior to survey efforts by government agencies, NGOs, and citizen scientists. Since the early 1990's, almost 300,000 acres of old-growth forest have been documented in the region using multiple lines of evidence. This talk will provide examples of how techniques such as dendrochronology, historical documents, US Forest Service records, geographic inference, and geospatial technology such as LiDAR have been used to identify and map the remnant old-growth forests of the Southern Blue Ridge.

10330 - Identifying Old Growth Forests in the Southern Blue Ridge Mountains

Robert Messick

independent researcher, Union Mills, NC

A decades long process of gathering old growth candidate sites on national forest and other ownerships in the southern Blue Ridge region (SBRR), verifying or rejecting them with a classification system, and cataloging candidate and visited sites separately culminated in a report and a book chapter that was published in 'Imperiled: The Encyclopedia of Conservation' in the summer of 2022. Candidate sites were generated by seeking and interviewing hikers, birders, nearby residents, hunters, and scientists including the NC Natural Heritage Program. A range of topographic features, based on years of field experience, were also used to generate candidate sites. Initial examinations and verifications followed the A and B classification system used by the Great Smoky Mountains NP Old Growth Team and Paul Carlson related to field work in the Chattooga River Basin (1995).

The cumulative result from 20 major contributors and numerous volunteers in the SBRR in 2020 was 110,275 ha (55% in the GSMNP and 45% in five national forests and other ownerships). This could place the SBRR third behind Minnesota and the Adirondacks in northern New York in terms of cumulative old growth acreage by region in the eastern US. The GSMNP has the largest old growth polygon in the SBRR, and three of the largest sites on national forests were ≥ 2023.4 ha. The Nantahala Mountains and the Black Mountains had the largest concentrations of old growth outside the park.

The old growth catalog of 2020 was paired with ArcGIS. 649 delineated sites and 191 visited-not-delineated sites were mapped and listed, and 732 candidate sites worthy of a site visit were cataloged. Additional field work has been done in the SBRR since the 2020 catalog including the Chattahoochee Headwaters, Big Fork Ridge in Pisgah NF, the Montreat easement, and numerous sites in the Balsam Mountains.

10089 - Landscape patterns in southern Appalachian forests: How do mature and old growth forests differ, and what does that mean?

Margaret Woodbridge[1], Martin Dovciak[2], Jason Fridley[3], Julia Burton[4]

[1]USDA Forest Service, Asheville, NC, [2]State University of New York College of Environmental Science and Forestry, Syracuse, NY, [3]Clemson University, Clemson, SC, [4]Michigan Technological University, Houghton, MI

Interest and efforts to conserve and steward old-growth forest conditions have come to the forefront in recent years. However, information is lacking on the characteristics that define old growth (OG), obscuring our understanding and ability to identify these important resources. This lack of information on OG characteristics is confounded in areas where forests are highly variable, such as those found across the topographically and environmentally diverse southeastern US, in addition to the scarcity of forests that escaped logging. In short, it is unclear how old growth forests differ from mature forests, which dominate our current forested landscape. Understanding these differences is required for effective management for old growth conditions in our aging forests-and evaluation of the efficacy of those management practices.

We evaluated the differences between mature (clear-cut before 1934) and old-growth forests using land-use history data from Great Smoky Mountains National Park, which maintains some of the largest tracts of old growth forest in the eastern US. Using a vegetation dataset compiled from multiple studies, we addressed questions about differences across multiple forest communities and strata (tree, shrub, and herbaceous layer). We found that old growth forests exhibited greater local (plot-level) richness compared to mature forests, but this difference varied by landscape position and strata. We found that lower richness in mature forests was most pronounced in the ground-layer in topographically sheltered locations receiving low solar radiation. We also found compositional differences between

mature and old growth were most pronounced in high elevations and lower-elevation mesic forests, but not in lower-elevation xeric forests. Our results suggest that managers looking to conserve or restore old growth characteristics at the landscape scale focus on 1. particular landscape positions: high elevations (e.g., spruce-fir) and lower-elevation mesic (e.g., cove) forests and 2. increasing herbaceous layer and shrub richness, but not necessarily tree richness.

10589 - Lunch

9994 - The thorniness of identifying old-growth forests: perspectives from a field-based approach

Neil Pederson

Harvard Forest, Harvard University, Petersham, MA

Conservation requires the identification of species and the state or trajectory of ecosystems. Identifying old-growth forests is one of the great challenges in conservation. Part of this is due to the many human constructs of what old-growth forest should look like – definitions. To be up front, my definition is simple: forests heavily cut within the last 200 years are not yet old-growth. Visual identification of old-growth forests might be harder in the Southeastern US than in other regions given that recovery from any kind of disturbance is relatively quick under warm and near temperate rainforest conditions, especially if one uses big trees as a key characteristic. Also, if one uses the amount of deadwood as a second, classic characteristic, this can be difficult as under such climatic conditions downed wood can decay relatively quickly. Broadly speaking, faster ecological processes can obscure classic old-growth characteristics in second-growth forests and make one doubtful of the forest's history. Lastly, old-growth forests can sometimes be unsteady and quite heterogenous over space. All these ecological realities make the visual identification of old-growth forests difficult. We have found it easier to identifying old-growth forests by looking at some non-traditional characteristics that are of a present/absent variety. Identification can be a bit easier by obtaining the life-history and ages of trees from their growth rings. And still, identification might be harder moving into the future: Time and the impact of exotic pests and pathogens is blurring stand structures. With a cup half full, the difficulty in identification is a good thing as it indicates we might be allowing more landscapes to return to old forest conditions. Opening the door for new old-growth ecosystems and accepting that old-growth forests are a process not a destination is an important first step to a better conservation of the world.

10018 - LiDAR and the quest for Old-Growth Forests: Promises and Shortcomings

Erik Danielson[1], Neil Pederson[1], David Orwig[1], Benjamin Poulter[2], Ralph Dubayah[3], Jamis Bruening[3], Amanda Armstrong[4]

[1]Harvard Forest, Harvard University, Petersham, MA, [2]NASA, Washington DC, DC, [3]Department of Geographical Sciences, University of Maryland, College Park, MD, [4]NASA Goddard Space Flight Center, Biospheric Sciences Laboratory, Greenbelt, VA

The last decade has seen intensifying interest in identifying and inventorying old-growth forests for the sake of management and conservation. Most agencies and NGOs hope to do the most they can with limited staff and funding while often confronting complex and rugged terrain, making remote sensing technologies appealing for predicting potential old-growth occurrences. But does mapping structural expectations from "classic" old-growth sites onto available LiDAR products succeed in detecting the stands that have escaped notice in the past? And do our expectations about what distinguishes old-growth from mature second-growth match what can be observed in the field in 2025? Outside of large-scale modeling, can finer-scale inspection of LiDAR products enhance fieldwork and save time and energy for researchers on the ground? Over the past several years we have applied widely available aerial and satellite LiDAR data in seeking out the oldest trees and the tallest trees- which rarely coincide- and have learned a lot along the way about what LiDAR can reveal, as well as its important blind spots. Improvements in technology will hopefully improve large-scale modeling outcomes in the future, but we hope that some of the information from this discussion can help you use LiDAR to improve your field approaches today.

10081 - Integrating forest inventory, remote sensing, and ecosystem modeling for old-growth mapping

Jamis Bruening[1], Paul May[2], Neil Pederson[3], Erik Danielson[3], Amanda Armstrong[4], Ralph Dubayah[1]

[1]Department of Geographical Sciences, University of Maryland, College Park, MD, [2]Department of Mathematics, South Dakota School of Mines & Technology, Rapid City, SD, [3]Harvard Forest, Harvard University, Petersham, MA, [4]NASA Goddard Space Flight Center, Biospheric Sciences Laboratory, Greenbelt, VA

Old-growth forests are characterized by old trees, unique characteristics, and immense ecological and cultural value. Their significance inspired a recent, government-sponsored US old-growth survey using the national forest inventory (NFI) system. While this effort produced important information about old-growth forest abundance in the US, the dependence on NFI plots precluded old-growth identification and mapping at fine-scale spatial resolutions necessary for decision making, and limited practical applications for management and conservation. In this talk, we explore possibilities for old-growth mapping at spatial resolutions necessary to support

specific management and conservation actions at regional to national scales, and discuss associated advantages and limitations to such an endeavor. As an example, we present a Bayesian mapping framework for the US that translated the national NFI-based old-growth definitions to a remote sensing context, leveraging forest information gathered by optical, lidar, and radar satellite remote sensing missions. The framework produced old-growth probability maps at 1 ha resolution, and area-level estimates of old-growth proportion and uncertainty at multiple spatial scales. We also show how this framework can be coupled with a ecosystem model to explore temporal dynamics within old-growth forests. Our findings advance efforts to merge ground and space data with ecosystem models for old-growth mapping across large spatial extents, and we discuss how this methodology could be improved or adapted for more localized and nuanced old-growth mapping at smaller scales.

10435 - Simulating Mature and Old Growth Forest with Associated Lidar Waveforms in four CONUS Study Sites

Amanda Armstrong[1,2], Jamis Bruening[3], Neil Pederson[4], Ralph Dubayah[3], Benjamin Poulter[5]

[1]NASA Goddard Space Flight Center, Biospheric Sciences Laboratory, Greenbelt, VA, [2]Earth System Science Interdisciplinary Center, College Park, MD, [3]Department of Geographical Sciences, University of Maryland, College Park, MD, [4]Harvard Forest, Harvard University, Petersham, MA, [5]NASA, Washington DC, DC

In support of the current US national monitoring efforts to map and conserve Mature and Old-Growth (MOG) forests (U.S. Executive Order 14072), our research effort seeks to understand the structural, functional and compositional characteristics that define MOG forests in the continental US. We parameterized the spatially-explicit individual-based gap model SIBBORK for four pilot National Forest study sites using species-specific light and environmental tolerances, and regionally derived USDA-USFS Forest Inventory and Analysis (FIA) allometric, biovolume, specific height and leaf area equations. Stem map simulation output from each site was then used to generate simulated lidar waveforms from modeled forest data. We compared our simulated waveform heights to a GEDI MOG probability map, as well as to a MODIS-NDVI derived function type classification. Our results improve our understanding of the structural, compositional and functional character and variability of mature and old growth forests.

10587 - Panel Discussion

SYMPOSIUM: QuillCon III: Systematics, Evolution, and Conservation of Isoetes

Peter Schafran[1], Jay Bolin[2], Richard A. Matthews[3] and Lytton Musselman[4], [1]Boyce Thompson Institute, Ithaca, NY[2]Catawba College, Salisbury, NC[3]Abraham Baldwin Agricultural College[4]Old Dominion University, Norfolk, VA

10580 - Introductory Remarks

10484 - Theory and implementation of species concepts in *Isoetes*

Peter Schafran

Boyce Thompson Institute, Ithaca, NY

The classification of life into representative groups is a foundational part of biology. While most modern taxonomic levels are considered to be subjective, for many practitioners the species holds a unique position as a natural group, existing irrespective of human classification. The variation inherent in the natural world has led to continued disagreement both about the boundaries of species and how individuals fit within species. The advent of systematics and phylogenetics brought taxonomy into an evolutionary framework, leading to a unified species concept that recognizes the only necessary condition of species as being part of an independently evolving lineage. However, phylogenomic studies have highlighted the commonness of reticulate evolution that complicates interpretation under a tree-like model of evolution.

The genus *Isoetes* (quillworts) has been a difficult group to classify. In eastern North America, extreme lumping and splitting occurred in the 19th and 20th centuries. The paucity of morphological features and widespread hybridization and allopolyploidy have made delimitation of species difficult. Here I review the species concepts traditionally applied to quillworts, developments in molecular phylogenetics, and new difficulties arising from population genetics and phylogenomic evidence for hybridization and introgression. I argue that many species as currently circumscribed are data deficient, with studies needed to test the evolutionary independence of

separate lineages and how this correlates with morphological and phylogenetic variation. I explore how reproductive genomics in *Isoetes* can illuminate processes responsible for reproductive boundaries. Finally, I discuss whether one species concept can serve the purposes of both evolutionary biologists and conservation biologists.

10485 - Paired morphologic and genetic studies of *Isoetes piedmontana* diversity in Georgia, U.S.A.

Gemma C. Milly[1], Peter Schafran[2]

[1]Milly Botany, Athens, GA, [2]Boyce Thompson Institute, Ithaca, NY

The seasonal wetlands of the Georgia Piedmont's granitic outcrops are home to two federally endangered rare quillworts—Isoetes melanospora Engelm. and I. tegetiformans Rury—as well as the more common I. piedmontana (N. Pfeiff.) C.F. Reed. Known to be genetically polyphyletic, I. piedmontana has long been recognized as the problematic dumping ground for any granite outcrop plants which lack the characteristic dark megaspores of I. melanospora and I. tegetiformans. In the footsteps of Heafner and Bray, our analysis continues examination of I. piedmontana diversity. In 2023 and 2024, Milly made dozens of I. piedmontana collections from populations across its Georgia distribution. Her morphological studies have examined corm shape, sexual arrangement, tissue colorations, and other conventional and unconventional characters. Schafran evaluated matched genetic samples from each collection and generated a phylogeny using the LFY intron. The unique linking of herbarium vouchers and morphological data matched with genetic sequences allows us to probe I. piedmontana from a coordinated perspective. Our results are finding additional complexity within I. piedmontana. Sequencing found a new genetic clade of I. piedmontana, dissimilar to previously published sequences. Morphological studies found a consistent assortment of differences between a population in western Georgia and other populations from the central and eastern regions. As we finish morphologic and genetic analysis for the remaining samples, we will work to determine if evidence from both perspectives supports taxonomic distinctions.

10166 - Thinking Outside the Box - Homoploid Hybridization and Animal Dispersal in *Isoetes lithophila*

Lisa George[1], Sylvia Kinosian[2], Peter Schafran[3], Jacob Suissa[4], Alejandra Vasco[1]

[1]Botanical Research Institute of Texas, Fort Worth, TX, [2]University of Arizona, Tuscon, AZ, [3]Boyce Thompson Institute, Ithaca, NY, [4]The University of Tennessee, Knoxville, TN

Recent state-listing of the Texas endemic rock quillwort (Isoetes lithophila) has spurred research into its taxonomic delineation, population dynamics, and ecological interactions. Specimens traditionally referred to as Isoetes lithophila include plants of two morphologically similar taxa and their hybrids. These diploid hybrids inhabit microhabitats that are distinctive from their parents and may represent a novel evolutionary direction if fertile and persistent in the environment. Analysis of Isoetes lithophila RADseq data indicates substantial gene flow among plants in different rock pools and discrete rock outcrops within a limited geographical area. At distances greater than 10 miles, there is substantial genetic differentiation between Isoetes lithophila populations and concomitant morphological and phenological variation. This pattern of genetic substructure is consistent with observations of potential mammalian dispersal agents identified in camera trap data. These unexpected findings should help expand our expectations of quillwort biology and better conserve this and other quillwort species.

10366 - Untangling the web: Using HybSeq to resolve the *Isoetes* phylogeny

David Wickell[1], Jacob Suissa[2], Peter Schafran[3]

[1]University of Connecticut, Storrs, CT, [2]The University of Tennessee, Knoxville, TN, [3]Boyce Thompson Institute, Ithaca, NY

Isoetes (quillworts) is a diverse, widespread, and ecologically significant lineage of plants. However, their phylogenetic relationships remain poorly resolved due to limited sampling, reduced morphology, and propensity for hybridization. While low-copy genes and chloroplast sequences have been useful in other plant lineages, they often fail to capture the complex evolutionary histories of *Isoetes*, particularly in groups with rapid radiations or reticulate relationships. To address these challenges, we employed hybridization-based sequencing (HybSeq) using the GoFlag probe set to target hundreds of nuclear loci across 114 individuals comprising at least 92 species. This approach provided phylogenetic signal at multiple evolutionary scales while allowing us to identify taxa of likely hybrid origin and phase alleles to resolve previously intractable relationships within *Isoetes*. Our results reveal new insights into the diversification of quillworts and highlights the utility of HybSeq for clarifying patterns of hybridization and speciation in phylogenetically challenging lineages.

10414 - Seeing the forest through its phylogenetic trees: uncovering the Carboniferous origins of *Isoetes* using phylogenetics and the fossil record

Megan Nibbelink, Mark Holder

University of Kansas, Lawrence, KS

The humble outward appearance of members of the genus *Isoetes* masks a fascinating evolutionary history from those with an untrained eye. Evidenced by a number of enigmatic anatomical and morphological features unseen in the euphyllophytes which primarily compose our modern landscape, *Isoetes* is the only modern representative of a lineage that once dominated the earth's surface with diverse forests of tall trees during the Carboniferous (~350 MYA). Tragically these 'scale trees' fell victim to a series of climate change events which punctuated the Isoetales' photosynthetic empire, and by the Triassic (~250 MYA) isoetalean lycopods exhibit markedly reduced body size and diversity. This transition in *Isoetes'* natural history is difficult to understand as the same climate events which influenced a dramatic shift in the ecology and morphology of these plants also suppressed rates of fossilization, and high-quality fossils which may enlighten our understanding of this transition are unlikely to be found.

We analyzed a a previously published matrix of Carboniferous isoetalean taxa (Bateman, DiMichele, Phillips 1992), amended slightly in character coding and with the addition of Mesozoic (~ 250 – 150 MYA) isoetalean representatives (i.e. *Annalepis*, *Pleuromeia*) utilizing RevBayes. We employed Bayesian phylogenetic inference and phylogenetic comparative methods to circumstantially inform our understanding of this pivotal gap in isoetalean evolutionary history and explore the possibilities of modern *Isoetes*' ancestry where the fossil record is unlikely to provide answers.

9696 - CAM-photosynthesis in aquatic lycophytes is an adaptation to low CO2 levels

Jacob Suissa

The University of Tennessee, Knoxville, TN

Crassulacean acid metabolism (CAM) is an adaptation to increase water use efficiency in dry environments. Similar biochemical patterns occur in the aquatic lycophyte genus *Isoëtes*. It has long been assumed and accepted that CAM in these aquatic plants is an adaptation to low daytime carbon levels in aquatic ecosystems, but this has never been directly tested.To test this hypothesis, populations of *Isoëtes engelmannii* and *I. tuckermanii* were grown in climate-controlled chambers and starved of atmospheric CO_2 during the day while pH was measured for 24 h. We demonstrate that terrestrial plants exposed to low atmospheric CO_2 display diel acidity cycles similar to those in both xerophytic CAM plants and submerged *Isoëtes*. Daytime CO_2 starvation induces CAM in terrestrial *Isoëtes*, substantiating the hypothesis that carbon starvation is a selective pressure for this physiological behaviour.

10457 - Advancing *Isoetes* Conservation Through Ex Situ Collections and Germination Research in the Southeast

Emily Coffey, John Evans, Laurie Blackmore

Southeastern Center for Conservation at Atlanta Botanical Garden, Atlanta, GA

The Southeastern Center for Conservation (SECC) at the Atlanta Botanical Garden is advancing the conservation of *Isoetes* species in Georgia and Tennessee, addressing critical knowledge gaps for these unique and often imperiled lycophytes. By integrating ex situ collections, tissue sampling, and spore germination trials, the SECC is developing comprehensive strategies to safeguard *Isoetes* diversity and support habitat restoration efforts.

Ex situ collections form the foundation of this work, ensuring the long-term preservation of genetic diversity while enabling research into propagation and germination methods. Tissue collections are carefully curated to facilitate genetic studies, which are essential for understanding population dynamics and informing in situ conservation strategies. Additionally, spore germination trials are conducted to optimize propagation protocols and explore the factors influencing spore viability and establishment.

Collaborating with regional and national partners, the SECC's *Isoetes* program exemplifies the integration of research, conservation, and restoration. These efforts are critical for protecting fragile habitats and securing a future for rare and endemic *Isoetes* species in the Southeastern United States.

10581 - Discussion

ASB Workshops

WORKSHOP: Honey, I Blew-Up the Molecules: Using 3D-Printing and Virtual Technologies as a Multi-faceted and Multi-disciplinary Pedagogical Practice

Carmony Hartwig, Andrew Jacobson and Zach Trivett, Catawba College, Salisbury, NC

WORKSHOP: After Graduation: Delving into Post-Baccalaureate Options and Graduate School Applications

Jeremy Rentsch, Francis Marion University, Florence, SC and Shoshana Katzman, Agnes Scott College, Decatur, GA

WORKSHOP: Eavesdropping of Ecosystems: Using Acoustic Data in Biology

Dr. John Quinn, Furman University, Greenville, SC

ASB Presentations

9593 - Microbial Communities in Standing Dead Trees in Ghost Forests are Largely Aerobic, Saprophytic, and Methanotrophic

Mary Jane Carmichael[1], Melinda Martinez[2], Suzanna Bräuer[3], Marcelo Ardón[4]

[1]Hollins University, Roanoke, VA, [2]USGS Eastern Ecological Science Center, Laurel, MD, [3]Appalachian State University, Boone, NC, [4]North Carolina State University, Raleigh, NC

Standing dead trees (snags) are recognized for their influence on methane (CH_4) cycling in coastal wetlands, yet the biogeochemical processes that control the magnitude and direction of fluxes across the snag-atmosphere interface are not fully elucidated. We analyzed microbial communities and fluxes at one height from ten snags in a ghost forest wetland. Snag-atmosphere CH_4 fluxes were highly variable (−0.11–0.51 mg CH_4 m^{-2} h^{-1}). CH_4 production was measured in three out of ten snags; whereas, CH_4 consumption was measured in two out of ten snags. Potential CH_4 production and oxidation in one core from each snag was assayed in vitro. A single core produced CH_4 under anoxic and oxic conditions, at measured rates of 0.7 and 0.6 ng CH_4 g^{-1} h^{-1}, respectively. Four cores oxidized CH_4 under oxic conditions, with an average rate of −1.13 ± 0.31 ng CH_4 g^{-1} h^{-1}. Illumina sequencing of the V3/V4 region of the 16S rRNA gene sequence revealed diverse microbial communities and indicated oxidative decomposition of deadwood. Methanogens were present in 20% of the snags, with a mean relative abundance of < 0.0001%. Methanotrophs were identified in all snags, with a mean relative abundance of 2% and represented the sole CH_4-cycling communities in 80% of the snags. These data indicate potential for microbial attenuation of CH_4 emissions across the snag-atmosphere interface in ghost forests. A better understanding of the environmental drivers of snag-associated microbial communities is necessary to forecast the response of CH_4 cycling in coastal ghost forest wetlands to a shifting coastal landscape.

9598 - Nesting Behavior and Habitat Selection of the Wood Thrush

Amelia Browning[1], Alexandra Price[1], John Lewis[1], Laura Cook[2]

[1]Lipscomb University, Nashville, TN, [2]Warner Park Nature Center, Nashville, TN

Wood Thrushes (*Hylocichla mustelina)* are a species of concern in Tennessee due to many factors. Historically, their nests have been found in low-hanging branches at the edge of dense forest (Evans et al. 2020). In 2021, a Wood Thrush nest was found in Warner Parks, a 3100-acre urban park sixteen kilometers south of Nashville, nesting eighteen meters off the ground and thirty meters from an active trail. We wanted to learn if this unusual nest height was a common occurrence in an active area of Warner Parks or an anomaly. We decided to compare nesting behavior and habitats at Warner parks with Timberland Park, a low-traffic 72-acre park in Williamson County, Tennessee. From May through July of 2024, we searched Timberland Park and each park within Warner Parks for Wood Thrush nests using binoculars and listening for vocalizations. We located eight nests between Warner and Timberland Parks. The nest heights in Warner Parks ranged between 11.8 to 18.3 meters above the ground with an outlier of 1.5 meters. Nest heights of Timberland ranged between 2.1 to 11.8 meters above the ground. Preliminary evidence suggests nest height may be affected by human presence in urban parks.

9599 - Beyond the classroom: Immersive learning through herbarium collections

Pamela Puppo

Marshall University, Huntington, WV

Herbaria, collections of dried plant specimens and their associated collection data, are invaluable resources for a variety of disciplines including taxonomy, systematics, ecology, biodiversity and conservation, among others. Herbarium specimens are also frequently used for teaching, providing material for classes such as Plant Taxonomy, Botany, and Ecology. In this talk, I will share ideas and experiences on courses developed around herbarium collections and how these classes constitute invaluable learning experiences for students outside the classroom. The Marshall University Herbarium (MUHW) in Huntington, West Virginia, is the second largest herbarium in the state with ca. 52,000 specimens. Our collection is mostly composed of vascular plants, but includes smaller collections of bryophytes, fungi, algae, plant fossils, and a small ethnobotanical collection and library. In Spring 2024, I developed a new class, Special Topics: Herbarium Curation where students learned how to curate and process plant specimens, including uploading information of the specimens they processed in our online database. At Marshall, undergraduate and graduate students can also do independent projects at the Herbarium for credit as part of our Independent Study class, and undergraduates can do an internship for their senior Capstone class. Working in the herbarium, students learn valuable transferable skills such as managing collections,

processing museum specimens, best practices on archives, working with online databases, etc. At the same time, students are significantly contributing to the visibility of our collection and making it more accessible to the broader scientific community and the general public through our online database. This presentation will detail the courses' structures, assignments, and individual projects students have developed using our plant collection.

9606 - Introducing a New Class of Ecosystems Literacy Tools to Protect Global Biodiversity Hotspots

Robby Thigpen

Marine Conservation without Borders, Florence, SC

When resource managers and marine scientists come to Creole and Indigenous fishing communities, oftentimes they arrive as outsiders. They speak a different language and use terms for which there are no apparent proxies within these linguistic communities. Frequently they ignore local ecological knowledge systems that have sustained these communities for millennia. This common scenario can lead to misunderstandings and numerous unintended consequences. Recently it has become popular for biologists to talk about using Indigenous ecological knowledge to better protect biodiversity.

My research with Caribbean Indigenous and Creole fishing communities began in 2005 through my internship with the Northern Fisherman Cooperative of Belize to fulfill my degree requirements for Appalachian State University. I have developed methods to seamlessly combine local ecological knowledge systems with Western science to create pan-Caribbean biocultural curricula where these fishers can readily identify their ecological knowledge and see it treated as equal to Western science. Furthermore, these curricula are indistinguishable from modern biology curricula to biologists and educators. My first pan-Caribbean biocultural prototype on mangrove ecosystems has been ethnotranslated into 10 seafaring languages of the greater Caribbean Basin. Additionally, I have begun working with inland communities because everyone deserves a science education in their mother tongue.

Our organization has an ongoing project in Quintana Roo using multiple chapter and grade ecology curricula written in Maya in Indigenous primary schools and active bilingual pilot projects in Bonaire, Curaçao [Papiamentu/Dutch]. Additionally, we are applying these methods to create our first university level content on *Lobatus gigas* and *Primate'ob tu Lu'umil México*.

Imagine the long-term effect on conservation efforts if we were using this STEM Plus Curriculum in every school in every biodiversity hotspot around the globe including locations such as Appalachia, Winyah Bay or anywhere in the low country of the Carolinas.

9610 - Distribution, Diversity, and Gene Flow of Crayfish Species Across the Eastern Continental Divide

Dylan Wolfe

Georgia Gwinnett College, Lawrenceville, GA

In the Appalachian region of the United States, Georgia is one of the hotspots for biodiversity. Based on ongoing research, gene flow across the eastern continental divide (ECD) using headwater stream fishes suggests a barrier to gene flow for some species. We have expanded this research to crayfish species in Georgia using the ECD and sampling opposing watersheds along this divide. Crayfish were collected using minnow traps, identified morphologically, and tissue sampled for molecular analysis. Hypotheses regarding the distribution and diversity of crayfish species were tested without prior assumptions since distribution and diversity data are limited for the proposed sample area. Our results suggest that the ECD does not act as a barrier to gene flow for crayfish as it does for some freshwater fishes. The preliminary data also suggests possible range expansion for one crayfish species and a potential invasive species in one of the sampled streams. We will discuss issues related to genetic versus morphological definitions and clarity, or lack of, in species designations. Geographical data is further examined along the ECD to question if certain species are ecologically competitive or if in certain watersheds species can coexist.

9612 - Chemical Mate Choice Copying in *D. melanogaster*

Philip Kohlmeier[1], Bloo Mitchell[1], Alexandria Abbott[2], Elmira Umarova[1], Ashanti Brown[2], Lacy Skinner[3]

[1]University of Memphis, MEMPHIS, TN, [2]University of Memphis, Memphis, TN, [3]Christian Brothers University, Memphis, TN

Mate choice is a critical decision, requiring time and energy to assess potential partners' genetic quality. Consequently, in many species females have evolved the ability to utilize social information by copying the mate choices of others, usually based on visual cues. However, chemical cues offer advantages, such as not requiring active observation of copulations. Using Drosophila melanogaster, we provide the first demonstration of chemical mate choice copying. Student females selected the same male genotype that a teacher female mated at higher frequently than expected by chance. Chemical mate choice copying requires sensing both male and female cues, which might indicate that that male genotype has been chosen by other females. Our work suggests that females, in the presence

of mated females, increase choosiness at the virgin stage, elevating sexual selection on male traits. This study provides novel evidence that exploiting social information is more prevalent in flies than previously assumed.

9613 - "Different Roads Sometimes Lead to the Same Castle": Development of Ventral Pigmentation in Dark-bellied Desmognathan Salamanders of Northern Georgia

Carlos Camp[1], Tyler L. Brock[2]

[1]Piedmont University, Demorest, GA, [2]University of Mississippi, University, MS

Homoplasy, the similarity of phenotypes between species not caused by common descent, is rampant in the salamander family Plethodontidae, often obscuring phylogenetic relationships. For many decades, large, dark-bellied semi-aquatic and aquatic dusky salamanders were known as the Black-bellied Salamander (*D. quadramaculatus*) and the Shovel-nosed Salamander (*D. marmoratus*), respectively. However, both taxa represented groups of cryptic, sometimes unrelated species. Georgia has three of the four species in the southern ("Nantahala") clade: the Dwarf Black-bellied Salamander (*D. folkertsi*), the Southern Black-bellied Salamander (*D. amphileucus*), and the Southern Shovel-nosed Salamander (*D. aureatus*). Both *D. folkertsi* and *D. amphileucus* are semi-aquatic and cryptic with completely black venters. However, *D. folkertsi* is phylogenetically sister to *D. aureatus*, which is completely aquatic and has a mottled belly. Because *D. folkertsi* and *D. amphileucus* share the common feature of a completely black belly even though they do not represent sister taxa, we investigated the pattern of pigment development to determine if it is similar in the two. We collected a series of different-aged specimens for each of the three species mentioned above and photographed the ventral surface of each. The larvae of all three species have unpigmented bellies. In our series of *D. aureatus*, the belly became mottled shortly after metamorphosis, and this pattern persisted into adulthood. The belly of *D. amphileucus* began to mottle shortly after metamorphosis; mottling expanded until the entire belly became black as salamanders neared or reached adulthood. However, *D. folkertsi* bellies were never mottled, pigment appearing uniformly across the ventral surface of the trunk shortly after metamorphosis. While the endpoint of a black belly is the same in *D. folkertsi* and *D. amphileucus*, the ontogenetic pattern of achieving it differs. The reason for dark pigment in this and the unrelated northern ("Pisgah") clade of dark-bellied desmognathans is unknown.

9614 - Crayfish genetic diversity, distribution, and endosymbionts across the Eastern Continental Divide

Elizabeth Doss

Georgia Gwinnett College, Lawrenceville, GA

The Appalachians are a proposed origin site for crayfish due to the high rates of endemism and genetic diversity. Many aspects of this diversity are underexplored, including the impact of the Eastern Continental Divide on species distribution and gene flow. Additionally, the presence of intracellular endosymbionts and their possible impact on crayfish genetics has not been assessed. The following project uses genetic, geographic, and morphological data collected across three different watersheds to create a baseline for future work on crayfish in the southern Appalachians. Preliminary results indicate the presence of five species, including a new invasive, as well as a possible range expansion for a native species. Preliminary results also indicate widespread rickettsia infection among all species surveyed. Topics of discussion include morphological versus genetic species definitions, impacts of invasive crayfish on local populations, and lack of clarity with regards to species within *Cambarus.*

9628 - Lafayette Frederick in Hawai'i (1945-1948)

Chris Havran

Campbell University, Buies Creek, NC

Lafayette Frederick (1923-2018) was a Mycologist and Plant Pathologist who made significant impacts on science and civil rights in the southeastern United States. Frederick spent just over two formative years in Hawai'i from 1945-1948. An account of Frederick's Hawaiian experiences were reconstructed to evaluate his impact on Hawaiian Botany and how these experiences informed his career. Frederick's herbarium specimens were attributed to him on Bionomia.net to determine the scope of his collections and the identity of his co-collectors. Newspaper articles, field notes, archived correspondences, and oral histories were also reviewed as primary sources. Frederick was enlisted in the U.S. Navy when he began a tour of duty on O'ahu in 1945. The next year he would enroll as a graduate student at the University of Hawai'i (UH), where he would study under prolific plant taxonomist Harold St. John. Frederick participated in botanical excursions across O'ahu and on interisland field trips to Hawai'i (1946) and Kaua'i (1947). Frederick was listed as collector or co-collector on approximately 190 Hawaiian herbarium specimens amassed during his graduate work. Among Frederick's collections are holotypes for Alectryon mahoe H. St. John & Frederick (Sapindaceae) and Cyrtandra frederickii H. St.John (Gesneriaceae), the latter being named in his honor. Frederick attributes an interaction with a mycologist, likely Donald Philip Rogers, in inspiring him to continue his graduate career in Mycology. Outside of his studies Frederick was involved in volunteering with his church and the YMCA. While he did not obtain a degree at UH, Frederick's collections helped to expand knowledge of Hawai'i's diverse flora while his interactions with field collaborators inspired him to pursue a lifelong career in Mycology.

9629 - Dynamic Landscape of the Venus Flytrap (Dionaea muscipula) Transcriptome

Jeremy Rentsch

Francis Marion University, Florence, SC

In this talk, we will explore the dynamic landscape of the Venus flytrap (*Dionaea muscipula*) transcriptome during various points of prey capture and digestion. Likewise, we will examine transcriptomic differences at several matched timepoints in traps triggered with prey and traps triggered without prey. We will then link a few key observations from this research back to the basic biology of the botanical carnivores.

9630 - Pollination niche partitioning in Rhexia (Melastomataceae)

Erin Burney[1], Darin Penneys[2]

[1]University of North Carolina Wilmington, NC, [2]University of North Carolina Wilmington, Wilmington, NC

Congeneric plants that co-occur often utilize a variety of pre-pollination barriers that serve both to reduce the possibility of hybridization between closely related species and reduce competition between pollinators. Pollination niche partitioning is one of these barriers, in which pollinator species exhibit strong preferences towards certain plant species. Meadow-beauties (Melastomataceae: *Rhexia*) are a genus of flowering plants common throughout the Coastal Plain of the eastern U.S.A. Twelve species are currently accepted in the genus, many of which display overlapping ranges, and can co-occur and co-flower in the same habitats. Hybridization is possible between some species; however, hybrids are not commonly observed. The co-occurrence of species in the genus provides an exemplary study system for determining if pollination niche partitioning is occurring between co-flowering *Rhexia* species. Observations of various urban and rural *Rhexia* communities were conducted in southeastern North Carolina, with pollinator groups compared between species and sites. All *Rhexia* species observed were *Bombus*-dominated in their pollination, though some subtle differences were observed between species, with certain *Rhexia* species supporting a greater variety of pollinator species than others. Additionally, urban and rural sites were shown to support different pollinator species, with urban sites receiving less visitation from pollinators than rural sites, and urban sites receiving almost zero visitation from two threatened pollinator species. The *Rhexia*-pollinator system has been largely unstudied in North Carolina, and the data collected in this study is providing important information about pollinator communities in the region and their reliance upon *Rhexia*.

9640 - Identification of biomarker genes in liver and kidney cancer progression: A shared high-throughput and molecular docking approach with potentials for targeted therapeutic interventions.

Jannatul Ferdoush[1], Maya Minkara[1], Shipan Das Gupta[2], Maisha Tasneem[2], Md Jubair Ahmed Jony[2]

[1]University of Tennessee at Chattanooga, Chattanooga, TN, [2]Noakhali Science and Technology University, Noakhali, Bangladesh

Liver Hepatocellular Carcinoma (LIHC) and Kidney Renal Clear Cell Carcinoma (KIRC) are leading causes of cancer death worldwide, but their early detections remain hindered by a lack of genetic markers. Our study aims to find prospective biomarkers that could serve as prognostic indicators for efficient drug candidates for KIRC and LIHC treatment. To detect differentially expressed genes (DEGs), four datasets were used: GSE66271 and GSE213324 for KIRC, and GSE135631 and GSE202853 for LIHC. Visualization of DEGs was done using heatmaps, volcano plots, and Venn diagrams. Hub genes were identified via PPI analysis and the cytoHubba plugin in Cytoscape. Their expression was evaluated using box plots, stage plots, and survival plots for prognostic assessment via GEPIA2. Molecular docking with PyRx's AutoDock Vina identified optimal binding interactions between compounds and proteins. Pharmacokinetic and toxicity analyses reinforced the drug-likeness and safety of these compounds. In this study, 47 DEGs were identified, with the top 10 hub genes being *TOP2A*, *BUB1*, *PTTG1*, *CCNB2*, *NUSAP1*, *KIF20A*, *BIRC5*, *RRM2, NDC80* and *CDC45*, chosen for their high MCC scores. Data mining revealed a correlation between TOP2A expression and clinical survival outcomes in KIRC and LIHC patients. Docking studies of the TOP2A structure identified a promising compound from *Andrographis paniculata* with high binding energy and interactions with TOP2A. Pharmacokinetic and toxicity assessments support its potential as a drug candidate. Our study emphasizes *TOP2A*'s prognostic significance in KIRC and LIHC and recognizes *Andrographis paniculata* compound as potential therapeutics, offering prospective for enhanced treatment and patient outcomes in these cancers.

9647 - Unraveling the Microbial Diversity of Freshwater Ecosystems Under Environmental Pollution

Elik Esquilin[1], Dr. Tammy Laberge, Ph.D[1], Jacqueline Valiente[2], Analuz Nieves[2]

[1]Miami Dade College, Miami, FL, [2]Miami-Dade College, Miami, FL

Increasing pollution levels are disrupting ecosystems worldwide including microbial ecosystems. As bacteria are foundational for life, playing vital roles in ecosystem stability by conducting various biogeochemical cycling processes, investigating the effects of pollution

on bacterial microbiomes is crucial for developing strategies to counter pollution's impact. This study focuses on understanding pollution's influence on bacterial ecosystems by collecting environmental DNA (eDNA) from urban and rural waterways and conducting DNA metabarcoding through DNA Subway. This research seeks to identify bacterial diversity and abundance across the different sample sites and discern significant variations in composition. Our current results reveal common foundational biogeochemical cycling bacteria as well as photosynthetic cyanobacteria across both urban and rural samples. Additionally, several urban sites revealed an overabundance of fecal bacteria, in turn, these same sites were found to be less diverse and abundant in bacteria when compared to the other urban and rural sites which were surprisingly similar. By illuminating the complex relationship between pollution and bacterial biodiversity, this study aims to inform the development of proactive measures to mitigate the spread of pollution, protect South Florida's waterways, and preserve our diverse ecosystems.

9658 - MiPner Analysis for Microbial Discovery and Classroom Experiential Learning

Jeffrey Bennetzen, Jeffrey Bennetzen, Josue Fernandez-Canela, Shaugnessy McCann, Phil Brailey Jones

University of Georgia, Athens, GA

Traditional microbiology focusses on studies of individual species, while recent metagenomic investigations have undertaken DNA sequence-based descriptive analyses of all of the microbes in an environment at once. The Bennetzen lab has developed a technique that begins to bridge this gap, between one and all, involving the isolation of pairs of microbes that have evolved specific binding interactions. This simple and robust technique, call Microbial Partner (MiPner) analysis, provides access to novel microbes and their interactions. At the same time, it provides a dependable platform for laboratory courses that teach both the techniques and the strategies/adaptations of discovery science. In our first applications of this approach to the soil-root environment, we have discovered numerous new species and genera of bacteria, have assayed their gene contents with full genome sequence assemblies, and have identified physiological interdependencies. The technique involves using one cultured microbe as a bait, and then isolating the microbes from a complex community (e,g., the rhizosphere of a particular plant) that bind to the bait. The binding sub-community can be characterized by metagenomic DNA sequencing, while individual “MiPners” can be purified by standard plate streaking procedures. In using over a dozen different soil bacteria as baits, we have never observed the same binding community twice, but the binder sub-community has always been a tiny subset of the starting microbial community. This presentation will briefly describe the MiPner approach, some of its results when used in lab courses, and how this type of lab class provides education in real-world microbiology, molecular genetics, genomics, genome computational analysis and microbial community analysis.

9674 - Barcode Barriers: Mitochondrial DNA in Freshwater Mussels

David Campbell[1], Charles Lydeard[2]

[1]Gardner-Webb University, Boiling Springs, NC, [2]Morehead State University, Morehead, KY

DNA sequencing is increasingly used for detecting and identifying species, such as in eDNA studies. However, this requires adequate and accurate comparative data. Freshwater mussels (Unionida) provide a test case, with 300 species in the southeastern US. Often they live buried, making detection a challenge. Over 70% of the species are of conservation concern. Some species are difficult to distinguish morphologically. Thus, reliable eDNA detection would be valuable. But are the reference data adequate? Sixty-eight currently recognized species in the region have no *cox1* sequences available. Globally, 17148 *cox1* sequences are available. However, 1269 (7.4%) have an incorrect genus and 2224 (13.0%) have an incorrect species in GenBank. Unlike some other mollusks, the *cox1* gene is not known to have highly anomalous but functional sequences in Unionida; however, some sequences are pseudogenes. Tracking the literature to identify updated names is also a challenge; 2464 records are listed as “in press” when they are actually published, and 3773 are listed as unpublished but are published, totaling over 1/3 of the records being bibliographically inaccurate and thus hard to trace. Additional sequences generated in this study add data for *“Lasmigona” holstonia, Ptychobranchus greeni, Toxolasma cylindrellus, T. germanum, T. granulatum, T. cromwelli, T. pullus,* and *T.* sp. nov. eastern Gulf. Although *cox1* generally seems to be adequate for species identification, hybridization occurs and some species are not well-differentiated. Also, large-scale phylogenetic analyses based on *cox1* alone have poor resolution of deeper branches; complete mitochondrial genomes or nuclear data give better results for such questions.

9692 - Assessing Niche Overlap of Isotopic and Morphological Space in Plethodontid Salamanders

Bailey Sauls[1], Benjamin Fitzpatrick[2], Jon Davenport[1]

[1]Appalachian State University, Boone, NC, [2]University of Tennessee, Knoxville, TN

Approximately 2.16 million living species have been identified on Earth. Determining the mechanisms for species coexistence has proven elusive and widely debated. Species are expected to differentiate along at least one dimension of niche space (i.e. alter diet, behavior, microhabitat use, temporal space, morphological space, etc.) to reduce resource overlap or else eventually become extinct.

The southern Appalachians are a biodiversity hotspot for salamanders, specifically plethodontids. Small-bodied plethodons play vital roles in the communities where they are found, yet the mechanisms for coexistence in these Appalachian ecosystems remain unknown. Southern Zigzag salamanders, *Plethodon ventralis*, and Southern Redback salamanders, *Plethodon serratus*, are two small-bodied woodland salamanders with areas overlap in the Great Smoky Mountains National Park. A total of seventeen populations, eight sympatric sites, five allopatric P. ventralis sites, and four allopatric P. serratus sites, will be studied to determine if niche overlap exists in isotopic niche and morphological space as character convergence could explain the successful sympatric populations found in the national park. Tail tissues approximately 5mm in length were collected in the field and processed for stable isotope analysis while photos were taken of live individuals for digitization and processing in geomorph, an R package. Based on preliminary results, overlap in isotopic niche space exists between all populations of *P. ventralis* and *P. serratus*. Morphological data are undergoing analysis.

9694 - Ramping it up: Assessing the genetic diversity of *Allium tricoccum* Aiton complex in Great Smoky Mountains National Park using Next-Gen sequencing

Lauren Gray, Matt Estep

Appalachian State University, Boone, NC

Our world today faces an unprecedented loss of biodiversity, and understanding theextent to which species lose genetic diversity is imperative for conservation efforts. Reducedgenetic diversity causes species to be less resilient to stochastic change and more susceptible to extirpation and possibly extinction. This is especially problematic for species that have small population sizes or have modes of reproduction that do not facilitate gene flow. *Allium tricoccum* complex is a highly sought-after edible plant that is culturally-significant to Native Americans, specifically the Eastern Band of Cherokee. However, due to its strong onion flavor and aroma, foraging for, and commercially harvesting this plant has become increasingly popular, leading to concern that some populations may be eradicated due to irresponsible harvesting. This study uses SNP genetic markers obtained via the Next-Generation sequencing technique, MIG-seq to assess the genetic diversity of *A. tricoccum* populations throughout Great Smoky Mountains National Park with the hopes of empowering sustainable, indigenous harvest. Populations throughout the park show low levels of genetic diversity and high levels of inbreeding, as to be expected in predominantly clonal plant populations. Analyses have revealed genetic structure and two distinct genetic clusters within the park, providing molecular evidence for the potential presence of the sister taxa, *Allium burdickii*. The data generated in this study will play a crucial role in the long-term monitoring of the *A. tricoccum* complex, as well as highlight genetic methods for obtaining population-level information that can be used in future studies analyzing seemingly abundant clonal plant populations.

9711 - Modeling NatureServe Subnational Conservation Status Ranks for Tennessee Vascular Plants

Julia Prins, Joey Shaw

University of Tennessee at Chattanooga, Chattanooga, TN

Plants are crucial components of our ecosystems and understanding their risk of extinction is important for ensuring effective and efficient conservation. Conservation status ranks measure this potential risk for species at the global, national, and subnational levels, taking into account rarity, threats, and species population trends. These ranks impact development initiatives, guide land management practices, and help establish conservation priorities. It is therefore important to have a complete list of ranks for all species. It is equally important that ranks are generated using a standardized system to reduce bias and misranking. The NatureServe ranking system has been used since 1978 and has generated over 100,000 conservation status ranks from critically imperiled to secure. They have developed a rank calculator based solely on scientific data to standardize the process. Prior to this study, 75% of Tennessee's flora did not have a subnational conservation status rank (s-rank) under the NatureServe ranking system. This study generated s-ranks for all 3,033 vascular plant species present in Tennessee using 5 methods: (1) looking at the s-ranks in the states surrounding TN, (2) calculating the percentage of counties each species had a known occurrence record in, (3) using ArcGIS Pro to calculate rarity criteria and assign a rank based on the NatureServe rank calculator, (4) using a python shiny app to calculate rarity criteria and assign a rank based on the NatureServe rank calculator, and (5) using FME to calculate rarity criteria and assign a rank based on the NatureServe rank calculator. Each s-rank was subject to review by several botanists to ensure accuracy. This study has resulted in a complete state flora being ranked, something only a few other states have accomplished. It shows the tools available for other states to complete their s-ranks and can tremendously impact conservation efforts.

9712 - Plant community dynamics and arbuscular mycorrhizal responses following early stages of drawdown in a large manmade lake

Matthew Reid, Braeden Hurley, Ty Tillman

Hendrix College, Conway, AR

Plant communities are dynamic in the face of environmental change. We explored the change in plant communities of Lake Conway, a large man-made lake in Faulkner County, Arkansas. Beginning in October 2023, the drawdown of Lake Conway commenced as part of a multi-year effort to improve habitat quality and fishing/boating infrastructure. The exposure of the lakebed offers an opportunity to examine early successional responses in plant and soil communities, as the area transitions from an aquatic to a terrestrial system. We documented changes in plant community composition and arbuscular mycorrhizal abundance along a drawdown gradient from the historical shoreline to current water levels in June-July 2024. For the plant community, we quantified species presences and abundances. We collected soil cores to extract and quantify extraradical hyphae of arbuscular mycorrhizal fungi (AMF). We collected covariate data on elevation, canopy cover, and soil pH to identify their potential effects on plant and soil responses. We found the drawdown gradient had no effect on plant species richness and Shannon diversity, but PERMANOVA revealed significant differences in the composition of the plant community along the drawdown gradient. Percent cover by species such as Polygonum and Juncus decreased by 50% and 90% respectively, along the drawdown gradient, while more aquatic species such as Nuphar and Ludwigia increased 3-fold and 5-fold, respectively. Across the drawdown gradient, AMF extraradical hyphal length was low (~11.6 mm g-1 soil) and did not show significant differences along the transects. Collectively, these results highlight the rapid shift in plant community structure because of the drawdown. However, colonization of the exposed lakebed sediments by AMF appears to be slow. With drawdown expected to continue for four more years, the area is likely to experience further rapid change in plant community composition, but colonization by AMF remains uncertain.

9714 - Of Hurricanes and Hellbenders: Catastrophic River Flooding from Hurricane Helene Offers Variable Impacts for Eastern Hellbender (*Cryptobranchus alleganiensis*) Habitat Restoration

Walter Smith[1], Zack Edwards[2], Bryce Cheers[1], Savanna Busick[1]

[1]The University of Virginia's College at Wise, Wise, VA, [2]Conservation Management Institute, Virginia Tech, Blacksburg, VA

Eastern Hellbenders *(Cryptobranchus alleganiensis*) have experienced declines due in part to the degradation of water quality and riverbed substrate. In response, federal funding has been allocated to support habitat reconstruction efforts across the species' range. However, it remains unknown how resilient both restored and reference river reaches may be to natural disturbance events that are increasing in frequency and severity across the Appalachian region. In late September 2024, precipitation from landfalling Hurricane Helene and an associated predecessor rainfall event triggered catastrophic flooding across portions of Southwest Virginia, Western North Carolina, and East Tennessee, including at the site of Virginia's largest hellbender habitat restoration project to date along the Middle Fork Holston River. Data reflecting the condition of rock cavity refugia have been collected annually since 2019 at both reference and restored reaches as part of the design and evaluation phases of this project. We combined these data with post-storm surveys to examine if and how impacts from Hurricane Helene affected riverbed substrate of the type used by hellbenders. Flooding significantly restructured riverbed substrate, with some cavity refugia eliminated due to boulder movement or sediment deposition and new refugia created via flood-scouring or boulder relocation. While riverbed boulders became significantly more embedded following the storm, mean cavity size was not significantly altered, with impacts consistent across both reference and restored reaches. Our data suggest that Hurricane Helene significantly modified but did not deplete available rock cavity habitat in the Middle Fork Holston River, although it is unclear how these attributes balance with other flood impacts, such as hellbender mortality. More broadly, our results underscore that riverbeds are dynamic ecosystems and that restoration projects should account for flood resiliency during their design, especially in the face of ongoing trends from anthropogenic climate change.

9718 - The effect of temperature and soil type on the growth of an imperiled, southern Appalachian endemic, *Houstonia montana* (Rubiaceae)

Kira Lindelof, Alexander Krings

Department of Plant and Microbial Biology, North Carolina State University, Raleigh, NC

An understanding of fundamental niche space for rare species, obtained experimentally through ex situ studies like common garden experiments and greenhouse studies, can shed light on optimal conditions and thus meaningfully inform management strategies. One species in which an understanding of the fundamental niche is largely lacking is *Houstonia montana*, a federally listed herbaceous perennial endemic to the high elevation rock outcrops and grassy bands of the southern Appalachians. Under controlled growing conditions at the NC State Phytotron, we experimentally assessed the growth response of *H. montana* to varying temperature and soil conditions with the intent to improve our understanding of its performance under a range of environmental factors. Plant height,

internode length, and leaf dimensions were examined for individuals stemming from two populations of *H. montana* grown in two soils of varying pH and mineral content and under three temperature regimes reflective of an environmental gradient of the southern Appalachians. We observed taller plants with larger leaves as temperatures increased. We also observed increased growth in soils with a higher pH and greater concentrations of calcium, magnesium, and manganese than the average of extant occurrences. Our results suggest that the species is not presently occurring in physiologically optimal soil and temperature conditions, appearing instead to benefit from higher temperatures and more nutrient-rich soils, factors considerably more abundant in the southern Appalachians in habitats other than those in which the species currently finds itself.

9720 - Secrets of the Swamp: Uncovering the Genetic Diversity of a Federally Threatened Wetland Species, Swamp Pink (*Helonias bullata* L.)

Kate Loughran, Matt Estep, Lauren Gray

Appalachian State University, Boone, NC

Helonias bullata L. (swamp pink) is a monotypic plant genus belonging to the Melanthiaceae family. *Helonias* is listed as federally threatened plant species and is a long-lived perennial evergreen herb that occurs in wetlands and bog subtypes in the eastern United States. While these habitats are already increasingly rare, development and urbanization has fractured and extirpated many *Helonias* occurrences, leading to a mosaic of small, isolated populations throughout its range. Due to the limited number of individuals within many of these populations, *Helonias* faces the perilous threat of genetic diversity loss which can lead to population instability and collapse. This research focuses on developing an in-depth genetic diversity analysis of the extant *Helonias* populations in North Carolina, as well as assessing the effect of genetic drift within smaller populations. Leaf samples from 15 Element Occurrences across the state were collected and DNA extracted using an advanced CTAB approach. MIG-seq, a next-generation sequencing method, was used to construct reduced-representation libraries for *Helonias*. After sequencing, single nucleotide polymorphisms (SNPs) within the genome of each individual sampled were identified. This data will be used to calculate genetic diversity estimates for each population, observed through nucleotide diversity and heterozygosity. This critical genetic analysis will identify populations within North Carolina containing high genetic diversity as well as at-risk populations experiencing genetic diversity loss via genetic drift. This data will, in turn, help inform future management decisions such as genetic rescue implementation and habitat conservation.

9727 - Effects of Lipid Raft Depletion on LL-37 Uptake in Human Monocytes

Lauren Byrnes[1], Maria Craig[2]

[1]Mary Baldwin University, VA, [2]Mary Baldwin University, Staunton, VA

LL-37 is a peptide of innate immunity that displays antimicrobial properties and that shows anti-inflammatory activity in some immune responses. As part of its role in innate immunity, LL-37 forms complexes with extracellular DNA and carries it across host cell membranes, alerting the immune system to pathogens but also contributing to immune conditions like psoriasis, cystic fibrosis, and lupus erythematosus. The exact mechanism for how LL-37 is able to cross membranes is unknown, but there is evidence that LL-37 is associated with lipid raft regions. Lipid rafts are membrane microdomains containing high concentrations of cholesterol and saturated lipids, specifically sphingolipids, and characterized by increased lipid packing and order and decreased membrane fluidity. These regions play a role in membrane organization and trafficking, and they are associated with some host-pathogen interactions. Cholesterol-depleting drugs that extract cholesterol from the cell membrane, such as methyl-β-cyclodextrin, have been observed to inhibit LL-37 uptake, indicating that lipid rafts may be associated with LL-37 endocytosis. However, methyl-β-cyclodextrin has side effects in addition to cholesterol depletion that confound the results. In this study, we investigate the effects of drugs that inhibit membrane lipid synthesis on the uptake of LL-37 and LL-37/DNA complexes by a human monocytic cell line (THP-1). By inhibiting cholesterol and sphingolipid synthesis individually and also in combination, we seek to determine whether LL-37 endocytosis is associated with a specific component of lipid rafts, like cholesterol, or if it is associated with the overall physical properties of rafts.

9728 - An Examination of Zooplankton Abundance and Diversity off the Eastern Georgia Coast and Estuaries.

Mark Schlueter, Dreanna Wildman, Mary Haney

Georgia Gwinnett College, Lawrenceville, GA

Zooplankton are small animals that drift along with the currents in marine and freshwater habitats. Zooplankton are a critical component of aquatic systems. They serve as a bridge from the primary producers (phytoplankton) to larger animals (e.g. fish). Zooplankton diversity and abundance was investigated in marine, estuary, and freshwater ecosystems. On October 19 -20, 2024, researchers aboard the R/V Savannah sampled zooplankton at 6 sites (2 marine sites, 2 estuary sites (brackish water), and 2 freshwater sites) near Savannah, Georgia. Zooplankton were sampled using a weighted plankton net that was dragged at a depth of 1 meter below the water

surface for 2 minutes. The zooplankton samples collected via the plankton net were examined within 5 minutes of their collection using a portable In-Situ Shadowgraph Imaging System that allowed the zooplankton to be visualized via a computer monitor. Portions of the samples were preliminarily examined in the wet lab aboard the ship, while the entire sample was videotaped and recorded for later analysis. Salinity, temperature, depth, and conductivity were measured using a CTD device (package of electronic sensors) directly lowered from the ship. Preliminary results indicated a larger diversity of zooplankton (jellyfish, comb jellies, arrow worms, and copepods) in the marine environments. As salinity decreased, however, fewer zooplankton species were observed. Freshwater samples often were limited to only copepods and an occasional crab larva. Copepods were the most numerous zooplankton in all samples.

9730 - Developing Conservation Tools: Microsatellite Markers for *Cypripedium parviflorum*

Elyssa Ghazali, Matt Estep

Appalachian State University, Boone, NC

Cypripedium parviflorum (Orchidaceae, Salisbury), commonly known as the Yellow Lady Slipper, is found throughout North America and is listed as a rare species by North Carolina's Natural Heritage Program. Despite its general security on a global scale (G5T3T5), it is considered imperiled or critically imperiled (S1S2) within the state. Botanists recognize three varieties—var. parviflorum, var. pubescens, and var. makasin—distinguished by subtle ecological and morphological traits, which often complicate accurate identification. In order to construct genetic tools for future conservation research, we identified 50 diverse microsatellite loci from sequence data, designed primers, and screened them for consistent amplification. Twenty-four primer pairs passed the 1st phase of development and are being used to genotype 69 individuals to assess polymorphism within a single population. We hope these molecular markers will be valuable tools in future conservation efforts for this species complex.

9732 - In Silico Screening of Stilbene Compounds to Identify Selective Binding to Estrogen Receptors ESR1 and ESR2

Dr. Lyndsay V. Rhodes, PhD

Florida Gulf Coast University, Fort Myers, FL

Estrogen receptors (ERs), ESR1 (ERα) and ESR2 (ERβ), are nuclear receptors critically involved in regulating cellular processes such as growth, differentiation, and reproduction. Dysregulation of ER signaling pathways is associated with various diseases, including hormone-responsive cancers like breast cancer. Stilbenes, naturally occurring polyphenolic compounds, have garnered interest for their potential as selective estrogen receptor modulators (SERMs) due to the similarity in structure and size to 17β estradiol. In this study, we computationally screened a library of 29 stilbene compounds to evaluate their binding affinity to ESR1 and ESR2 in both agonist and antagonist conformations using AutoDock, a molecular docking tool.

The docking analysis aimed to identify compounds with high binding affinity and potential selectivity for ESR1 or ESR2. Target protein structures were sourced from the Protein Data Bank and prepared for docking by ensuring the appropriate receptor conformations. Stilbene analogues were curated and optimized using Avogadro, a molecular editing software. Docking simulations were conducted under standardized parameters to ensure reproducibility, and results were evaluated based on binding energy scores and interaction profiles.

Preliminary findings indicate that several analogues demonstrate strong binding affinity to ESR1 and ESR2, with distinct conformational preferences. Select compounds exhibited differential binding patterns that suggest potential as ESR-selective agonists or antagonists. These results highlight key structural features critical for receptor interaction and provide insight into the mechanisms underlying ligand selectivity.

This research underscores the utility of in silico approaches for the initial screening of bioactive compounds and guides subsequent in vitro and in vivo studies. Further validation of the identified stilbene analogues may contribute to the development of novel therapeutics targeting estrogen receptor-associated pathologies.

9733 - Climate Growth Relationships Among Longleaf and Associated Pines in Southeastern Virginia

Sarah Durham[1], Arvind Bhuta[2]

[1]Old Dominion University, Norfolk, VA, [2]United States Department of Agriculture, Washington, DC

Dendroclimatology examines the relationship between climate and growth in annually formed tree rings. We created total ring-width, earlywood, and latewood chronologies from living *Pinus palustris* (longleaf pine), *Pinus taeda* (loblolly pine), and *Pinus serotina* (pond pine) in the Blackwater Ecological Preserve, Isle of Wight county, southeastern Virginia. Response functions analyses were conducted

between growth and climate variables (precipitation, Palmer Drought Severity Index (PDSI), minimum temperature, maximum temperature) resulting in positive associations between growth and winter temperatures and precipitation during the late growing season for all species. The latewood chronologies demonstrated more sensitivity to climate than the earlywood or total ring width chronologies, including a strong positive association between precipitation and late growing season while conditions of the previous year also influenced growth during the current year. Results varied between species and chronology type, but precipitation during the previous September had a positive effect on growth during the current year while maximum temperature of the previous October had a negative effect in the earlywood chronologies. We also utilized moving plots, which visualize how climate-growth relationships change over time. Associations between summer temperatures and precipitation became stronger over time, primarily from the 1970's onward. This may suggest that, at least within this study site, annual variability within ring width is becoming more sensitive to a changing climate.

9740 - Age influences environmental preference choices of Flamboyant Cuttlefish (*Ascarosepion pfefferi*)

Henderson Gull[1,2], Alisha Fredrickson[3]

[1]Research Associate - Walt Disney World, Lake Buena Vista, FL, [2]Research Associate - New College of Florida, Sarasota, FL, [3]Senior Aquarist - Walt Disney World, Lake Buena Vista, FL

Little is known about the ecology and life history of the Flamboyant cuttlefish (Ascarosepion pfefferi) despite its popularity in public aquaria. To better understand their environmental preferences, we created an environment with two distinct habitat designs cuttlefish could freely go between. The first was a simple side with open space, small caves and replica coconut husks, while the second side was complex and contained artificial seagrass and large rock structures providing visual barriers. We observed a cohort of 17-27 cuttlefish across five months, documenting their environmental use through 501 scan observation sessions. We collected data on overall counts across the two habitats, camouflage use, as well as conspecific grouping choices. This data was collected for each object type (and open space) within the environment in each habitat. We found that while cuttlefish had an overall bias towards a complex environment ($P = 8.92e-16$, Wilcox $V=79337$, $n =501$) and statistically significant preferences between objects ($P<2.2e-16$, $Chisq=994.25$, $df=6$, $n=8016$), age was an extremely influential factor throughout the data. We began watching these cuttlefish at the onset of sexual maturity (approximately 90 days old) and started observing reproductive behaviors at 5 months old. Within our data, there are statistically significant changes in preferences for habitat and object-use that began at five to six months old ($P<0.05$). One of the most noticeable trends was increased use of simple habitat with age ($P=2.63e-15$, $Chisq=77.62$, $df=5$, $n=501$) and a strong increase in the use of open space ($P=1.45e-12$, $Chisq=64.46$, $df=5$, $n=1004$) and replica coconuts. ($P<2.2e-16$, $Chisq=22.85$, $df=5$, $n=1003$) as age increased. These results suggest ontogeny is an important factor to consider for A. pfefferi's behavior in both ecological studies and husbandry. A lack of ontogenetic data in common cephalopod study methods may have introduced biases in our interpretations of their ecology and life history.

9744 - The effects of stilbene compounds on a triple-negative breast cancer 3D cell culture model

Gavriel Burger, Dr. Lyndsay V. Rhodes, PhD

Florida Gulf Coast University, Fort Myers, FL

Triple-negative breast cancer (TNBC) is an aggressive, metastatic subtype of breast cancer that lacks the three commonly targeted receptors for treatment, estrogen receptors (ER), progesterone receptors (PR), and human epidermal growth factor receptor 2 (HER2). Due to the increased difficulty in treating this cancer, as well as the cancer's ability to form drug resistance, new drug therapies are needed to increase prognosis and drug availability in patients. Resveratrol (RSV), a stilbene compound, is a phytoestrogen that is produced naturally in plants like grapes and peanuts. RSV has been popularized due to its antioxidant and anti-inflammatory abilities, as well as some anti-cancer properties. In this study, RSV and four other stilbene compounds derived from RSV were screened for anti-cancer and anti-metastatic abilities in two TNBC cell lines through both 2D and 3D cell culture. Migration and invasion assays showed that these drugs do affect TNBC cell's ability to metastasize in both MDA-MB-157 and BT-549 cells. In addition, the formation of a multicellular tumor spheroid (MTS) model was developed using low adhesion cell culture plates to produce a high-throughput drug screen protocol. The MTS model was used to determine the stilbenes effect on already formed tumors, as well as the drugs' ability to prevent tumor formation. Using the MTS model, hypotheses on how these drugs might react in vivo can be made, due to the similarities in the tumor microenvironment. Changes in MTS formation or integrity can provide insight on how a drug may affect tumor growth, proliferation, and metastasis in TNBC patients. Results of this study show a significant effect on MTS structure and formation in response to some stilbenes, which suggests a potential for the compounds to be used as anti-cancer agents in TNBC treatment therapies, as both a preventative treatment, and as an established cancer treatment.

9746 - Infanticide and Neonaticide: How Often are these Crimes Concealed?

Gillian Johnson, Dr. Ed Mondor, BSc, MSc, PhD

Georgia Southern University, Statesboro, GA

Homicide rates in infants (under 1 year of age) and neonates (under 1 day of age) are greater than in any other childhood age group. Using the National Violent Death Reporting System (NVDRS) we aimed to determine the biological characteristic of infanticide and neonaticide perpetrators and victims, the incidence rates of both crimes, and the circumstances in which these deaths were concealed. Here we report that perpetrators of infanticide were most often male, while neonaticide was most often committed by a female. Perpetrators of both types of homicide were most often black, aged 20-30, the parent, and also the caregiver at the time the crime was committed. Victims were most often male and black. Neonaticides were significantly more likely to be concealed than infanticides. Concealed victims were most often placed in bags or in the trash, respectively. It is important to increase awareness of these heinous crimes, as they are easy to conceal and likely underreported. By identifying how infant deaths are most often concealed, it could improve the ability of forensic entomologists to assist in legal investigations.

9747 - A Severe Head Lice Infestation in a Pediatric Fatality: Forensic Insights

Dr. Ed Mondor, BSc, MSc, PhD[1], Marina Eremeeva[1], Lance Durden[1], Jonathan Eisenstat[2], Brian Hargrove[3]

[1]Georgia Southern University, Statesboro, GA, [2]Eisenstat Forensic Pathology LLC, Atlanta, GA, [3]Georgia Bureau of Investigation, Region 6 Field Office, Milledgeville, GA

Lice are assuming an increasing importance in forensic entomology cases, given their capacity to provide information about an individual's care. Prolonged and chronic infestations may result in serious outcomes including anemia. This talk will describe an investigation of a head louse infestation in a 12-year-old child who experienced severe anemia and subsequent death. Numerous lice were found postmortem on the head, face and neck of the patient, as well as on bedding and clothing. Analysis of nits on individual hairs determined that the louse infestation had been present for at least 166 days. All lice were heterozygous for the T917I *kdr* genotype, a marker of permethrin resistance. Head louse pediculosis can be severe on children with limited parental attention, and may serve as a warning sign of neglect.

9749 - Shifts in Avian Community Composition in Response to Eastern Hemlock Decline in Great Smoky Mountains National Park

Nicole Mooradian

University of North Carolina Asheville, Asheville, NC

The eastern hemlock (*Tsuga canadensis*) is a foundation tree species that provides important habitat and foraging opportunities for many organisms. Since the introduction of the hemlock woolly adelgid (HWA) (*Adelges tsugae*) in the 1950s, hemlocks have been under threat across their range, showing accelerated declines in the Southern Appalachians, where effects of the adelgid may be amplified by a recent lack of harsh winters. Studies from the northeastern United States have shown that hemlock-associated avian species have declined in areas of high hemlock mortality. This study investigated how avian communities in the Southern Appalachians have been affected by the loss of this important tree in a region that is ecologically distinct from those of previous studies. At 202 sites in the Great Smoky Mountains National Park, vegetation surveys were conducted to assess the current size and health of hemlocks to develop an index of hemlock decline since before HWA reached the Southern Appalachians. Avian point count surveys were also conducted to describe current avian abundance and diversity as compared with historic survey data. Results show that sites with high hemlock mortality are significantly less similar in bird species composition between current and historical surveys than sites of low hemlock mortality, indicating that species composition has shifted more in areas with greater hemlock decline. Data suggest that, in response to hemlock decline, generalist and disturbance-adapted birds such as the Brown Creeper (*Certhia americana)* have increased in abundance, while hemlock-associated species, such as the Acadian Flycatcher (*Empidonax virescens*) have decreased. While there is no evidence for the strong obligate relationships observed in the northeast, findings suggest that hemlocks in the Southern Appalachians are an important tree for several avian species and further decline of hemlocks could continue to alter the composition of bird communities in this region.

9752 - Exploring the Potential of Equine Herpesvirus Type-1 as an Oncolytic Agent for the Treatment of Human Prostate Cancer

Jacob Mayer, Arthur Frampton

University of North Carolina Wilmington, Wilmington, NC

Prostate cancer is the second most frequent cancer and the fifth leading cause of cancer death in men globally. An intriguing option for cancer treatment is oncolytic virotherapy, in which native or genetically modified viruses are used as anti-cancer agents. In this study, we investigated the oncolytic potential of 4 strains of the animal virus equine herpesvirus type 1 (EHV-1) on human prostate cancer cell lines, PC-3, LNCaP, and C4-2B. We first measured the amount of virus mediated cell death at 24, 48, and 72 hours. Cell death steadily increased in each cell line from 24-72 hours with total cell death at 72 hours on PC-3 ranging from 84% to 90%, 75% to 85% on LNCaP, and 83% to 88% on C4-2B. We also infected the normal prostate epithelial cell line (RWPE-1) with the four EHV-1 strains and observed cell death ranging from 58% to 83% after the 72-hour infection. In addition to the cell death assays, the amount of virus produced in these cell lines was also measured at 24, 48, and 72 hours. To date, we have collected virus yield data for the 24–72-hour time points with the 4 EHV-1 strains on the 3 cancer lines and the yields range from 1.0×10^5 pfu/mL to 2.3×10^7 pfu/mL indicating EHV-1 is able to productively infect the three prostate cancer cell lines. Future work will assess the utility of combining anti-cancer agents such as docetaxel and histone deacetylase inhibitors, including valproic acid (VPA), with EHV-1 to evaluate synergistic cytotoxicity. Additionally, based on our finding that wild-type EHV-1 lyses the normal prostate epithelial cells (RWPE-1) cells, we will engineer the virus to increase the probability of selectively eliminating prostate cancer cells while reducing cell death on the RWPE-1 cells.

9753 - Assessing Avian Species Change in Response to Hemlock Decline: A 25-Year Follow-up in Great Smoky Mountains National Park

Allison Melrose

University of North Carolina Asheville, Asheville, NC

This study investigated changes in avian species abundance following the decline of eastern hemlocks (*Tsuga canadensis*) in the Southern Appalachian region. Eastern hemlocks are a foundation species, providing unique structure and microclimates that support forest biodiversity. However, since the spread of the invasive hemlock woolly adelgid (HWA) to the Southern Appalachians, eastern hemlocks have experienced widespread die-off. Previous studies in the northeastern US suggest that hemlock loss leads to the decline of regionally hemlock-associated bird species, such as the Black-throated Green Warbler (*Setophaga virens*). Expanding on previous research, our study applied a before-after approach to the Southern Appalachian region, using bird survey data collected from 1996-1999 in Great Smoky Mountains National Park, prior to HWA infestation. We compared pre- and post-HWA bird abundance data at 201 sites using 10-minute point counts during the breeding seasons from 2018-2024. At each site, we calculated a decline value by counting all hemlocks within a 30-meter radius and categorizing them by size and health class. To account for differences in detectability across species, we used dynamic occupancy modeling. Our results suggest that three species have declined as a result of hemlock loss: Ovenbird (*Seiurus aurocapilla*), Veery (*Catharus fuscescens*), and Blackburnian Warbler (*Setophaga fusca*). In contrast, we found that some species have increased in former hemlock sites, likely reflecting preferences for disturbed habitats or standing dead trees. These increasing species include Brown Creeper (*Certhia americana*), Eastern Towhee (*Pipilo erythrophthalmus*), Northern Parula (*Setophaga americana*), and Swainson's Warbler (*Limnothlypis swainsonii*). Our results suggest that while hemlock-associations in the Southern Appalachians may not be as strong as in the northeastern US, hemlock decline has still driven significant differential shifts in avian abundances, reflecting varied species responses to environmental change.

9757 - Increasing the Accuracy of Tree-Ring Data Processing to Improve Models for Reconstructing Climate

Bailey Reutinger, Nicholas Bussberg, David Vandermast

Elon University, Elon, NC

Tree-ring data is used to reconstruct past climate and to predict future climate trends. In each year of a tree's lifespan, a distinct ring is added to the tree's width, and the widths of individual rings vary depending on the climate that year. To process tree-ring data, two cores from each tree are typically extracted, and then all cores are combined before analysis. We aim to improve the modeling of future climate scenarios using tree rings by assessing the accuracy of tree-ring data collection. Our investigation of data from the International Tree-Ring Data Bank found that cores sampled from the same tree do not necessarily have the same ring widths, and trees with low correlation may have a worse correlation with local climate data. These findings imply that only trees with moderate or better internal correlation should be used for climate modeling. To more directly target differences among tree-ring data processing methods, we collected 47 tree cores from Virginia pines (*Pinus virginiana*) in Elon University Forest. With this data, we combined and correlated the widths of the rings on each core with local climate data. We compared the existing standard method of combining cores for processing with a new method. The standard method treats each core in the stand independently despite each belonging to a pair or triplet of a single tree. We proposed a new method that processes measurements on the tree level instead of a core level. We compared each

method to recommend the approach that produces better fits with local climate data. The proposed method produces a higher correlation for annual average temperature (r = 0.20) and precipitation (r = 0.12) data than the standard method (r = 0.13, r = -0.01, respectively).

9762 - Stream Health of the Little River in Townsend, TN as Determined by Biological Indicators, Aquatic Macroinvertebrates

Kaitlin Koster, David Unger

Maryville College, Maryville, TN

The Little River in Townsend, TN is an important source of drinking water and recreation while also hosting abundant biodiversity. The Little River originates in the Great Smoky Mountain National Park and is widely loved and used recreationally throughout Townsend. The city government recently requested that stream health be monitored and thus partnered with Maryville College (Maryville, TN) to conduct this study. In this aspect of a larger study, the stream health of the river was determined by the use of aquatic macroinvertebrates as bioindicators. Previous water quality studies had indicated that E. coli values sometimes exceeded those expected for excellent water quality. In addition, a spike in E. coli noted at the input of a small tributary (Cedar Creek) into the Little River warranted further investigation through bioindication. Kick-net sampling technique was used to collect triplicate samples at 10 sampling sites along 8 kilometers of the Little River, 3 control sites in a less human-impacted location, and 2 specific sites of interest in Cedar Creek and just below in the Little River. Samples were collected from 5 to 7 August 2024, then sorted and identified to order and to family. Methods were performed following the Tennessee Department of Environment and Conservation's (TDEC) macroinvertebrate sampling protocol, and results were analyzed using the NCBImod Index. No significant differences in water quality were observed throughout the City of Townsend, and no significant differences were observed between upstream and downstream of the input of interest. Possible reasons for this lack of significance could include dilution of polluted water or the potential use of E. coli as a food source by macroinvertebrates.

9771 - Indole Treatment of *C. elegans* Rescues Illness Induced by the Opportunistic Pathogen *Cronobacter sakazakii*

Joshua Asselin, Kyle Brawner

Lipscomb University, Nashville, TN

Necrotizing enterocolitis (NEC) is a severe and often life-threatening inflammatory condition of the intestine primarily affecting premature infants. The opportunistic pathogen *Cronobacter sakazakii* (Cs) has been implicated in NEC. While activation of the ligand-dependent transcription factor aryl hydrocarbon receptor (AhR) has been shown to prevent NEC in a mouse model, its potential as a therapeutic target for established NEC remains unclear. We hypothesize here that the AhR ligand indole can reverse Cs-mediated illness in the model organism *Caenorhabditis elegans*. Our results demonstrate that exposure to live Cs, but not heat-killed Cs, significantly impaired worm motility, demonstrating Cs is an effective pathogen of *C. elegans*. Treatment of Cs-infected worms with indole improved motility and enhanced survival under heat stress. These effects were dependent on *ahr-1*, the *C. elegans* ortholog of the human *AHR* gene. Finally, wild-type worms infected with Cs maintained higher motility scores and heat stress survival rates than their *ahr-1* knockout counterparts, even with no exogenous indole supplied but fed a diet of indole-producing commensal *Escherichia coli* prior to Cs infection. Our findings indicate that indole enhances health outcomes in Cs-exposed worms, suggesting a potential therapeutic avenue for NEC. Further investigation into AhR ligands could reveal new treatment strategies for managing NEC in premature infants.

9777 - Ghosts in Glass: Ghost Crabs as Judges of Glass Sand for Coastal Restoration

Emily Parrish, Jonathan Pérez, Jeremiah Henning

University of South Alabama, Mobile, AL

Coastal erosion impacts ecosystems worldwide. Restoration typically involves replenishment of sand that is dredged from deep water despite evidence of high ecological damage and economic costs. As an alternative, sand made from recycled glass bottles may provide more sustainable substrate while reducing glass entering landfills. Our goal is to determine whether glass sand is a viable option for coastal restoration via its impact on a critical indicator organism in coastal dune ecosystems, the Atlantic Ghost Crab, Ocypode quadrata. Ghost crabs were live-trapped from Dauphin Island, Alabama and reared in sand environments containing full beach sand, half beach sand and half glass sand, and full glass sand for 8 weeks. In order to compare the stress responses of each treatment, the crab's initial and final stress hormone levels (Crustacean Hyperglycemic Hormone), carapace widths, weights, and claw dimensions were collected. There were no significant differences in mortality ($F=2, 62=0.1805$, $p=0.8353$), carapace widths ($F2,34=0.0114$, $p=0.9887$), weights ($F2,35=0.2571$, $p=0.7747$), or claw dimensions (dominant $F2,35=0.07$, $p=0.9325$ and non-dominant $F2,35=0.9081$, $p=0.4126$). Overall, our growth and survival data indicate that recycled glass substrates may be a viable option for beach restoration

projects, as evidenced by the lack of differences between ghost crab growth and survival between natural and glass substrates. Follow-up studies will focus explicitly on physiological and behavior changes in ghost crabs between our substrates.

9782 - Using machine learning techniques to predict the spread of invasive species: Cyperus blepharoleptos as a case study.

Maxwell Gebhart, Samuel Schmid, Gray Turnage

Mississippi State University, Miss State, MS

The biogeography of invasive species is integral to the study of invasion ecology and one of the most important research questions in this respect asks where invasive species are expected to spread. In the past few decades, many statistical tools have been developed that use machine learning to predict the ecological niches of species. One such tool is MaxEnt which can make use of small datasets of presence-only data to develop ecological niche models (ENMs) with environmental predictors. The objective of this study is to use a MaxEnt ENM to predict the distribution of suitable habitat of the poorly studied *Cyperus blepharoleptos* (Cuban bulrush) in present-day and future climate scenarios. Publicly available records of *C. blepharoleptos* and BioClim rasters (BIO1, BIO7, BIO12, BIO14, and BIO15) were used in this modeling effort as the response variable and predictors, respectively. MaxEnt models were iteratively tuned using combinations of four different feature classes and three different regularization multipliers to build 12 different candidate models. The best-fit model was selected using three criteria: omission rate < 0.05, corrected Akaike information criterion (AIC), and model parsimony. A jackknife analysis was run in MaxEnt to determine the relative importance of the BioClim variables through stepwise inclusion/exclusion. The best-fit model was used to predict the geography of suitable habitat in North and South America in five climate scenarios: present-day, SSP1-2.6 in 2040, SSP1-2.6 in 2060, SSP5-8.5 in 2040, and SSP5-8.5 in 2060. Model predictions show the expansion of suitable habitat in all future climate scenarios, with the greatest expansion occurring in SSP5 by 2060. We compare our findings with a study that used a different niche modeling approach to highlight the strengths and weaknesses of either approach as well as how these different approaches can complement each other.

9784 - Assessing the foraging habits of two sunflower specialist bees (Melissodes, Apidae) using DNA barcodes ITS2 and trnL

Rebecca Foy[1], Beth Ferguson[2], Jarrad Prasifka[2], Pamela Puppo[1]

[1]Marshall University, Huntington, WV, [2]USDA-ARS-ETSARC, Fargo, ND

Many plants rely on insect pollination, including economically important crops like sunflower (Helianthus, Asteraceae). Long-horned bees (Melissodes, Apidae) are solitary species native to the Americas that specialize in sunflower pollination and are more effective pollinators than honey bees. Other than their preference for Helianthus pollen, little is known of the foraging range and plants visited by Melissodes. This study uses metabarcoding to investigate the foraging habits of two understudied Melissodes species, M. trinodis and M. agilis. We collected a total of 138 female bees from three sunflower fields near Fargo, ND. Bees were identified to species morphologically, and pollen was washed off their bodies. DNA was extracted from the pollen and amplified using the ITS2 (nuclear) and trnL (chloroplast) regions. Resulting sequences were matched to PLANiTS2 (ITS2) and NCBI (trnL) databases to identify pollen origin. Our results show that both species have a clear preference for sunflower pollen, as 99% of the sequences recovered from the pollen were from Helianthus. We also found small amounts of pollen from other plant species visited by these bees, mostly other Asteraceae genera, as well as species in the legume family, Fabaceae. This overabundance of Helianthus pollen illustrates just how specialized and effective Melissodes are at sunflower pollination. Overall, our results prompt future research on maximizing sunflower pollination services provided by Melissodes for applications in both agriculture and prairie restoration.

9789 - Mississippi Macrophyte Monitoring: Surveys for detecting aquatic invasive plants

Samuel Schmid, Gray Turnage

Mississippi State University, Miss State, MS

A large fraction of the Earth's freshwater is stored in small lakes and a major threat to these ecosystems is the introduction of invasive aquatic plants. Despite their importance, small lakes are often neglected in research and management. To address the issue of invasive aquatic plants, the most effective method is the implementation of early detection and rapid response (EDRR) strategies. This talk introduces an ongoing early detection effort conducted by Mississippi State University, funded by the Mississippi Department of Environmental Quality. This strategy entails surveys of aquatic plant communities across the state of Mississippi with an objective of detecting new incursions of invasive plants and a focus on small lakes and rivers. Point surveys of the littoral zone were conducted by boat and all species observed at sample points were reported. Data from these surveys identified several new incursions of invasive species and these early detections were presented to appropriate management bodies for rapid response. These data were also used to predict the patterns of invasion of four prominent invasive species: *Alternathera philoxeroides* (alligatorweed), *Cyperus*

blepharoleptos (Cuban bulrush), *Panicum repens* (torpedograss), and *Triadica sebifera* (tallowtree). In addition to detecting new instances of invasive species, these surveys helped describe the native flora of Mississippi. Several state and county records were observed, improving our understanding of the Mississippi's aquatic and wetland flora.

9797 - The effect of a Charcot-Marie-Tooth Mutation on Lifespan, Sleep Behavior and Motor Function in *Drosophila melanogaster*

Emma McBane, Katelynn Corder

Samford University, Homewood, AL

Charcot-Marie-Tooth disease (CMT) is a group of genetically inherited peripheral neuropathies commonly characterized by distal sensory and motor involvement, with muscle weakness and atrophy, frequent sensory loss, and foot deformities. In addition, sleep disturbances have been suggested to be associated with the disease as well. In this study, we used a *Drosophila melanogaster* line with a mutation in the dynamin-2 gene, modeling an autosomal dominant form of CMT. In this study, we investigated the lifespans, daily activity, sleep patterns, and climbing ability of this *Drosophila* model of CMT to determine its viability as a basic research model for further research. We found that this model mirrors some aspects of the human disease, including potential sleep disturbances.

9821 - "Case" studies of the caddisfly (Trichoptera) Linnean shortfall

Alexander Orfinger

Dalton State College, Dalton, GA

Caddisflies (Trichoptera) represent the most diverse primary aquatic insect order with well over 17,000 nominal species. These cosmopolitan insects are widely used in freshwater biomonitoring, for which taxonomic resolution positively corresponds to biomonitoring accuracy. As with many animal taxa, however, a significant but unequally distributed Linnean shortfall exists with the caddisflies. In this presentation, I discuss cases of unresolved taxonomy of this fascinating group of insects, highlighting challenges and opportunities for aquatic entomologists.

9829 - Behavioral and Morphological Insights into Water-Associated Ecological Classification of *Pteroptyx* Fireflies

Wanvimol Juneau

Agnes Scott College, Decatur, GA

Beetles (*Coleoptera*) are often difficult to designate as aquatic, semi-aquatic, or terrestrial due to unclear parameters for these classifications, as well as diversity within the order. Our study investigates behavioral diving patterns and morphologies of *Pteroptyx valida*, *Pteroptyx malaccae*, and *Pteroptyx tener* via scanning electron microscope (SEM) imaging to assess and potentially correct their current terrestrial classification while simultaneously contributing to refining the current parameters of water-associated classifications in Coleoptera. We hypothesize that if *Pteroptyx* larvae show behavioral patterns that suggest statistical inclination towards breaching water in an intertidal zone and opened eversible respiratory organs during submersion, it will provide strong evidence for reclassifying these *Pteroptyx* fireflies as semi-aquatic. The behavioural diving experiments reflect the natural environments during firefly larval stages, which include aquatic, sloped, and terrestrial zones. Larvae were placed in a dry aquatic zone which was then gradually flooded to mimic the tide. Diving or escaping behaviours and total time spent in water was recorded for further analysis. Results assessed possible statistical significance of diving and escaping during tidal cycles, providing insight into whether *Pteroptyx* fireflies exhibit terrestrial or semi-aquatic behaviors. SEM imaging was conducted, with a focus on eversible respiratory organs. Both specimens submerged in water and out of water were frozen and preserved for observation and analysis. We will examine the eversible organs to see if they are open or closed. Future results will determine if these organs play a role in underwater respiration. SEM images will also reveal whether functional eversible organs during submersion are a morphological adaptation to water, a characteristic commonly found in semi-aquatic beetles. Overall, our study seeks to clarify ecological classifications of *Pteroptyx* fireflies contributing to a more precise understanding of *Pteroptyx* firefly behavior and morphology in water-associated environments, and refining the parameters used to distinguish aquatic, semi-aquatic, and terrestrial species.

9830 - Assessment of spatial and temporal variation in relative frequencies of alternative reproductive tactics in the Blue Ridge Two-Lined Salamander (*Eurycea wilderae*)

Cooper Kework[1], Todd W. Pierson[2]

[1]Kennesaw State University, Kennesaw, GA, [2]Department of Ecology, Evolution, and Organismal Biology, Kennesaw State University, Kennesaw, GA

Alternative reproductive tactics (ARTs) are discrete intrasexual differences in reproductive behavior and are often accompanied by morphological differences. In the Appalachian Mountains, ARTs exist in populations of the Blue Ridge Two-Lined Salamander (*Eurycea* cf. *wilderae*) in the form of "searching" and "guarding" males. Searching males perform courtship mostly terrestrially. During their reproductive season, searching males develop elongated cirri that help detect and locate potential mates. On the other hand, guarding males are found more frequently at aquatic nesting sites and develop hypertrophied jaw musculature utilized in aggressive mate-guarding behavior. The long-term maintenance of these two distinct reproductive tactics raises many questions, including what evolutionary mechanisms may support their coexistence. For example, we hypothesize that spatial and temporal heterogeneity may create distinct reproductive niches that support the persistence of each male phenotype. Here, we present *Eurycea* ART frequency data from: 1) ten sites (five small stream and five large stream environments) sampled in a single season (Summer 2024); and 2) a single small stream site sampled in three consecutive years. To do this, we collected tissues, extracted DNA, and used a PCR assay to genotype more than 1,300 salamanders. Understanding how the frequencies of these ARTs vary across space and time within their heterogeneous habitats will provide a better understanding of the maintenance of this polymorphism. These findings will also contribute to a more general understanding of the ecology and evolution of ARTs.

9833 - Those Dam Parasites: How Human activity impacts the parasite communities of fishes surrounding Allatoona Dam over time

Mr. Nicholas Tsangarides, Jade Salis, Whitney Preisser

Kennesaw State University, Kennesaw, GA

Anthropogenic climate change and growing human populations will put immense pressure on the natural environment. The need for access to water drives governments to build reservoirs by way of damming rivers and streams. Damming waterways can cause devastating changes in biotic communities; specialist fish species can be pushed to extirpation and even extinction after the damming of a reservoir, as generalist species tend to take over after a large disturbance. However, less is known about how parasites of fishes respond to such changes in the host community. We predict that generalist parasites and those with direct lifecycles will have a greater prevalence than specialist species in areas impacted by reservoir damming and other human activity. To assess the validity of the predictions, we used fluid-preserved fish specimens that were collected from 1999 to 2016 in the Etowah River catchment around Allatoona Dam in northwest Georgia, USA. We dissected each fish specimen for their parasites, removing them from host tissues and identifying them to the lowest taxonomic level. Latent environmental variables from each of the 57 sampling sites, such as land use and impervious surface percentages, were accessed through the United States Geological Survey. We analyzed the potential impacts of these anthropogenically altered variables on parasite communities from 316 number of fish specimens using various models. The preliminary results of these analyses and their implications will be discussed.

9850 - Presentation Withdrawn

9869 - Using iNaturalist to Engage Students in Biodiversity Inventories

Annkatrin Rose, Marta Toran

Appalachian State University, Boone, NC

University campuses provide conveniently positioned habitats for biodiversity studies. In October 2022, Appalachian State University joined UNC Greensboro (and since 2023 UNC Wilmington) in a friendly BioBlitz competition aimed at raising student awareness of biodiversity on campus. We have conducted this BioBlitz three times at AppState so far (in fall 2022, spring 2023, and fall 2023), utilizing iNaturalist as an online platform to engage students in creating a comprehensive biodiversity inventory of campus properties, discovering undocumented species, and monitoring invasive species. Participants have consistently added new species, particularly plants, fungi, and invertebrates, with more still to be found and identified. The project has bridged various disciplines and roles within the university, attracting participation from a wide range of majors, faculty, staff, and community members, with most active participants being students spurred by the competitive nature of the event. The first iteration of the BioBlitz saw many new iNaturalist users making casual observations, primarily of cultivated plants. This shifted to fewer casual and more wild observations after providing additional training material to participating instructors and students. We found participation tends to be higher in the fall, with new recruits compensating for any losses in the spring. Unfortunately, hurricane Helene canceled our 2024 BioBlitz, but we are curious to see how

it changed the campus landscape and biodiversity in future iterations. It is our hope that keeping the competition going not only fosters a deeper understanding of local biodiversity but also strengthens community ties and promotes environmental stewardship among students and the broader community.

9873 - Benthopelagic divergence in Percidae impacts trait, lineage and ecological diversification: a case of ecological filtering or exaptation

Jessica Arbour

Middle Tennessee State University, Department of Biology, Murfreesboro, TN

Ecological filtering and exaptation are linked concepts in which prior adaptations facilitate transitions to new habitats or niches, sometimes by being co-opted for a new function (e.g., feathers in dinosaurs). We investigated possible ecological filtering/exaptation in Percidae, a diverse clade of freshwater fishes that shows its highest diversity in small benthic fishes living in creeks and small streams in the Nearctic (the Etheostomatinae "Darters"), but also includes pelagic and larger river species. We hypothesize that traits associated with transitions to benthic living (e.g., loss of the gas bladder, body size and shape) subsequently facilitated the colonization of small river habitats. We collected ecological and body size data for 201 species, and whole body 3D shape data using an Artec Space Spider structured light scanner and 3D geometric morphometrics for 89 species. Using phylogenetic comparative approaches, we found that transitions to small river habitats were dependent on prior transitions to strictly benthic lifestyles, but not vice versa. Based on body size and body shape datasets we found that selection towards smaller bodies and longer caudal peduncles in benthic species in large rivers appears to have enabled transitions to small rivers; but this also considerably slowed rates of shape and size evolution in darters, biasing transitions between habitats. Pelagic species also colonized small rivers, but at a much lower rate and tended to frequently transition back to large river habitats, and similarly showed selection to small body size in these habitats. Small rivers may serve as a stable refugia for benthic percids, while providing cradles of diversification for more mobile pelagic species. As a result, ecological filtering and exaptation may impact both the biodiversity and phylogenetic composition of fish assemblages in small Nearctic streams.

9875 - Using Terrestrial Laser Scanning to Evaluate the Impacts of Forestry Management Practices on the Understory Complexity of a Longleaf Pine Savanna in Southern Mississippi

Noah Williamson, Kayla Stan

University of Southern Mississippi, Hattiesburg, MS

One of the most important ecosystems to the Southeastern United States is the longleaf pine savanna, supporting a diverse variety of herbaceous flora and endemic fauna. However, due to various destructive practices, this ecosystem has been reduced to 3% of its original range. The intent of this study is to understand how the longleaf pine savanna ecosystem responds to different management practices including Fire Suppression, Annual Prescribed Burning, Mulching, Herbivore Grazing, and how these practices influence the understory complexity. To do so, an affordable terrestrial laser scanning (TLS) system was used to generate point clouds of areas experiencing different treatments. From these point clouds, an Understory Complexity Index (UCI) value was calculated and used to compare the complexity of each treatment. Overall we found that regular prescribed burning, often considered necessary for longleaf pine savanna health, produced the least complex understory. Grazing also produced a uniform, low complexity understory. Both mulching and fire suppression treatments produced a highly complex understory. These findings help further the understanding of these endangered ecosystems, provide a solid foundation for future comparisons, and refine an accessible metric for comparing ecosystems.

9879 - What lies beneath: Fungal associations of native *Dionaea muscipula* (Venus Flytrap) roots.

Anna Carnaggio, Michelle Barthet

Coastal Carolina University, Conway, SC

Dionaea muscipula, commonly known as the Venus Flytrap, is well known for its carnivorous leaf trap but little is known regarding fungal associations of this interesting plant species. *D. muscipula* is a plant native to the nutrient poor acidic soils found in the rims of the Carolina Bays located in the southeast corner of North Carolina and the northeast corner of South Carolina. *D. muscipula* has a vestigial root system compared to non-carnivorous plants suggesting that an alternative mechanism is used to increase nutrient acquisition from the surrounding nutrient poor soils. Although the carnivorous leaf trap provides increased nutrients through insect digestion, previous studies demonstrated that nitrogen as well as other nutrients in the roots are not sourced from insect digestion but instead acquired primarily from the roots themselves. The combination of the vestigial root system and the nutrient poor soils suggest that *D. muscipula* must rely on another mechanism for increasing nutrient uptake from the soil such as mycorrhizae. We instigated the first investigation into fungal associations of native *D. muscipula* roots. We provide evidence for the presence of arbuscular mycorrhizae as well as species of endophytic fungi in *D. muscipula* roots that may contribute to the success of this plant species in the Carolina Bays ecosystem.

9884 - PAR-1 Activation Interferes with Normal Axon Development in C. elegans through the PLC and ROCK Pathways

Isabel Greco, Victoria Turgeon

Furman University, Greenville, SC

Thrombin, an enzyme in coagulation, also affects neurons through the protease-activated receptor-1 (PAR-1), a G-protein coupled receptor. Neuronal PAR-1 activation appears to impact cell survival and axon formation through downstream activation of Phospholipase C (PLC) and Rho-kinase (ROCK). While the PLC pathway is responsible for axon depolymerization, the ROCK pathway regulates overall axon polymerization. Therefore, understanding thrombin's role in axonal growth is crucial, as vascular damage following injury leads to thrombin accumulation in the nervous system and the subsequent activation of these pathways. In *Caenorhabditis elegans*, embryonic exposure to thrombin causes axon deformities, but its specific mechanism is unclear. This study aims to clarify PLC and ROCK signaling in thrombin-mediated axon development in *C. elegans*. If either pathway is involved in thrombin-mediated axon development, then inhibiting both should prevent the creation of axon deformities. To examine axon formation, *C. elegans* eggs were exposed to one of six conditions: control, PAR-1 activation (100 mM thrombin), Rho-kinase inhibition (250 mM Y27632), PLC inhibition (100 mM U73122), Rho-kinase inhibition + PLC inhibition, and PAR-1 activation + Rho-kinase inhibition + PLC inhibition. A Kruskal-Wallis rank sum test and Wilcoxon post-hoc test (95% CI) showed a significant difference in the percentage of axon deformities between all the groups. Overall, the PAR-1 activated group co-treated with PLC and ROCK inhibitors had the most axonal deformities compared to other groups, demonstrating that thrombin binding to PAR-1 activates both pathways resulting in abnormal axons. Understanding how the pathways are initiated upon PAR-1 activation interact and relate to each other provides insight into how thrombin interferes with axon growth following injury.

9894 - Prevalence of Trypanosoma cruzi in populations of Nine-Banded Armadillo (Dasypus novemcinctus) in Southwest Georgia: Implications for Chagas Disease and Public Health.

Richard A. Matthews[1,2], Douglas S. Wright[3,4]

[1]Old Dominion University, Norfolk, VA, [2]Abraham Baldwin Agricultural College, Bainbridge, GA, [3]Abraham Baldwin Agricultural College, Tifton, GA, [4]Auburn University, Auburn, AL

Chagas disease, or American Trypanosomiasis, is caused by the flagellated protozoan parasite *Trypanosoma cruzi*, and is spread by kissing bug vectors in the subfamily Triatominae. The disease is of major social and public health concern in Latin America and has been regarded as a neglected tropical disease by the World Health Organization. It affects many poor and disadvantaged people, and the estimated annual global burden of the disease is between $627-646 million in health care costs. The disease has also been reported in the southern United States.

In this study, we examined the prevalence of *Trypanosoma cruzi* in sylvatic populations of nine-banded armadillo (*Dasypus novemcinctus*) in Southwestern Georgia. We collected heart tissue from 50 road-killed and hunter donated armadillos from 2019 to 2024. The presence of *T. cruzi* DNA was determined using real-time PCR methods. Threshold values (Ct) below 24 were considered positive for *T. cruzi.* The data are expected to be consistent with other studies conducted in rural Georgia. Knowledge of the prevalence of these pathogens in reservoir populations can lead to a better understanding of the risk of infection and can have important implications for disease management in these areas.

9897 - Examination of control methods to kill Chinese Privet (*Ligustrum sinense*) in a Tennessee State Park

Jordan Brison

TN State Parks, Chattanooga, TN; University of Tennessee-Chattanooga, Chattanooga, TN

Chinese Privet (*Ligustrum sinense*) is an invasive shrub species that has spread throughout the Southeastern forests of the United States. Forming dense thickets that can lead to a decrease in native plants, forest succession and decrease native pollinator abundance. Land managers seek to control this invasive species before it can be established but in areas that already have dense *Ligustrum sinense* groves must weigh the best method for removal. Direct heat, herbicide and a combined method were completed over a Fall and Spring season to compare efficacy, cost, and time spent for removal. The study indicates that a combined method of herbicide and direct heat treatment may be the most effective and could indicate the ability to lower concentration of herbicide used in areas with sensitive plants or other concerns.

9898 - Material and mechanical properties of the mandibles of the invasive granulate ambrosia beetle, *Xylosandrus crassiusculus* (Curculionidae), through different life stages and sexes.

Kendall Myers[1], Jessi Raubenolt[2], Lingyan Li[3], Christopher Ranger[2], Matthew Lehnert[1]

[1]Kent State University at Stark, North Canton, OH, [2]Ohio State University, Wooster, OH, [3]University of Akron, Akron, OH

The granulate ambrosia beetle, *Xylosandrus crassiusculus*, is native to Asia and is currently considered an invasive species in North America. These beetles have a unique life history in that the females use their mandibles to bore holes into sickly trees, creating galleries that are used to farm their fungal symbiont, which they feed on. This process suggests that the mandibles must be significantly hard in order to bore through the wood, and cuticular hardness among insects has been associated with the presence of transition metals. Here, we hypothesized that the distal regions of the mandibles have high concentrations of transition metals to enable boring, and these concentrations are higher in the mandibles of females as compared to the mandibles of adult males and larval life stages. To study this, we employed confocal microscopy, energy dispersive x-ray spectroscopy, and nanoindentation to study the material and mechanical properties of the mandibles. Through confocal microscopy, we found that the females had significantly higher amounts of red autofluorescence, indicating high levels of sclerotization. In addition, the concentrations of the transition metal zinc in the tip regions of the female mandibles were significantly higher than other mandible regions, and the mandibles of females also had higher concentrations of zinc than the mandibles of adult males and larval life stages. Our hardness tests with nanoindentation confirmed that the regions with high levels of zinc were also significantly harder than other regions. These findings help explain the successfulness of this invasive species in its ability to damage trees and provides insights into the mechanism by which insects acquire transition metals for cuticle augmentation.

9914 - Scientific Illustration of Amphipod Crustaceans from Sapelo Island, GA

Kali Holierhoek[1], Kristine N. White[2]

[1]Georgia College and State University, Milledgeville, GA, [2]University of Tampa, Tampa, FL

Amphipod crustaceans inhabit most aquatic ecosystems. Despite their small size (2–15 mm), amphipods are an important food source for larger organisms, recycle nutrients, and maintain ecosystems by acting as ecological links. Because of their imperative roles, amphipods can be used as important bioindicators to assess the health and stability of their ecosystems. Coastal marine amphipods are poorly studied in the state of Georgia. The goal of this study was to document amphipods from Sapelo Island, Georgia, as the first step in understanding amphipod diversity within the state. Amphipods were collected, identified, and imaged to create a preliminary checklist and identification key. The next step is to illustrate the amphipod structures used in the identification key to aid experts and non-experts alike when identifying amphipods. This addition to the key will allow amphipods to be easily identified and incorporated into ecological studies as bioindicators of the health of their environments.

9920 - A Snapshot of Intertidal Crustaceans from Sapelo Island, GA

Elise Mirabella[1], Kristine N. White[1,2]

[1]Georgia College & State University, Milledgeville, GA, [2]University of Tampa, Tampa, FL

Intertidal crustaceans play important roles in marine ecosystems as they are a primary food source for fish and other invertebrates and can act as bioindicators for the health of the environment. The intertidal zone, the area between high and low tide, supports a diverse group of organisms, but wave action can have a large impact on the distribution of intertidal crustaceans. Both the diversity and impact of wave action on intertidal crustaceans are poorly studied in coastal Georgia. Therefore, intertidal crustaceans were collected from one protected and one exposed beach at Sapelo Island to document the diversity and to aid in understanding the effect of wave action on the distribution of intertidal crustaceans. Three sampling methods were used: D-net, beam trawl, and yabbi-pump to eliminate bias in collection method. Crustaceans were then identified and quantified. As hypothesized, the exposed beach had a higher biodiversity than the protected beach based on both abundance and species richness. These data will aid in incorporating intertidal crustaceans in regional ecological studies and monitoring programs.

9922 - Oak mistletoe, *Phoradendron leucarpum* (Viscaceae), alters host tree architecture

Nicholas Flanders, Lytton Musselman

Old Dominion University, Norfolk, VA

Oak mistletoe is the best-known parasitic plant in the Southeastern United States and though common remains little studied. Like all parasitic plants, mistletoes form a haustorium which is the morphological and physiological bridge between host and parasite. We report the effect of mistletoe infection on the growth patterns of trees as well as the increased morbidity and death of the host. These impacts

are due to the unique life history of the parasite, including germination, attachment, penetration, and hypodermal spread via strands extending from the point of haustorial attachment and breaking through the host bark to produce new plants. The stem distal to the haustorium dies and the terminal infection produces a swelling composed of mistletoe and host tissue. We suggest the term lignotuber for this unique structure, also known as woody galls. As the lignotuber grows, host stems emerge in a fastigiate pattern from the tip of the lignotuber. In older trees, most prominently tupelo (*Nyssa aquatica*), lignotubers can be very large and contort the host tree in a dramatic way. While the anatomical features of parasitism in this species have been studied, the impact on tree architecture has received scant attention despite the obvious impact on forest ecology.

9926 - Some insects breathe with their mouths: Gas exchange in the elongated proboscises of Lepidoptera

Matthew Lehnert

Kent State University at Stark, North Canton, OH

Insects rely on a vast network of tubes, the tracheae, to transport respiratory gases from spiracles on the body wall to tissues inside the body. For butterflies and moths (Lepidoptera), this would require the respiratory gases to also travel through the elongated mouthparts (proboscis), which can attain lengths up to 30 cm in Darwin's sphinx moth. How Lepidoptera overcome the challenge of gas exchange through the tracheae of the proboscis remains an open question. Here, we show with x-ray imaging that the distance effects of gas exchange are overcome by previously unreported micropores on the proboscis surface and by superhydrophobic tracheae that prevent water loss and entry. We find that micropore dimensions support the diffusion of respiratory gases. We consider these adaptations as key innovations vital to proboscis elongation, which facilitated lepidopteran biodiversification.

9937 - The Effects of Female Age on Eastern Bluebird White Blood Cell Counts

Kiley Nansel, Jennifer Newbrey, Michael Newbrey

Columbus State University, Columbus, GA

Female birds can experience age-related changes in their health across their lifespans, but most bird species do not exhibit post-reproductive life stages like many species of mammals do. Prior reproductive effort can also affect the health of female birds and impact their future reproductive success, which has been previously shown in several bird species. To better understand the effects of female age on the health of female birds, we quantified heterophil to lymphocyte ratios (H:L) of 24 known-age female Eastern Bluebirds (Sialia sialis) using white blood cell counts obtained from blood smears. To determine if H:L ratios varied significantly with female bluebird age, we analyzed the H:L ratio data using One-way Analysis of Variance (ANOVA) with Least Significant Difference post hoc tests. The results of the ANOVA showed that H:L did not vary significantly with female age in Eastern Bluebirds, which suggests that immune system function did not decline as female bluebirds aged. However, when examining H:L ratios of individual female bluebirds, we did find that H:L ratios varied across their lifespans, which is likely due to unique health challenges they experienced at different times in their lives.

9943 - Increased EMG activity supports the presence of movement evoked reflexes during the tail nociceptive withdrawal response

Emily Myers, Linda Wenger, Corey Cleland

James Madison University, Harrisonburg, VA

The nociceptive withdrawal response (NWR) is a response to noxious stimuli that causes the movement of a limb or appendage away from the stimulus. Previous behavioral studies from our laboratory demonstrated that the heat-evoked NWR of the rat tail consists of four components: local bend, caudal bend progression, tail-based rotation, and tail stiffening. We hypothesize that tail stiffening is an evolved mechanism to lessen the neural computational burden the CNS faces during the NWR. The specific aim of this study is to determine if movement evoked reflexes contribute to tail stiffening during the NWR by comparing electromyographic (EMG) responses to noxious heat stimuli during *movement* and *isometric* (no movement) conditions. In adult rats (n = 7), fine-wire EMG electrodes were inserted bilaterally into 8 tail muscles (6 intrinsic, dorsal lateral; 2 extrinsic; M. sacrocaudalis dorsalis). The NWR was then evoked using a heat stimulus (980 nm laser diode) applied bilaterally to 12 locations distributed rostral-caudally on the tail. The tail was secured to a rigid rod to confine tail movement to rotation at the base of the tail. Tail responses were recorded in two conditions: *isometric* (no tail-based rotation, accomplished by fixing the rigid rod during the trial) and *movement* (tail-based rotation), using high-speed video. Our results revealed the presence of increased EMG activity, especially in the intrinsic tail muscles, during *movement* trials when compared to *isometric* trials, which is consistent with the presence movement evoked reflexes. Our results suggest the presence of movement evoked reflexes such as the stretch reflex in the intrinsic tail muscles during the NWR, which may contribute to tail stiffening.

9952 - A History, Summary, and Description of the Vascular Flora of Tennessee

Joey Shaw

University of Tennessee at Chattanooga, Chattanooga, TN

Augustin Gattinger (1901) provided the first detailed vascular plant checklist for TN, but writing keys remained elusive until a symposium on the flora and vegetation of Tennessee (Chester, 1989) focused workers on a 25-year, three-phased plan to produce a revised checklist, plant atlas based on authenticated county records, and a cumulative guide with keys, family treatments, and other information. The first edition of the *Guide to the Vascular Plants of Tennessee* was published in 2015. Publication sparked growth in botanical knowledge as workers began presenting evidence for omitted species or expanded distributions. From 2015-2019, though funding from the National Science Foundation (#1410087 & #1756382), J. Shaw and others led a statewide effort to barcode, image, and database Tennessee's herbaria as part of the larger SERNEC initiative. At the time writing the second edition, over 340,000 Tennessee-collected herbarium specimens were available online, significantly enhancing our understanding of Tennessee's plant species and distributions. It is from this totality of specimens that the Tennessee-Kentucky Plant Atlas, a companion to the second edition was created in 2021 (https://tennessee-kentucky.plantatlas.usf.edu/). Publication of the second edition of the *Guide* is expected in fall 2025. Today, our cumulative knowledge of Tennessee's flora contains 3153 species (2640 native, 513 naturalized) within 921 genera and188 families. Our native flora of 2640 species and lesser taxa is represented by 747 genera and 177 families. To the second edition were added 156 species or lesser taxa (84 native and 72 nonnative) that are either historic, likely to be part of our flora because they are known from adjacent counties of neighboring states, or ubiquitous ornamental taxa likely to be encountered. In total, this second edition contains keys and descriptions to 3310 species and lesser taxa as well as notes or accounts of several hundred other taxa reported or present but not naturalized.

9959 - Characterization of the Interaction Between Adenoviral Protein E4 11k and the DNA-PK-dependent DNA Damage Response

Kindle Reeves, Heather Vincent, Kasey Karen

Georgia College & State University, Milledgeville, GA

Adenovirus (Ad) can cause upper respiratory infections, gastroenteritis, and conjunctivitis. The linear, double-stranded DNA Ad viral genome can be broken up into early and late phase genes. Our protein of interest, E4 11k, is a product of one of the early genes that works to disrupt normal cellular function to enhance the viral replication cycle. One of the mechanisms E4 11k uses to achieve this disruption is through the inhibition of the DNA damage response (DDR). The DDR is responsible for repairing double-stranded DNA breaks (DSBs) through non-homologous end joining (NHEJ). During DDR, DNA-dependent protein kinase (DNA-PK) becomes activated via phosphorylation. During an infection, Ad's genome triggers the DSB repair pathway due to the genome's structural similarity to a cellular DSB. The DDR tries to "repair" the viral genome by ligating the viral genomes into concatemers, disrupting viral DNA replication. Ad, however, has evolved mechanisms to prevent activation of the DDR. Previously, E4 proteins have been shown to regulate the activation of DNA-PK. In this study, we aim to determine E4 11k's ability to inhibit DNA-PK phosphorylation in response to cellular DSBs. HeLa (cervical cancer) cells were treated chemically with different combinations of either etoposide (drug that induces DSBs), Nu771 (inhibitor of DNA-PK phosphorylation), or an Ad E4 11k only viral infection. The phosphorylation status of DNA-PK was analyzed through immunoblotting. In addition, we want to characterize DNA-PK localization during an Ad infection. Immunofluorescence microscopy was also used to visualize protein localization. Our results indicate that E4 11k is a novel inhibitor of DNA-PK activation. It has also been shown that etoposide treatment combined with the inhibition of DNA-PK activation results in cancer cells that have less adherence. These findings suggest a potential mechanism for which E4 11k can be used as a novel chemosensitizer for therapy-resistant cancer cells.

9961 - You Can Help Cure Blood Cancers & Diseases

Matthew (Matt) Kroeger

NMDP. Find Cures. Save Lives., Minneapolis, MN

Each year more than 12,000 people in the United States are diagnosed with a blood cancer (including leukemia and lymphoma) or blood disease (such as sickle cell disease). 70 percent of patients who need a blood stem cell or bone marrow transplant DO NOT have a fully matched genetic donor within their family. When they need to find a donor they turn to NMDP, who has managed the most diverse registry in the world for more than 35 years and impacted more than 137,000 lives. At NMDP, we believe we believe each of us holds a key to cure blood cancers and disorders. With the help of blood stem cell donors from the world's most diverse registry and our extensive network of transplant partners, physicians and caregivers, we are expanding access to treatment so that every patient can receive their life-saving cell therapy. Information will be shared on how the patient & donor matching process works; the donor experience; and how students, faculty, staff and others can join the life-saving movement.

9964 - Enhancing *Sarracenia leucophylla* Germination: The Role of Water and Substrates

Kevin Kelly[1], Julie Ballenger[1], Kerri Shelton[1], Ramneet Kaur[2]

[1]Columbus State University, Columbus, GA, [2]Department of Biology, University of North Georgia, Oakwood, GA

This research investigates the optimal germination conditions for *Sarracenia leucophylla*, a carnivorous plant species adapted to nutrient-poor environments. Understanding the germination requirements is crucial as instances of habitat loss and climate change rapidly increase, for plant conservation. This study focuses on substrate selection and water treatments required for achieving the highest germination rates. Seeds undergo a 6-week cold stratification at 3.8°C/39°F before being planted in three different substrate combinations: peat moss/perlite, peat moss/sand/sphagnum, and coco coir/perlite. Water treatments include distilled water, distilled water with GA_3, and an H_2O_2/water mix. Germination and growth will be monitored for 60 days, with data collected on plant height, number of pitchers, number of cotyledons, and dry weight. Hormone testing will assess gibberellic acid (GA) and abscisic acid (ABA) levels during the various germination stages to better understand their impact on germination. The study anticipates that the peat moss with GA_3 treatment will yield the highest germination rates, contributing valuable insights for both horticultural use and conservation efforts aimed at preserving *Sarracenia leucophylla*.

9981 - Diversity of Panamanian Amphipods (Crustacea) Within the Parvorder Caprellidira

Sally Sir, Kristine N. White

Georgia College & State University, Milledgeville, GA

Marine amphipod crustaceans inhabit many ocean habitats and support higher trophic levels, acting as a food source and breaking down detritus. They can be used as bioindicators measuring the health of their environment due to their sensitivity to pollution and disturbance. The amphipod parvorder Caprellidira contains 1244 described species in 17 families and typically inhabits coral rubble, seagrasses, sponges, algae, and sand. These amphipods are also common fouling organisms exhibiting a diversity in their morphology and ecology. Caprellidiran amphipods are detritivores that frequently feed on decaying organic matter in the water column. Enlarged antennae support this feeding strategy by catching drifting matter, in turn recycling the nutrients back into the environment. 70 Caprellidiran species had previously been documented within Panamanian waters, with only one species, *Paracaprella barnardi* (McCain, 1967), documented from Caribbean Panama which seems unlikely based on the known diversity of the area. Collections from 2005, 2009, 2021, and 2023 revealed the presence of 20 Caprellidiran species from Bocas del Toro, Panama, five of which are new to science. All species collected are diagnosed and described herein. This study provides species list and dichotomous key to the Caprellidiran amphipods of Panama, both of which may be applied to a variety of projects including those associated with environmental monitoring in Bocas del Toro, Panama.

9983 - Stable isotope analysis reveals demographic variation in diet between adult and juvenile eastern box turtles

John Roe, Kathryn Davis

University of North Carolina Pembroke, Pembroke, NC

Box turtles are generalist omnivores that play potentially important roles of seed and spore dispersal and nutrient cycling in forest ecosystems. Box turtles can eat a wide variety of foods, but little is known about how diet varies among individuals within a population or how populations in different environments vary in diet. Here, we examined sources of variation in diet within and between two populations of Eastern Box Turtles (*Terrapene carolina carolina*) using carbon (^{13}C) and nitrogen (^{15}N) stable isotopes sampled from claws and compared isotope values of turtle tissues to that of locally available food sources to determine the primary foods consumed. Isotope values did not vary between populations in Coastal Plain and Sandhills regions. ^{15}N values varied from 1.1 ‰ to 8.6 ‰ and ^{13}C values from -24.8 ‰ to -21.0 ‰ among individuals, a range spanning two to three trophic levels. ^{15}N values remained consistent within individuals over time, and both ^{15}N and ^{13}C values increased with body size. Isotope mixing models indicated adult diets were comprised of 56% mushrooms, 41% animals, and 3% plants, while juvenile diets were comprised of 71% animals, 17% plants, and 13% mushrooms. Direct observations of foraging for radiotracked turtles generally supported isotope mixing model results. Demographic variation and individual specialization in diet may have important ecological, evolutionary, and conservation implications, especially when concerning how local resource management practices may impact food resource availability and abundance in forest ecosystems.

9987 - Seeing the Spectrum: Investigating Color Vision in Freshwater Crayfish

Katherine Torrance, Zackary A. Graham

Department of Biological Sciences, West Liberty University, West Liberty, WV

The visual abilities of crayfishes are understudied. In the context of color vision, physiological evidence suggest that crayfishes are either monochromatic or dichromatic. However, there are no behavioral studies that support or refute these findings. Using classical conditioning, we test the hypothesis that crayfish are dichromatic and can differentiate between colored shelters from non-colored shelters. Shelters were provided in seven different shades of gray and four shades of blue for each crayfish in each tank to represent achromatic and chromatic stimuli, respectively. Blues were selected to have brightness values near their gray counterparts to prevent the crayfish from using brightness/achromatic cues to differentiate them. Thus far, thirteen *Cambarus monongalensis* were provided a randomized order of shelters. Shelters were randomized again every other day for sixteen days. At the same time each day, one commercial crayfish pellet was provided in a randomly chosen blue shelter. On the seventeenth day, the crayfish were no longer provided food, and their location and behavior in the tank was monitored for the next four days. Preliminary results show that crayfish resided in gray shelters more frequently than blue shelters overall.

9990 - Field Botany Made Easy: A Practical Guide for Educators

Kunsiri Chaw Grubbs

Winthrop University, Rock Hill, SC

Field botany courses present unique educational opportunities and challenges that requires a blend of theoretical and practical knowledge to be successful in local outdoor environments. This presentation is designed to share tips and techniques for educators to use to enhance students' learning experiences in field botany courses. The talk emphasizes the importance of preparation and planning by encouraging instructors to familiarize themselves with local flora and field sites in advance. This presentation highlights effective planning and the design of detailed excursions that are focused and aligned with curriculum goals for the course. This includes examples of engaging learning activities, such as plant identification exercises and assignments, along with diverse assessment methods like field journals, quizzes, and group projects. Additionally, considerations for ensuring student safety during field trips are included. Furthermore, the session emphasizes the importance of teaching ethical practices in plant collection and conservation to foster responsible future botanists. Ultimately, the presentation aims to demonstrate how field botany courses can encourage curiosity and critical thinking by motivating students to ask questions, make observations, and engage in discussions that deepen their appreciation of plant diversity and ecological relationships. By implementing these strategies, field botany experiences can become more dynamic and effective learning environments that equip students with the knowledge and skills valuable for their future careers and personal lives.

9991 - Transcriptomic Analysis of the Endangered Manatee: Identification of Immune-Specific Gene Signatures

Mackenzie McKillop[1], Annalaura Mancia[1], Anmari Alvarez-Aleman[2], Jamal Galves[2], Celeshia Glaves[2], Antonio Mignucci-Giannoni[3], Carla Rivera-Perez[3]

[1]Jacksonville University, Jacksonville, FL, [2]Clearwater Marine Aquarium, Clearwater Beach, FL, [3]Ross University School of Veterinary Medicine, Basseterre, Saint Kitts and Nevis

The West Indian Manatee (Trichechus manatus) consists of two endangered subspecies: the Florida manatee (T. m. latirostris), found in the southeastern United States, and the Antillean manatee (T. m. manatus), which inhabits various coastal areas across the Americas, from Mexico to Brazil, including the Greater Antilles. These species face threats such as habitat destruction, human interference, climate change, and harmful algal blooms. Current conservation efforts do not focus on molecular-level responses, which are essential to fully comprehend the health status of the species. Although genomic data is available for the Florida manatee, little is known about the Antillean manatee subspecies. Each tissue expresses specific genes, or RNA transcripts, which, taken together, form the tissue transcriptome. This study aims to analyze the skin and blood transcriptomes of the Antillean manatee, two tissues vital for immunity. RNA extraction methods are being optimized using blood and skin samples collected from live-captured individuals in Belize and Puerto Rico, from both healthy and diseased animals. High-quality RNA will be sequenced to identify genes associated with skin and blood functions and to uncover gene signatures that reflect immune responses linked to environmental threats. These gene signatures will also be used to explore the transcriptome of the Florida manatee to relate immune mechanisms to population-specific challenges. Understanding the resilience mechanisms of these species to environmental changes is crucial for improving conservation efforts for vulnerable and endangered populations. This project proposes to characterize the transcriptomes of the skin and blood from selected T. manatus individuals. Acquisition of RNA data from the skin and blood can be extremely useful for understanding skin physiology, diseases and health status.

10010 - *Streptococcus equi* subspecies *equi* biofilm formation and role in environmental and host persistence

Hannah Blanton, DeLacy Rhodes

Berry College, Mt. Berry, GA

Streptococcus equi subsp. *equi* (SEE) is a globally significant equine pathogen and is the causative agent of the highly contagious disease, strangles. Strangles is characterized by a severe upper respiratory infection with abscessed lymph nodes that may rupture and disrupt breathing. SEE persists well in hosts, resulting in chronic infections that can be both symptomatic and asymptomatic, yet the pathogenicity of SEE is poorly understood. One virulence strategy that allows many bacterial pathogens to persist inside of a host is the formation of biofilms. The purpose of this study was to investigate SEE biofilm formation and the role that SEE biofilms potentially play in antibiotic susceptibility and environmental persistence. To determine if SEE is able to form biofilms, *in vitro* microtiter biofilm assays were performed with both a lab strain and clinical isolates of SEE. These assays showed that SEE forms biofilms optimally when supplemented with 6% sucrose and incubated for 48 hours with 5% CO_2. Once a biofilm assay protocol had been established, antibiotic assays testing four different antibiotics were performed utilizing SEE growing both planktonically and in biofilms. Additionally, soil samples were taken from two horse stables and isolates of soil bacteria were co-cultured with SEE in a biofilm assay to investigate the role of biofilm formation on environmental persistence. Antibiotic assays showed that SEE growing in a biofilm displays a decreased susceptibility to the antibiotics amoxicillin, penicillin, tetracycline, and azithromycin while biofilm assay results with soil isolates demonstrated that SEE grows denser biofilms when assays are performed individually rather than through microbial co-culture. Collectively these results indicate that biofilm formation may play a larger role in SEE survival and persistence inside an infected horse than in the external environment. Current research is evaluating if SEE can form a tissue-associated biofilm through co-culture with mammalian cells.

10013 - Comparing current population trends with previous population viability analysis predictions

Pamela Rueda Cediel[1,2], Jake M Ferguson[1]

[1]University of Kentucky, Lexington, KY, [2]Hebrew University of Jerusalem, Rehovot, Israel

Forecasting population dynamics is crucial to develop management plans for populations at risk of extinction. This enterprise is often pursued with the use of population viability analysis (PVA). PVA consists of the use of demographic population models to determine probabilities of population extinction or establishment. We aim to test the accuracy of historical PVA, by contrasting past PVA predictions with publicly available data, to assess the relative strengths and weakness of different model structures and practices across different life histories and ecological traits of populations.

Our preliminary survey includes a density independent time series model of the Yellowstone Grizzly bear population that can be compared to 10 years of subsequent monitoring data, a stage structured model of Atlantic salmon spawners in Maine rivers to 11 years of subsequent returns, and a model of piping plovers that integrates population surveys, nest monitoring, and mark-resight data along with 7 years of subsequent abundance observations. Our preliminary results indicate that the predictions made for the Piping plover match the current status of the population, this is supported by finding consistency between the subsequent population abundances and the predicted PVA mean abundances as well as consistency of subsequent observations with the 95% prediction intervals from the PVA. In the case of the Atlantic salmon, we obtain a similar finding in which the predictions match the available data, this is supported by the positive correlation between subsequent observations and the mean abundances and the consistency of subsequent observations with the 95% prediction intervals. In the case of the grizzly bear there was no evidence to consider a match between the population viability analysis predictions and the available data. We will discuss the value of revisiting past forecasts, these and additional populations, and the conditions under which some models might fail.

10026 - *Helianthus waccamawensis*, a new species of sunflower endemic to the Cape Fear Arch region of North and South Carolina, United States.

Eric Ungberg[1], Jay Horn[2], Derick Poindexter[3], Keith Bradley[4], Alan Weakley[5]

[1]South Carolina Department of Natural Resources, Georgetown, SC, [2]Florida Gulf Coast University, Fort Myers, FL, [3]University of North Carolina at Chapel Hill, Chapel Hill, NC, [4]SCDNR Botany and Plant Conservation Program, Columbia, SC, [5]University of North Carolina Herbarium, Chapel Hill, NC

A new species of Helianthus (Asteraceae), Helianthus waccamawensis Ungberg, sp. nov., is described from the Cape Fear Arch Region of North and South Carolina. Most recently, it has been included in H. floridanus A. Gray ex Chapm. but differs in its narrower leaves, achene and floral morphology, and habitat preferences. It superficially resembles H. angustifolius L. but differs in its extensively rhizomatous habit, shorter leaves, and achene and floral morphologies. It is further differentiated from the diploids H. floridanus and H.

angustifolius by being hexaploid, and molecular phylogenetic data do not indicate a close relation to either species.

10027 - Shell histology of leatherback turtles (Testudines: Dermochelyidae) with a new specimen from the Oligocene of Alabama

Michael Burns[1], Andrew Gentry[2], Jun Ebersole[3], Kimberly Gregson[2], Emma Martinez[4], James Parham[4]

[1]Jacksonville State University, Jacksonville, AL, [2]Alabama School of Mathematics and Science, Mobile, AL, [3]McWane Science Center, Birmingham, AL, [4]Department of Geological Sciences, California State University Fullerton, Fullerton, CA

The leatherback sea turtles stand out for their extreme diving capabilities and unique carapace adaptations, which allow them to withstand deep-sea pressures and optimize physiological demands. Unlike other marine turtles, the shell comprises flexible, interlocking ossicles and lacks keratinous scutes, providing structural integrity and flexibility. This study investigates the osteology and osteohistology of a near-complete fossil leatherback shell from the lower Oligocene (Rupelian) Glendon Limestone Member of the Byram Formation in Monroe County, Alabama. Histological analysis reveals an external compact cortex, a porous cancellous core, and an absent basal cortex, consistent with adaptations seen in highly pelagic marine turtles. The lack of basal cortex distinguishes it from neritic relatives and aligns with its presumed pelagic lifestyle. This new specimen allows the opportunity to study the shell histology of this enigmatic group of turtles.

10028 - Urban Stream Syndrome Reduces Macroinvertebrate Functional Feeding Diversity in Headwater Streams

Helena Loucas, Kenneth Fortino

Longwood University, Farmville, VA

Urban Stream Syndrome is a suite of characteristics associated with streams in proximity to urbanized areas and is characterized by increased concentrations of contaminants, altered stream morphology, and reduced taxonomic richness. In streams with Urban Stream Syndrome, the chemical and physical alterations put stress on macroinvertebrate communities resulting in reductions to aquatic macroinvertebrate taxonomic diversity. Because aquatic macroinvertebrates differ in their tolerance to environmental stressors, the loss of taxonomic diversity is not equally distributed among taxa. This biased loss of taxonomic diversity has implications for stream function because aquatic macroinvertebrates are specialized feeders, and macroinvertebrate specialized feeding contributes to in-stream processes such as the decomposition of organic matter in the stream. Because some feeding groups are primarily represented by sensitive species, macroinvertebrate function is not uniformly distributed within the tolerance categories. This means a reduction in macroinvertebrate taxonomic diversity may not affect stream function uniformly, and urban streams, which have less functional diversity, are likely to have a reduction in functions such as organic matter processing. Our study compares the macroinvertebrate functional diversity of a piedmont, headwater stream impacted of the Urban Stream Syndrome to an un-affected stream. We found that each of the functional feeding groups were well represented in the non-urban stream, while the urban stream was dominated by collectors and predators with low counts of filterers and shredders and zero scrapers. Both the urban and non-urban streams were dominated by chironomids, a highly tolerant macroinvertebrate. This is the reason for the high counts of predators and collectors in both systems. Our findings so far support our hypothesis that the altered environmental conditions associated with Urban Stream Syndrome reduce the presence of intolerant macroinvertebrate taxa, ultimately altering environmental processes due to reduction in functional feeding diversity.

10034 - Phage-Host Interactions: Getting Closer to Discovering Phage Gene Functions

Jessica Morgan, Victoria Frost

Winthrop University, Rock Hill, SC

ExplosioNervosa is a bacteriophage that infects Mycobacterium smegmatis. Through both sequencing and amplification techniques, two different populations of ExplosioNervosa have been identified: a Wild-Type and a Mutant. In the mutant population, 11 annotated genes have been deleted out of the genome, the majority of which have no predicted function. This has posed questions about the effect of gene loss on overall phage biology, and phage-host dynamics. All 11 genes missing in the mutant population have been amplified, assembled into a plasmid, and sequence confirmed. These 11 genes then proceeded through a characterization technique called a cytotoxicity assay, which provides a visual indication of an interaction occurring between the phage gene product and host proteome. Cytotoxicity is identified through a decrease in host growth. Of the 11 genes, gp80 and gp81 displayed this cytotoxic character. To investigate the possible function of these genes, each proceeded through a Bacterial-2-Hybrid (B2H) Assay. A B2H assay utilizes a specifically engineered dual hybrid system that allows for the identification of the host protein that is interacting with the phage gene product. One plasmid contains the phage gene and the other contains random fragments of the M. smegmatis genome. If gene products from both plasmids interact, stabilization of the RNA polymerase occurs and allows for the expression of the reporter genes.

We then "pick" bacterial colonies expressing the reporter genes (termed "hits") and sequence the plasmid containing the M. smegmatis fragmented genome. This allows us to identify which host protein(s) the phage gene product is interacting with, and provides clues to the potential role of the phage gene under investigation. Ongoing inquiries are also examining any differences in infection timelines with regard to the presence of this mutation. In tandem, these experiments provide a glimpse into phage-bacterial host interactions, potential phage gene function, and relevance.

10036 - Microbial Biodiversity of the James River Rock Pool Ecosystem

Jordan Heydt, Kristin Yoshimura

James Madison University, Harrisonburg, VA

Rock pools are ephemeral aquatic environments formed in rock depressions by overflow from a larger surrounding body of water. They provide a unique opportunity to study complex communities and their adaptation to environmental changes because they represent a wide array of ecological environments within a small geographic area by varying in size, water depth, percent of shade cover and vegetation. Due to their small size, the microbial community composition of rock pools is tightly linked to the surrounding environment, making the system an environmental health indicator. Microbial communities provide necessary ecosystem services, therefore understanding their composition and function is vital. This information gives important insights into the specific ways these communities respond to environmental variables including river flood height, shade cover, time since last flood, etc. The unique James River rock pool system comprises over 700 individual rock pools varying in size and depth, located in a heavily trafficked urban environment. The microbial community of this system was characterized by extracting DNA from water samples, 16S rRNA gene sequencing, and analyzing taxa relative abundance with environmental metadata. The analysis of taxa across pools shows there is variation in microbial community composition of the individual pools in relation to flood height with pools at similar flood heights exhibiting similar microbial communities, suggesting that the height and frequency of the flooding pools influences microbial community composition. Further analysis of chlorophyll, nitrogen and phosphorus concentrations showed influence on the microbial community composition of the pools. Additionally, tracking the microbial community before, during, and after a seasonal flooding event showed the resilience of the microbial community, despite a disruptive event. This study provides a baseline for long-term studies investigating how the microbial community of the James River rock pool ecosystem changes over time and in response to drastic environmental conditions initiated by climate change.

10047 - Swimming behavior of longfin squid *Doryteuthis pealeii* paralarvae

Mel Lhuillier[1], Ian Bartol[2]

[1]*Old Dominion University (Department of Biological Sciences), Norfolk, VA,* [2]*Old Dominion University, Norfolk, VA*

Upon hatching, squid paralarvae must become proficient at locomotion and prey capture before their yolk reserves are depleted, while also contending with the physical constraints associated with low/intermediate Reynolds number (Re) environments. Although some aspects of behavior and jet dynamics have been examined in squids during early ontogeny, little is known about routine behaviors in paralarvae, whether repeatable patterns are employed, or how these behaviors are achieved dynamically. To better understand swimming behaviors and the propulsive flows that drive them in young squids, high-speed video data and particle image velocimetry (PIV) data were collected simultaneously from longfin squid Doryteuthis pealeii paralarvae swimming in a viewing chamber. A catalog of repeated behaviors was created along with transition matrices, behavioral percentage breakdowns, and a kinematic diagram. Jet properties, such as mean and maximum jet velocity and jet length-to-diameter ratios based on the vorticity extent, were also determined. A wide range of behaviors was identified, including vertical bobbing, spiral motions, and tail-first and arms-first swimming, with several repeatable behavioral sequences being present across paralarvae. Many of the observed behaviors involved short and long jet pulses with prominent vortex ring elements, some near or even below the Re limit of vortex-ring-based jet propulsion reported in other jet-propelled animals. The observed diversity of swimming behaviors and jet flows in paralarvae facilitates survival during a critical ontogenetic stage.

10058 - Does the presence of a generalist predator affect water quality within a southeastern pond?

Michael Bocchieri, Brian Helms

Troy University, Troy, AL

Sunfishes (Centrarchidae) have been widely used as model organisms to study food web dynamics and energy transfer within aquatic systems. However, little is known about how centrarchids affect water quality within small impoundments in the Southeast United States (SE). Given their often high abundance, we hypothesized that *L. macrochirus* regulates water quality in SE ponds. To test this, we conducted a mesocosm study on Mullis Pond, a 1-ha meso-eutrophic pond in Troy, AL. We predicted that if *L. macrochirus* is removed, nitrates, phosphates, chlorophyll-*a,* and total suspended solids (TSS) will increase, and ammonia will decrease over time. Experimental mesocosms (10 x 10 x 3 m) were constructed using 1.2 m x 3 m minnow seine mesh (6.35 mm mesh), PVC pipe, and T-posts and

placed in the littoral zone. Twelve experimental groups were randomly assigned to one of three treatments in a randomized block design: an enclosure, an exclusion, and a control group. Enclosures were stocked with ten *L. macrochirus* split into size classes based on total length (0.3 cm—0.35 cm and ³ 0.36 cm) according to observed ambient density of *L. macrochirus* from Mullis Pond. Exclusions were not stocked with fish. Control groups were created with PVC pipe without a net. Dissolved oxygen, temperature, pH, chlorophyll *a*, TSS, nitrates, phosphates, and ammonia were monitored monthly for 12 months in each mesocosm. Ammonia, nitrate, and phosphate levels ranged from 0.001 to 0.92 mg/L. Chlorophyll -*a* concentrations fluctuated from 4.604 to 75.77 Chlorophyll -*a* per ug/liter. TSS concentrations ranged from 0.689 to 86.886 mg/L. Preliminary data suggests trends show strong temporal variation with physicochemical and nutrient parameters; however, the link with fish presence is unclear. The degree to which *L. macrochirus* regulates water quality necessitates further analysis.

10061 - Regurgitation Unraveled: Plant Microstructures and Hairball Formation in Cats

Kara Bensel, Megan Rudock-Bowman, Nicole Hughes

High Point University, High Point, NC

Carnivores, including wild and domestic felids and canids, have been widely observed eating fibrous plant material such as leaves and stems. Previous studies have hypothesized that this behavior aids in the expulsion of parasites or hair trapped in the digestive tract. While previous studies have observed direct interactions between leaf matter and parasites expelled in stool, no such interactions have been reported concerning hairs expelled as hairballs or stools. We used scanning electron microscopy (SEM) to observe interactions between hairs and leaf microstructures from six hairballs produced by two indoor/outdoor domestic cats belonging to one of the authors. No manipulation or experimentation was involved, and only hairballs containing visible plant matter were examined. DNA barcoding (rbcL gene) was used to identify plants in hairballs. Leaf blades in all six hairballs exhibited serrations and/or trichomes, and these plant microstructures were observed directly ensnaring animal hairs in all samples. Consumed plant matter spanned multiple taxonomic groups, and included Poaceae, Lauraceae, Commelinaceae, and Araceae. These findings support the hypothesis that plant microstructures assist in the removal of hairs from the gastropharyngeal tract of carnivores and suggest that access to plant matter with leaf microstructures, such as grasses, is a healthy supplement to diets of domestic and captive animals.

10076 - Mapping Change using GIS: Land Use Dynamics in Paulding County Georgia Amidst Rapid Population Growth

Ericka Walczak[1], Jessica Osborne[2]

[1]Georgia Highlands College - Rome, GA, ACWORTH, GA, GA, [2]Georgia Highlands College, Rome, GA

Paulding County, one of the fastest growing counties in Georgia and the 13th largest, has increased nearly twice as fast as other counties and is projected to grow by 56% over the next 15 years[4]. As a rapidly expanding suburban area outside Atlanta, Paulding County has experienced notable land cover changes from 2018 to 2023, though not to the extent hypothesized. This study employs ArcGIS Pro to analyze spatial data from the USDA Forest Service using the Land Change Monitoring System, LCMS, to illustrate vegetation loss or gain and overall land cover changes during this period. This research is significant as it underscores the environmental implications of urban sprawl and aids in urban planning and conservation efforts. Understanding the relationship between population growth and land use changes is vital for developing strategies to mitigate adverse environmental impacts and promote sustainable growth. Contrary to the initial hypothesis of significant forest reduction due to population growth, the data indicated that land use changes were minimal and the percentages of forest and developed land remained similar over the studied period. Developed land grew by 3.4%, correlating to approximately 1,462 acres over this five-year period, while forested land lost approximately 513 acres.

Though changes to land use have led to small changes in acreage numbers overall, fragmentation could be a larger issue and needs further research. The increase in developed land use by 3.41% and the decrease in forest land use by 1.4% suggest that Paulding County has managed to balance development needs with the preservation of forested areas. With a slowly decreasing forest acreage, additional preservation should be reviewed to ensure significant changes to forest land do not develop over the next decade with anticipated population growth.

10084 - Historical Land Change in Charleston Harbor: Insights from Digitized Maps and Landscape Metrics

Erin Vaughn, Dr. John Quinn

Furman University, Greenville, SC

Coastal landscapes are inherently dynamic and undergo constant change due to the forces of erosion driven by waves, currents, and wind. These processes reshape coastlines over time, making it crucial to understand the historical evolution of these landscapes for effective land management and future environmental predictions. However, quantifying historical land change, particularly before the

advent of satellite imagery, presents significant challenges. To address this gap, we used digitized historical maps to create rasters of the Charleston Harbor landscape between 1858 to 2024, creating a spatiotemporal dataset representing coastal changes over time. We used the landmetrics package for R to calculate metrics (e.g., total edge and total perimeter) to evaluate the change in the coastal landscape over time. Total edge and total perimeter had significant positive correlations with time, with coefficients of 0.767 and 0.733, respectively ($p = 0.021$, $p = 0.031$). The use of digitized historical maps could be a productive way to quantify historical landscapes and provide insight into how land has changed over time. The use of digitized historical maps in this study demonstrates a promising approach for quantifying historical landscape changes and understanding the long-term impacts of natural and anthropogenic factors on coastal environments. By integrating historical data with contemporary observations and future projections, we can develop more robust models for predicting coastal landscape responses to ongoing environmental changes and human pressures.

10085 - Seeing Spots: Long term study on the margay at a mid-elevation site in the eastern Andean foothills of Ecuador

Natasha Vanderhoff[1], Marlena Warren[2], Brian Arbogast[3], Travis Knowles[4]

[1]Jacksonville University, Jacksonville, FL, [2]Jacksonville Univerity, Jacksonville, FL, [3]University of North Carolina Wilmington, Wilmington, NC, [4]Francis Marion University, Florence, SC

The margay *Leopardus wiedii* is a small Near Threatened felid found throughout much of the neotropics. Despite its large geographic range, relatively few long-term studies have examined their population dynamics. Since 2008 we have utilized camera traps to assess mammal diversity at Wildsumaco Wildlife Sanctuary (WWS). Although margays have special adaptations for an arboreal lifestyle, they have been one of our most frequent captures. We report population trends at our site on the eastern slope of the Andes and compare our findings to other studies in the neotropics.

10086 - Temporal Dynamics of Grassland Bird Communities in Response to Agricultural Disturbances

Kara Justus, Dr. John Quinn

Furman University, Greenville, SC

The nature of agricultural land management, in particular arable land, requires frequent disturbances including harvest, tillage, and chemical application. Past research has broadly considered the impact of these practices on a year by year basis. New data collection tools, including passive acoustic monitoring (PAM) allows for additional insight at a finer temporal scale. We examined the effects of agricultural disturbances on grassland breeding bird populations on fields enrolled in General Mill's regenerative agriculture program in Kansas between 2020 and 2022. We collected data on bird detections using PAM over a 7 month window, sampling on the hour, for 24 hours at each location. Cooperating farmers reported on planting and harvesting dates for cover and row crops, as well as nitrogen, phosphorus, potassium (NPK) fertilization and pesticide application. Preliminary analysis reveals that short-term agricultural disturbances, such as planting, harvesting, fertilization, and pesticide application, influence bird species in distinct ways. Species-specific responses to the temporary changes in habitat conditions that these activities generate ranges from displacement to attraction. For instance, species like the Dickcissel and Eastern Meadowlark experience significant declines in detections and fail to return to baseline population levels within a week following disturbances. In contrast, other species, such as the Horned Lark, appear to benefit from harvesting activities, with population detections often exceeding baseline levels within the post-disturbance timeframe. The study illustrates the species-specific near-term impacts of agricultural practices on grassland birds, emphasizing the importance of temporal and spatial considerations when managing agricultural land for biodiversity conservation. By identifying species that are particularly vulnerable or adaptable to these disturbances, these results provide actionable insights for cooperating farmers to balance agricultural productivity with ecological health.

10090 - Anatomical and performance traits associated with fight outcome in male fall field crickets

Jeremy Morris, Landon Foster, Katharine Spence, Shelton Laney, Hannah Scott

Wofford College, Spartanburg, SC

The outcome of male-male contests plays a significant role in determining reproductive success in many species. As a result, specific traits that improve male fighting performance are often more pronounced in males that win fights as compared to those who lose. In this study, we explored a set of morphological, physiological, and performance traits to understand their potential influence on contest outcomes in male fall field crickets (*Gryllus pennsylvanicus*). We conducted contests between size-matched males and collected data on a set of traits that may be associated with winning. For these comparisons, we only included fights that reached the highest level of aggression, in which competitors lock mandibles and try to push or flip each other (occurred in 43 of 53 total fight trials). We predicted that hindlimb muscle mass and jump energy, which is determined by hindlimb muscle power generation, would be greater in winning males, because they use the same muscles when pushing and grappling with their opponents. Winning males were also predicted to

have larger heads and maxillae because these jaws are the primary weapons used in combat. We also predicted that males would have lower standard metabolic rates, given that this is associated with a more "bold" behavioral phenotype in crickets. Finally, we predicted that winning males would have higher maximum metabolic rates, given that this trait is a major determinant of sustainable power output that is likely important during prolonged physical fighting. Our results indicated that winners had significantly larger heads and maxillae, greater jump energy, and marginally greater hindlimb muscle mass. We found no significant differences for standard or maximum metabolic rates. This integrative approach to analyzing multiple traits simultaneously provides a detailed understanding of the factors influencing success in male-male contests.

10102 - Investigating the mechanism of isopropyl BPZ as a treatment against *Toxoplasma gondii*

Miranda Gough[1], Robert Charvat[2]

[1]High Point University, NC, [2]High Point University, High Point, NC

Toxoplasma gondii is an obligate intracellular parasite affecting roughly one-third of the world's population. Toxoplasmosis is the second leading cause of death from food-borne illnesses in the United States, after salmonellosis, highlighting the demand for an effective treatment. As an intracellular parasite, current treatment methods are poorly tolerated by patients, as the drugs tend to destroy healthy host cells. Past research from this lab identified novel anti-cancer bisphenol Z (BPZ) derivatives as effective at targeting and destroying T. gondii cells. These drugs inhibit the growth of the parasitic cells by preventing them from replicating. This project aims to explore the mechanism of these compounds to address the need for new therapeutic strategies against T. gondii. To accomplish this, the primary focus was identifying the gene targets that allow the most promising BPZ derivative, isopropyl BPZ, to destroy T. gondii cells. This was achieved through the creation of a mutated parasite line that is resistant to isopropyl BPZ. The intracellular replications of this mutated line were tested in varying concentrations of the compound via doublings assays, which demonstrated adequate resistance as compared to that of the parental strain. To understand the mechanism of action, transcriptional analyses were completed through RNA sequencing between the parental and mutant strain under normal conditions and following isopropyl BPZ treatment. This identified several genes that reacted differently in the mutated strain versus the parental as a result of treatment. The genomes of each strain were investigated via DNA sequencing to compare RNA genes of interest to DNA genes of interest. These sequencing results can be used to create custom gene knockouts using CRISPR-Cas9 technology, which could further uncover the mechanisms of drug activity. The outcomes of this project have the potential to identify a novel treatment of toxoplasmosis that is more effective than current treatment methods.

10107 - Epigeal arthropod community dynamics as a function of urbanization in Guilford County, NC

Maggie Garr[1], Tyler Wright[1], Daniel Greene[1], Bella Perez[2]

[1]High Point University, High Point, NC, [2]Northwest Guilford High School, Greensboro, NC

Urbanization is one of the least reversible forms of anthropogenic action and is a principal driver of species extinctions and habitat loss. Highly urbanized areas can be delineated by large areas of impervious surfaces, lower humidity, and a warmer temperature than more undisturbed rural areas. To assess the effects of urbanization on arthropod abundance in Guilford County, NC, we conducted weekly (4 weeks) faunal community assessments across 20 sampling sites from 12 June-10 July 2024. We predicted that common epigeal arthropod (i.e., Araneae, Carabidae, Collembola, Formicidae, and Isopoda) abundance would be highest in sites with higher humidity and a low percentage of impervious surfaces and lowest in sites with low humidity and a high percentage of impervious surfaces. Each sampling site featured two covered pitfall traps and belonged to one of two grids (Grid A, 6.71km ^{2}; Grid B, 5.62km^2) that differed in their level of urbanization. The number of pitfall-collected Araneae, Carabidae, Collembola, Formicidae, and Isopoda were separately analyzed via generalized linear mixed modeling using land cover and environmental data as predictor variables. We hypothesized that taxonomic groups whose members occupy different trophic levels such as ants (Hymenoptera: Formicidae) and groups who fill a more generalist role such as detritivores including isopods (Isopoda) would be less affected by urbanization than taxonomic groups whose members represent a distinct trophic level (e.g., herbivore or predator). The results from our study are important as we seek to enhance ecosystem services as urban expansion continues across the planet. The identification of distinct drivers of arthropod abundance among various taxonomic groups within urban arthropod communities is a critical first step towards the modification of anthropogenic habitats to increase their suitability for arthropod occupancy.

10110 - STM and ATH1: Key regulator of floral organ abscission

Sabnam Ojha, Sarah Liljegren

The University of Mississippi, Oxford, MS

Plants shed leaves, fruit and other organs through a regulated process known as abscission. After *Arabidopsis* flowers are pollinated, their outer floral organs are shed to facilitate healthy fruit and seed development. Organ detachment occurs within abscission zones that form at the boundaries between the bases of the floral organs and pedicel. Two homeodomain transcription factors–ATH1 and

STM–regulate the development of these boundaries. Mutations in either *ATH1* or *STM* prevent stamen abscission, while mutations in both genes block sepal and petal abscission as well. Scanning electron microscopy has shown that the sepal-pedicel boundaries are less distinct in *stm* and *ath1* single mutant flowers and largely absent in *stm ath1* double mutant flowers. Furthermore, we have discovered that abscission zone cells at the sepal bases of *stm ath1* flowers are significantly larger than those of wild type. Within the wild-type sepal abscission zones, a lignin brace provides mechanical support and facilitates precise organ detachment by confining the enzymes responsible for cell separation and cell wall modification. Visualization with confocal microscopy has revealed that lignification of these cells is disorganized in *stm* and *ath1* flowers, and is absent from the sepal bases of some *stm ath1* flowers. Hydrogen peroxide is a reactive oxygen species utilized by peroxidase during lignin polymerization that accumulates at the base of wild-type sepals. Staining with 3,3'-diaminobenzidine has shown that hydrogen peroxide is missing from the sepal bases of some *stm ath1* flowers. These findings highlight key contributions of STM and ATH1 to the formation of sepal-pedicel floral organ boundaries and differentiation of abscission zone cells.

10115 - Multi-Dimensional Assessment of Species Composition and Vegetative Health Via Aerial Imagery and Machine Learning Modeling

Grant Erbelding

University of Louisiana Monroe, Monroe, LA

As the effects of global climate change continue to intensify, consistent monitoring of valuable and vulnerable ecosystems is vital to their preservation. To this end, remote sensing via satellite, and increasingly, via Unmanned Aerial Vehicles (UAVs) has continued to grow as an effective tool for high-resolution ecological monitoring. This project focuses on leveraging time-series aerial multispectral photogrammetry, Machine Learning (ML), and intensive ground validation to develop a comprehensive methodology for monitoring the old-growth Bottomland Hardwood Forest ecosystem native to Northern Louisiana.

Using a multi-temporal and multi-dimensional approach, this project has two major goals. First, the automation of identification of canopy-contributing tree species via ML model developed in the R programming environment. This model will delineate and isolate canopy extent, as well as identify the eight dominant tree species within this ecosystem. Second, spectral indices and vegetative health markers will be used to detect indicators of stress in trees across the forest, providing insight into how this ecosystem is responding to changes in temperature and precipitation patterns. Preliminary results demonstrate promise in aerial stress detection, and ground-truthing through phenological and cellular analysis of stressed individuals will aid in corroborating signs of biotic and abiotic stress factors.

The aim of this project is to produce a scalable and automated ecosystem monitoring system capable of providing actionable insights into forest health, and inform forest management in a changing climate.

10134 - An Update on the Carnivore Fauna of Wildsumaco Wildlife Sanctuary, Ecuador

Brian Arbogast[1], Travis Knowles[2], Anne-Marie Hodge[3], Santiago Burneo[4], Natasha Vanderhoff[5], Paul Zwiers[2], Jeff Camper[2], Jonas Nilsson[6]

[1]University of North Carolina Wilmington, Wilmington, NC, [2]Francis Marion University, Florence, SC, [3]Bakersville College, Bakersfield, CA, [4]Pontificia Universidad Catolica del Ecuador, Quito, Pichincha, Ecuador, [5]Jacksonville University, Jacksonville, FL, [6]Wildsumaco Wildlife Sanctuary, Pacto Sumaco, Napo, Ecuador

We conducted camera trap surveys at Wildsumaco Wildlife Sanctuary (WWS), Ecuador from 2010-2024. In 2015, Hodge and Arbogast published a summary of the carnivore fauna (Order Carnivora) documented with camera traps at WWS from July, 2010-June, 2011. They reported a total of 9 species from 3 families (4 species of Felidae, 3 species of Mustelidae, and 2 species of Procyonidae). Here we report the subsequent documentation of 3 additional species of carnivore: the jaguar (*Panthera onca*; Felidae), bush dog (*Speothos venaticus*; Candidae) and eastern lowland olingo (*Bassaricyon alleni*; Procyonidae). The former two were photographed with trail cameras and the latter was photographed foraging in the lower branches of a tree (*Isertia laevis*; Rubiaceae) by TWK. These new records are notable because the elevation of WWS (approximately 1250m-1500m) is above or near the upper elevational limit reported for the bush dog, eastern lowland olingo and jaguar in Ecuador (1400m, 1600m and 1660m, respectively), and can be attributed to both the strong biogeographic connection between Sumaco Volcano and the western Amazon basin and the existence of at least some suitable habitat corridors that connect the two. Furthermore, a total of 12 non-marine carnivore species have now been documented on the approximately 600-ha WWS, which represents 43% (12 of 28) of all such carnivores known from the entire country of Ecuador.

10136 - The Biology Cafe: Learning in a Social Setting

Megan Gibbons[1], Mickie Powell[2], Cynthia Tant[2], Ketia Shumaker[2]

[1]UAB, Homewood, AL, [2]UAB, Birmingham, AL

Forming social connections with peers can be critical in helping students manage the stress and anxiety that accompanies academically challenging courses. Current research suggests that university students prefer informal learning environments where they can study alone or with peers or just "hang out". Such settings can meet the increasing needs of students in academically rigorous courses, while also increasing opportunities for students to build social networks with peers. In Fall 2023, a team of Introductory Biology faculty at The University of Alabama at Birmingham initiated The Biology Café. The Biology Department serves ~850 undergraduate Biology majors every year; the majority of those students enroll in our Introductory Biology courses as first-year students. Peer facilitators, who have been recruited from past courses and trained to assist current introductory students, staff the Café throughout the day and assist students who have questions about course material. Facilitators can instruct and engage students about course concepts, study tactics, time management strategies, and metacognition learning skills. Since its inception, we have monitored several aspects of The Biology Café, including the number of Introductory Biology students who visit the area each term, how many hours they spend there, and whether these parameters are correlated with overall satisfaction with the course and whether they feel a sense of community with their Introductory Biology classmates. Initial results suggest that attendance at the Biology Café is steadily increasing, with over 45% of students utilizing the resource in Fall 2024, without any "points" incentive. In addition, students who utilized this resource indicated that they were more satisfied with their Introductory Biology course and experienced a greater sense of community than the students who did not utilize the resource. We are encouraged by these results, and we continue to explore ways to improve the effectiveness of the Biology Café.

10163 - Phenotypic Analysis of Phage-Host Interactions

Lidia Peralta, Victoria Frost

Winthrop University, Rock Hill, SC

Bacteriophages compete among themselves to infect and gain control of their bacterial host. Once inside the cell it is evolutionarily advantageous for an established phage to protect the host for its own use. In our lab, we have been attempting to reveal which phage genes may play a role in this defensive process by using a phenotypic defense assay. Individual genes from mycobacteriophage ExplosioNervosa are transformed into the bacterial host Mycobacterium smegmatis. Lawns of the transformed host are created, ExplosioNervosa's gene of interest is induced, and dilutions of external phage lysates are spotted onto the lawn. Several phage lysates from both the same, and different, subclusters were applied in this way. ExplosioNervosa itself (wild-type and mutant variants) was investigated for its ability to infect the host as a specific ExplosioNervosa gene was expressed by the cell (homotypic defense). Other phage lysates tested include Ashballer (A1), Bombitas (J), and Jinnie (unclustered). We have studied nine of ExplosioNervosa's genes so far, including gp1, 19, 23, 32, 41, 55, 57, 73, and 75. Of this group, gp75 has shown potential defense of the host against external phage infection, which is particularly interesting as this gene product is predicted to be an immunity repressor. Immunity repressors are known to maintain lysogeny, as well as play a role in host defense. Understanding these phage-phage interactions can add to our knowledge of phage biology and behavior. Grant/ Funding Support: This project was supported by grant P20GM103499-20 (SC INBRE) from the National Institute of General Medical Sciences, National Institutes of Health. Support has also been provided by the SEA-GENES project of the Howard Hughes Medical Institute, and by a U.S. Department of Education Ronald E. McNair Postbaccalaureate Achievement Program grant (#P217A230073). Affiliations: Department of Biology, Winthrop University, Rock Hill, SC

10164 - Experimental adjustments to hatching asynchrony between brood parasites and their hosts reveal patterns of parental feeding effort and nestling survival.

Rin Pell, Ph.D. student[1], Kelly O'Neil[2], Kelly Miller[1], Shelby Green[1], Madison Mash[1], E. Keith Bowers[1]

[1]University of Memphis, Memphis, TN, [2]University of Florida, Gainesville, FL

In altricial songbirds, hierarchies of competitive advantages among nestmates are often induced through hatching asynchrony (HA), a reproductive strategy in which incubation onset differs between eggs within a nest. This affects the order in which eggs hatch and creates size asymmetries among brood-mates that impact nestling development and survival. HA allows some nestlings to hatch earlier and obtain parental provisions before other nestmates hatch, enhancing their body condition and survival before independence. Brood parasites that lay eggs in the nests of other species may benefit from HA by providing their earlier-hatched offspring a competitive advantage over smaller host young. However, even where HA confers a size advantage for parasitic young, hosts may nevertheless gain indirect, brood-level benefits in some cases: If the presence of a large nestling elicits higher feeding rates to the brood, nestlings reared alongside a brood parasite may receive greater per-capita food than unparasitized conspecifics. Here, we explore how host-parasite size asymmetry impacts provisioning behavior and reproductive outcomes by experimentally altering the degree of HA between prothonotary warblers (*Protonotaria citrea*) and their common brood parasite, the brown-headed cowbird (*Molothrus ater*). We adjusted

the hatching date of cowbirds relative to their hosts by swapping eggs between naturally parasitized nests in which incubation onset differed (±1-2 days), creating experimental groups with cowbird young that hatched earlier or later than their "expected" hatch date. We monitored nestling growth and survival throughout the nestling period and assessed parental provisioning effort and feeding decisions at multiple developmental stages to determine how the degree of HA affects feeding preferences between parasites and progeny as they grow. In this ongoing project, we aim to understand the role of HA in parental feeding decisions and—ultimately—host growth and survival.

10168 - Species distribution modeling of invasive wood boring beetle *Anoplophora chinensis*

Travis Rhodes, Sibyl Bucheli, Christopher Randle

Sam Houston State University, Huntsville, TX

Anoplophora chinensis, otherwise known as the Citrus long-horned beetle, is a woodboring beetle native to eastern Asia, and is considered an invasive pest that decimates populations of citrus trees, maple trees, willow trees, and others. It is a pest even in its own home range, infesting trees that are seemingly heathy. *Anoplophora chinensis* has appeared in the US in the past and was eradicated, but presents a continual threat. To aid in early detection, species distribution models were developed to predict highly suitable environments in the US for this forest pest. We used an ensemble approach, including three different models, Generalized Additive Model, Maximum Entropy, and Boosted Regression Trees.

10170 - Species distribution modeling and connectivity analysis as tools for predicting patterns of invasion: a case study of the spotted lanternfly (*Lycorma delicatula*: Hemiptera)

Christopher Randle[1], Lekisha Nagpal[2], Sibyl Bucheli[1]

[1]Sam Houston State University, Huntsville, TX, [2]Woodlands College Park High School, Academy of Science and Technology, The Woodlands, TX

Species distribution modeling is a valuable tool in predicting habitats most likely to harbor invasive species following invasion. Initially, when an invasive species is brought into a new territory through human commerce, it is expected to occupy sub-optimal environments. However, as the species persists and spreads to adjacent areas, it is likely to choose areas more suitable for establishment of viable populations. Natural dispersal routes are likely to follow gradients of habitat suitability. Following initial invasion, therefore, two processes interact to create a pattern of geographical invasion: habitat suitability and natural dispersal. Habitat suitability can be predicted using species distribution modeling, and ability to disperse naturally through suitable habitat can be modeled using connectivity analysis. In this study, we test our ability to model these two factors using the recent invasion of the spotted lanternfly (*Lycorma delicatula*). Spotted lanternfly is native to China, the Koreas, and Japan, where it uses the tree of heaven (*Ailanthus altissima*) as a naural host. Spotted lanternfly has recently invaded the United States and Canada. It was first detected in Berks County, Pennsylvania in 2018, and has since spread to 19 states and provinces. Easy identification, high visibility, and citizen science tools like iNaturalist have provided more than 30,000 date-stamped observations of this invasive species in the US and Canada. Using these data points, we derived ensemble habitat suitability predictions to test the hypothesis that species will occupy increasingly more favorable habitats over the course of invasion. We then used connectivity analysis to predict geographical locations of new populations following the initial invasion, and tested our predictions against the known pattern.

10171 - Factors Influencing Stream Macroinvertebrate Diversity

David Rai, Clifton Ruehl

Columbus State University, Columbus, GA

Urbanization often leads to declines in water quality and subsequent loss of biodiversity and ecosystem structure. Along an urbanization gradient, biodiversity declines could be gradual as more sensitive taxa are progressively eliminated from aquatic communities. Alternatively, biodiversity declines may be abrupt if biodiversity rapidly declines after a threshold of poor water quality is reached. We determined the nature of biodiversity decline of macroinvertebrates along an urbanization gradient from seven different sites along six different streams in the greater Columbus, GA area. Biodiversity declined sharply between two ex-urban sites and four increasingly urban sites suggesting evidence of a threshold decline. However, biodiversity rebounded at the most downstream site and model selection with a variety of abiotic parameters revealed that flow rate accounted for much of the variation in biodiversity among sites. These results suggest that most aquatic biodiversity is lost once a threshold of urbanization is reached and that improving flow conditions through management could restore some of the biodiversity loss.

10173 - Species distribution modeling for predicting invasions by *Lymantria mathura* (Rosy moth)

Zyra Johnson, Christopher Randle, Sibyl Bucheli

Sam Houston State University, Huntsville, TX

Lymantria mathura (Lepidoptera: Lymantridae), also known as Rosy Moth, it is native to south Asia, where it thrives in cool environments, with frequent rainfall and dry periods. The moth's life cycle begins with around 50 to 1,200 eggs laid in mid-April or June and hatching within three to four weeks. The larvae emerge from early June to late September and develop for 2-3 weeks before pupating on the underside of branches or other protected habitats. *Lymantria mathura* is a polyphagous pest of many deciduous trees in 45 genera of 24 families, with the most frequently targeted including oak (*Quercus*) species, sal tree (*Shorea robusta*), Java plum (*Syzygium cumini*), arjuna (*Terminalia arjuna)* and east Indian almond (*T. myriocarpa*).Larvae damage host trees by mass defoliation. Invasion into the Koreas and Eastern Russia has resulted in heavy damage to forest ecosystems. Though the moth has not infiltrated the United States, it has been identified as a priority pest species by the USDA. In this study, we used species distribution modeling to predict habitat suitability for *Lymantria Mathura* in the contiguous US to assist in early detection and containment should this pest be transported to US forests.

10174 - Elevational structuring of medium-large species of mammals on Sumaco Volcano, Ecuador.

Travis Knowles[1], Brian Arbogast[2], Anne-Marie Hodge[3], Kai Curry-Lindahl[2], Santiago Burneo[4], Roland Kays[5], Natasha Vanderhoff[6], Jeff Camper[1], Jonas Nilsson[7]

[1]Francis Marion University, Florence, SC, [2]University of North Carolina Wilmington, Wilmington, NC, [3]Bakersville College, Bakersfield, CA, [4]Pontificia Universidad Catolica del Ecuador, Quito, Pichincha, Ecuador, [5]NC Museum of Natural Sciences and NC State University, Raleigh, NC, [6]Jacksonville University, Jacksonville, FL, [7]Wildsumaco Wildlife Sanctuary, Pacto Sumaco, Napo, Ecuador

Assessing the occurrence, geographic distribution, and spatial and temporal activity patterns of species is essential for a full understanding of their ecology, biogeography and interactions with sympatric species. Camera trapping techniques are useful in conducting such studies on mammals, as they are non-invasive and minimize disturbance of natural activity patterns. We report findings of camera trap studies of medium-large mammals on Sumaco Volcano, Ecuador, between 2010 and 2016. We characterize the medium-large mammal fauna at five elevational zones on Sumaco Volcano: one located in the lower montane rainforest at approximately 1350m, and four located in the cloud forest at approximately 1750m, 2200m, 2500m, and 2900m. We determined species diversity for each zone and species turnover (beta diversity) between zones. Our major conclusions are 1) that species turnover between the 1750m and 2200m sites was the most pronounced; however, we also found substantial turnover among upper elevation sites, suggesting that elevational differences in mammalian communities within Neotropical upper montane rainforest biomes also can be surprisingly high; and 2) that typical Amazonian lowland species occurred at all elevations (including 2900m, far above the rainforest-cloud forest ecotone), but that no "Andean" species were found below this ecotone.

10175 - Hybridization and the distribution of color phenotypes in great smoky mountains *Plethodon* salamanders

Benjamin Fitzpatrick

University of Tennessee, Knoxville, TN

The iconic Red-cheeked Salamander (*Plethodon jordani*) is endemic to the higher elevations of the Great Smoky Mountains. Although its geographic (and elevational) range has been surprisingly consistent through decades of climate change, a more subtle change has been proceeding in some parts of the mountains. Red-cheeked salamanders often hybridize with slimy salamanders (*P. glutinosus* and *P. teyahalee*) and while hybrid zones in some locations have been stable for decades, we are finding new locations where extensive hybridization appears to be changing the face of *Plethodon* populations. Here we present preliminary evidence from DNA and color patterns that hybrid populations are expanding in the western part of the mountain range. We find that this expansion is associated with forest type. We hypothesize that this expansion might be a consequence of differences in the light environment and/or predator communities between northern hardwood and coniferous forests, making the fitness effects of red cheek patches dependent on forest composition.

10183 - Preliminary Vascular Plant Flora of Cloudland Canyon State Park, Dade County, Georgia.

Andy Wall, Joey Shaw

University of Tennessee at Chattanooga, Chattanooga, TN

Cloudland Canyon State Park (CCSP), situated in Dade County, Georgia, spans more than 1,431 ha and is managed by the Georgia Department of Natural Resources. CCSP lies at the southern extent of the Cumberland Plateau ecoregion, an area that has received limited attention in terms of floristic studies compared to its northern counterparts in Tennessee and Kentucky. CCSP encompasses diverse habitats across its elevation range (240-600 meters) featuring higher elevation ridges with dry acidic soils, a canyon floor with moist calcium-rich soils, and a treacherous escarpment in between. This environmental variation presents a wide range of ecological niches, likely to host a diverse array of species. Our research aim is to catalog all vascular plant species within CCSP, contributing valuable insights to the understanding of the flora of the southern Cumberland Plateau. Since November 2023, 24 collection trips were conducted. 413 specimens thus far represent 310 species in 211 genera in 92 families. The largest plant families are Asteraceae with 43 species, Poaceae with 26 species, and Fabaceae with 13 species. Nonnative species make up 9% of the flora, the most aggressive threats being *Microstegium vimineum* (Poaceae), *Lespedeza cuneata* (Fabaceae), and *Ligustrum sinense* (Oleaceae). Notable rare species of conservation concern include: *Agalinis gattingeri* (Orobanchaceae; SH), *Brachyelytrum aristosum* (Poaceae; S1), state endangered *Lilium philadelphicum* (Liliaceae; S1), and the federally listed *Spiraea virginiana* (Rosaceae; S1). Thus far, 14 S1-S2 species have been documented in CCSP and this effort is providing critical baseline data for the park, laying the groundwork for informed management and preservation efforts of this understudied region.

10187 - "Exploring The Miniature Marvels of The Forest and Fields" Transforming Approaches to Study Myxomycete Diversity and Collection Preservation.

Brogin Van Skoik[1], Chinyere Knight[2]

[1]Tuskegee University, AL, [2]Tuskegee University, Tuskegee, AL

Advancing the understanding of myxomycete biodiversity and phylogeny by focusing on two key objectives: creating a comprehensive reference database of SSU sequences from 25 of the 350 specimens in the Lafayette Frederick collection, encompassing all five orders of *Myxogastria,* and conducting whole genome sequencing of *Clastoderma debaryanum* and related *Clastoderma* species to clarify the phylogenetic relationships within the *Echinosteliales.* The study will utilize bark samples preserved for over forty years from diverse regions of the world and fresh bark samples from regions within the United States, providing a unique opportunity to explore the genetic diversity of these understudied organisms. This research will fill critical gaps in the molecular taxonomy of myxomycetes and contribute to the broader understanding of their evolutionary history and ecological roles. The resulting data will be archived in publicly accessible databases to support future research and educational initiatives.

10194 - Isolating confounding abiotic and biotic effects on the phenotype of *Physa acuta* snails

Ashley Bauer, Clifton Ruehl

Columbus State University, Columbus, GA

Spatial and temporal habitat heterogeneity creates many challenges for organisms across their range. Organisms optimize fitness by matching their phenotypes to prevailing environmental conditions leading to habitat-specific polymorphisms within and between populations. Polymorphisms arise from genetic divergence, phenotypic plasticity, or a combination of both processes. We examined the presence of habitat-specific polymorphism in Physa acuta snails collected from three streams and their corresponding downstream reservoir. Snails exhibited both shared and unique aspects of phenotypic divergence. Regardless of stream-reservoir pair, snails from lotic systems had rotund shells with larger apertures, while those from lentic systems were comparatively more elongate with smaller apertures. Unique responses included the degree of aperture change and elongation. In a reciprocal transplant lab experiment that crossed flow regime and crayfish predator cues with F2 snails from both stream and pond habitats, we tested for the underlying mechanisms responsible for the observed phenotypic differences. We found no evidence for plasticity in relation to flow regime suggesting genetic divergence may be responsible for the observed shape differences. However, there was a habitat-specific plastic response to crayfish predator cues. Regardless of the flow regime during the experiment, snails experiencing crayfish cues that originated from the pond became more elongate, while snails from the stream became more globose. Surprisingly, genetic differences were apparent over small (<1km) spatial scales. Shell shape differences arising from flow regime are likely genetic, while those from predator cues seem to be plastic. Most importantly, the nature of shape change in response to predator cues depended on flow regime. These results add to a growing body of literature on the importance of abiotic factors that influence how organisms respond to biotic factors.

10214 - Impact of powerlines Right-of-way (ROW) on Non-migratory birds: Field Sparrows, Northern Cardinals, and Song Sparrows.

Nahom Estifanoes, Jill Penn, Mia Malloy, Maribel Fernandez

Georgia Gwinnett College, Lawrenceville, GA

Human Developmental activity has led to many species going extinct, and others threatened; birds are no exception. This is caused by habitat loss, climate change, and other species-specific factors. The main culprits for bird mortality are cats, buildings, automobiles and powerline collisions and electrocution, in that order. In contrast, some studies showed contradictory evidence to this trend, where powerlines may help thrive early successional habitat dependent species like Field sparrows. This is because AC overhead powerlines (69 kv - 765 kv) need a low vegetation path, creating a good early successional habitat along the way. Therefore, this warrants a deeper study to understand the nuances of powerlines ROWs effect on birds. The three species, namely, Field Sparrows, Northern Cardinals, and Song Sparrows are stable and listed as species of least concern (LN) in the International Union for Conservation of Nature (IUCN) metric, but they were selected for this study because these species are present all year round and can make use of the low vegetation created by the powerline ROWs. The bird samples will be collected from Atlanta metropolitan area sites such as, Georgia Gwinnett College, Panola Park, Collins hill park, and Harbins Park. The impact will be studied by assessing the genetic diversity of the birds using the cytochrome c oxidase subunit I (COI) gene and employing bioinformatics tools to analyze them.

10228 - Zoning, not vegetative productivity, best predicts insect biomass in an urban complex

Sarah Parsons[1], Elsa Youngsteadt[2], Peter Willadsen[2], Isaac Jackson[1], Harlan Chapman[1], RJ Wardell[3], Sophia Cox[3], Jack Balint-Kurti[3]

[1]Western Carolina University, Cullowhee, NC, [2]North Carolina State University, Raleigh, NC, [3]Duke University, Durham, NC

Recent reports of insect biomass decline have raised concern about the future of insect-dependent food webs and ecosystem services, such as pollination and nutrient cycling. The causes of insect decline are difficult to pinpoint, but urbanization is a clear threat. Cities, however, are mosaics of land uses, which likely have different effects on different insect groups. Moreover, patterns in non-urban systems predict that urban forests will support the greatest net primary productivity (NPP) and insect biomass. Here we examine links between land use, NDVI (Normalized Difference Vegetation Index) as a proxy for NPP, and insect biomass across different land uses (greenways, parks, residential, commercial, and industrial areas) in Raleigh, NC. We sampled insects with malaise traps and pitfall traps at 30 sites in Raleigh across all land use types. We then measured NDVI and canopy cover within 200m and 1km of sites and correlated this data with insect biomass data. We hypothesized that land uses with greater canopy cover would have greater NDVI and more insect biomass. We found that land use was predictive of canopy cover and NDVI, such that industrial and commercial areas had less canopy cover and NDVI compared to other land uses. We also found that greenways and parks had the highest amount of insect and herbivore biomass, as well as herbivore abundance, while commercial sites had the lowest. Contrary to prediction, sites with less canopy cover had more insect biomass in late summer. Together our results suggest that land use rather than canopy cover may be better at predicting urban insect biomass and identifying areas for insect biomass conservation. Furthermore, NPP-insect biomass relationship in cities may not exist as they do in non-urban systems. Our findings are useful for city planners who are exploring how to conserve insect biomass and wildlife within cities and beyond.

10231 - Assigning coefficients of conservation to the vascular flora of Tennessee and Kentucky.

Sevyn Brothers, Joey Shaw

University of Tennessee at Chattanooga, Chattanooga, TN

Floristic Quality Assessments (FQAs) measure ecosystems' quality and can be applied to any ecosystem. FQAs consist of two parts: a species checklist and each species' coefficient of conservatism (c-value). C-values are integers that describe species' tolerance and fidelity to anthropogenically disturbed habitats. C-values should be applied to species per ecoregion; however, difficulty arises due to resource allocations, and therefore it is common to apply c-values at state level or below.

Tennessee and Kentucky (TNKY) share many native and naturalized species and ecoregions, and both states lacked established c-values, putting TNKY in a prime position for combined c-value assignment. Previously, two TNKY botanists (J. Shaw and D. Estes) created individual draft c-value lists for most species and two previous attempts by Shaw, where a panel of botanists was assembled to assign c-values; however, none of these attempts resulted in a complete c-value assignment study. Although using a panel to assign c-values is most common, here we show that using a combination of pre-existing and newly assigned TNKY botanist data and two supplemental databases is an effective means of c-value establishment. To ensure accuracy of c-values assignment with unconventional methodology, species and corresponding c-values underwent public review. Furthermore, correlation and similarity of botanists' draft c-values was analyzed, and TNKY's native flora was analyzed against the native floras of six other states. Overall, c-

values were successfully applied to 99% of TNKY's flora (3,351 species). The remaining one percent (48 species) were marked "TBD" due to either a lack of, or conflicting botanist data.

10234 - A novel approach to retention pond renovation projects and the effect on the local turtle population.

Todd Rimkus, Mark Rimkus

Marymount University, Arlington, VA

Retention ponds exist for many planned communities around the US. These ponds can be completely isolated from natural waterways or reservoirs that only temporarily disrupt their flow. Over the years, a number of these ponds, have provided important habitat for local species. These retention-type ponds have become standard practice for many new-construction housing projects for the last 30 years. Now many of the older ponds need work and some even require total renovation. Construction plans do not always account for the impact on the species that inhabit the ponds. Even if they do account for the impact, the plan is usually a wait-and-see plan. Using a wait-and-see plan usually puts the animals at higher risk for injury or death while someone figures out what to do with the species encountered. This study took a new, proactive approach and yielded some remarkably interesting results. Prior to any construction, we identified several low-density ponds by trapping those ponds. Once the low-density ponds were located and approved by the Virginia Department of Wildlife Resources, we began trapping in the pond scheduled for renovation. All trapped turtles were marked using PIT tags and released into one of the low-density ponds. 66 turtles representing four species were relocated. Using the time needed during the trapping efforts along with the costs of supplies allowed us to determine the relocation costs on a per turtle basis. Based on similar projects where we were involved that used the wait-and-see method, we were able to estimate those costs on a per turtle basis for comparison. In studying the literature, we found this is the first known project that had a relocation phase prior to reconstruction of a retention pond. We propose that future renovation projects should employ the proactive plan, and the costs should be built into the budget.

10242 - Detection and Prevalence of Citrus Blight Infection in Florida Varieties of Citrus

Daniel Stanton[1], Jason Hurlbert[2], Bill Schneider[1], Ron Brlansky[1]

[1]University of Florida IFAS Citrus Research and Education Center, Lake Alfred, FL, [2]Winthrop University, Rock Hill, SC

Citrus Blight (CB) the second leading causing of declining and unproductive citrus trees in Florida. This has posed a significant problem for growers especially when trees are co-infected with Huanglongbing (HLB). and tree death. Water transport is reduced in Blighted trees trees due to plugged xylem, a symptom of an active CB viral infection. The problem is exacerbated by coinfection with HLB, resulting in trees rapidly dying due to a loss of phloem transport from HLB infection and the reduced water movement in the xylem from CB. Previously, our research group identified a Citrus blight associated Pararetrovirus (CBaPRV) where CB symptoms were tightly correlated (96%) with active CBaPRV. Pararetroviruses are unique plant viruses that insert a copy of their viral DNA into the host DNA and remain dormant until the proper conditions activate or 'trigger' the virus to begin its life cycle. Existing detection methods are limited; accordingly, we developed a more sensitive antibody-based detection method. This detection method is more reliable and can delineate active CBaPRV infection from genomic integration. This newly developed detection assay is vital to answering basic biological questions regarding the pathology of this disease including testing triggers that may activate dormant CBaPRV. Additionally, we examined the prevalence of CB in varieties of citrus grown in Florida. We determined that CBaPRV DNA is present in at least five different citrus species (orange, lime, lemon, grapefruit, tangerine and pomelo) as well as every rootstock tested to date, suggesting that breeding with clean stock is not an option. We have begun to investigate if CRISPR is a viable option to use to inactivate key domains of the integrated CBaPRV in order to prevent viral activation. If successful, the prevention of viral activation can prevent CB symptoms and reduce citrus decline associated with CB.

10243 - Hidden in plain sight, a new species of *Phacelia* for the Southern Appalachians

Jonathan Evans[1], J.T. Michel[1], Skyler Fox[2], Ashley Morris[3]

[1]University of the South, Sewanee, TN, [2]Georgia Southern University, Statesboro, GA, [3]Furman University, Greenville, SC

New plant species are often first discovered through careful analysis of herbarium specimens, but not all diagnostic characters are well preserved in such contexts. As a result, other taxa may go unnoticed without a thorough examination of individuals and populations in the field. In this study, we identified a new species of *Phacelia* from the southern Cumberland Plateau. Distinct morphotypes were first observed in Shakerag Hollow, Sewanee, Tennessee. Extensive ecological, morphological, and genetic surveys both in Shakerag and other locations support the recognition of *Phacelia sewaneensis*, which can be distinguished from *P. bipinnatifida* on the basis of corolla color, stamen length, presence or absence of watermarks on basal leaves, and dissectedness of basal leaves. Genetic analysis of sympatric populations of the two morphotypes using genotype-by-sequencing of microsatellite loci clearly defines the two taxa as separate entities. *Phacelia sewaneensis* is more typical of rocky substrates, while *P. bipinnatifida* is found on a broader variety of substrates. Because the original type specimen for *Phacelia bipinnatifida* does not provide the characters needed to distinguish between

the two species, we establish a new epitype for *P. bipinnatifida* and holotype and isotypes for *P. sewaneensis*. This new species is currently known from four sites, two in Tennessee and one each in Alabama and Georgia. Given the limited distribution based on our current understanding, we propose that *P. sewaneensis* be considered of special conservation concern. With additional information from subsequent field surveys, a formal conservation assessment would be warranted.

10247 - Forest Management Effects after Tornado Disturbance on Abiotic Conditions and Tree and Soil Microbial Communities in a Mixed Hardwood Forest in Kentucky

Julio Benedicto Pérez[1], Marvin Ruffner[2], Carlos Rodríguez López[3], Dr. Jonathan Moore[1]

[1]Campbellsville University, Campbellsville, KY, [2]Asbury University, Wilmore, KY, [3]University of Kentucky, Lexington, KY

Tornado prevalence has shifted during recent decades, increasing in the eastern United States. Consequently, forest managers must decide upon management strategies that account for changes in tree and soil microbial communities, which interact during succession and jointly facilitate ecosystem services. Thus, we studied early forest succession after tornado disturbance, focusing on salvage logging and no intervention management strategies. Our study site, Clay Hill Memorial Forest (Taylor County, KY, USA), was severely disturbed by an EF3 tornado on December 11, 2021. Twelve 20 x 20 m plots were chosen and grouped in four blocks. Each block comprises one control, one tornado disturbed, and one salvaged plot. In 2023 and 2024, we identified and measured DBH of all uprooted trees and all standing trees taller than 1.8 m in every plot. We monitored air and soil temperature, light, and soil moisture at the center of each plot. Soil bacterial and fungal community diversity and taxonomical composition were analyzed using a metabarcoding approach from nine soil samples per plot taken in Spring 2023. We expected disturbed plots to have more extreme abiotic conditions and higher tree and microbial diversity than controls. We predict salvaged plots to have a lower tree diversity compared to no intervention plots and compared to themselves before salvaging. Opposite to our predictions, tree diversity has decreased in salvaged plots and composition has changed across treatments. Specifically, importance of invasive trees increased in no intervention managed plots. Diversity of fungal and bacterial communities increased in disturbed plots. Air temperature highs and lows were more extreme in disturbed plots compared to controls, and more light reached the forest floor during the growing season in salvaged plots. These results indicate a divergence of abiotic and biotic conditions that correlates with management strategies and that could affect forest succession.

10248 - Navigating Polluted Waters: Examining the Role of Host-Associated Microbes in Aquatic Ecosystems

Rachel E. Diner

University of Memphis, Memphis, TN

Many human activities generate pollutants that enter aquatic systems, including coastal development, urban events, and industrial and agricultural operations. These pollutants are often toxic to marine and freshwater organisms and can negatively impact sensitive, keystone, and economically important species. While macro-organism responses to pollutants are frequently examined in the field of ecotoxicology, impacts on the microbes that live on and in these host organisms are poorly understood. Microbial communities associated with animal hosts (i.e., their “microbiomes”) are responsive to pollution and can play important beneficial roles for both hosts and the ecosystem. Furthermore, they may represent an untapped source of potential for bioremediation and probiotic applications. Here I discuss a framework for how host-associated microbes can mitigate the negative impacts of anthropogenic pollution in aquatic systems, citing examples from multiple environmental systems. I will also present research from our group using bivalves, including oysters and clams, as model systems to understand how pollutants and natural toxicants (e.g., harmful algal toxins) can impact aquatic hosts and their microbiomes, and the beneficial role microbes may play in these systems.

10253 - Integrating Authentic Learning into Large Microbiology Classes: A Case Study on Glyphosate-Degrading Microbes

Rachel E. Diner

University of Memphis, Memphis, TN

Authentic learning engages students in solving real-life problems to enhance their understanding of a subject while promoting creativity and critical thinking. These activities can be very effective but are often inaccessible to large lecture classes due to costs, time commitment, and the scale of original research. I developed and examined the effectiveness of an authentic learning module integrated into a large General Microbiology class (BIOL3500, student enrollment = 68). The project goal was to isolate microbes capable of degrading glyphosate, a widely used herbicide that can negatively impact aquatic ecosystems. Time and skill-intensive laboratory protocols were conducted by students conducting research for credit (BIOL4000), while General Microbiology students collected the samples, developed hypotheses, conducted bioinformatic analyses using NCBI blast, and wrote final reports on a single “adopted”

microbe. A post-activity survey completed by students (N = 57/68 students) assessed the activity's impact on various outcomes including student's perceived ability to generate and test hypotheses, understanding what microbiologists do and the role microbes play in their everyday lives, and their interest in pursuing related careers and engaging in undergraduate research. Most students indicated that the activity helped them better understand the lecture material (75%), increased their understanding of the role microbes play in their everyday lives (91%), and helped them understand the work that microbiologists do (83%), suggesting a beneficial impact of the activity towards achieving critical course objectives. Additionally, many students indicated an increased desire to participate in undergraduate laboratory research (65%) and take hands-on microbiology classes (58%) in the future. Most students reported a similar or increased interest in pursuing careers related to microbiology, agriculture, and environmental sustainability, while some (7-14%) indicated a decreased interest. Finally, most students indicated only moderate confidence that they could develop and test a scientific hypothesis, representing an important area for improvement.

10261 - Missing the mammals for the trees: Comparative biogeography of the sky island mammals of the southern Appalachians

Kimberly Cook[1], David Webster[2], Jules Stowe[1], Trinity Johnson[1], AJ Hopkins[1], Lisa Gatens[3], Travis Knowles[4], James Krupa[1], Rada Petric[5], JR Burger[1]

[1]University of Kentucky, Lexington, KY, [2]University of North Carolina Wilmington, Wilmington, NC, [3]North Carolina Museum of Natural Sciences, Raleigh, NC, [4]Francis Marion University, Florence, SC, [5]Institute for the Environment, University of North Carolina at Chapel Hill, Chapel Hill, NC

High-elevation refugia in the southern Appalachians serve as critical habitat for small mammal species that have persisted since the last glacial maximum. Several of these species have a contiguous range in the northeastern United States and Canada, and disjunct populations in the southernmost portion of their ranges. The patchy distribution of high elevation spruce-fir and northern hardwood forests, which forms a "sky island" archipelago along the southern Appalachian mountains, is often used as a surrogate for the distribution of these disjunct mammal populations. We used a species distribution modeling approach to predict past, present, and future distributions of 5 mammal species: *Sorex dispar*, *Microtus chrotorrhinus*, *Synaptomys cooperi, Glaucomys sabrinus coloratus,* and *Sylvilagus obscurus* along the southern Appalachians. We then compared the modeled distribution of suitable habitat to "islands" defined by elevation cutoffs for spruce-fir and northern hardwood forest. This comparison revealed variation in island size, connectivity, and suitability across mammal species and mountaintops 21,000 years ago to the present. Our comparative approach highlights how species-specific microhabitat requirements (e.g. mesic vs. xeric) and traits (i.e. body size) influence their use of high-elevation habitats, challenging traditional assumptions about forest-type associations in these systems. These findings underscore the importance of species-specific requirements when forecasting distributions and conserving sky island species in the southern Appalachians and elsewhere.

10265 - Investigations into the physiology, phytoremediation, and environmental impacts of *Alternanthera philoxeroides*, an undergraduate research project story

Christopher Beals

Abraham Baldwin Agricultural College, Tifton, GA

Over the last ten years, 12 different students and 17 different conference presentations examined the holistic ecosystem effects of *Alternanthera philoxeroides*. *A. philoxeroides* is an invasive plant species found infesting freshwater systems along the southeast United States. Student projects have investigated the plant's tolerance to heavy metals (Ag, Ni, Cd, Cu, Pb, and Cr) and translocation of metals within plant tissues. In addition to assessing the phytoremediation potential of *A. philoxeroides*, research students have also performed experiments on the plant's allelopathic effects on phytoplankton and *Daphnia magna*, a common microcrustacean used in toxicological studies. Current research has shown how plant absorption of copper inhibits flea beetle herbivory, which could impact efforts to control the spread of the plants. This presentation will summarize these students' efforts to show how a research idea can drive multiple connected projects.

10272 - Exploring the Impact of Nontraditional Science Education

Kayla Quincy

Agnes Scott College, Decatur, GA

This study investigates the impact of nontraditional science education, specifically summer camp programs, on students' scientific knowledge, connection to nature, and scientific identity. Conducted with 39 participants, the camp focused on tree identification, biodiversity, ecological importance, and scientists' roles in environmental sustainability. Pre- and post-test surveys assessed participants' knowledge retention, critical thinking, and environmental awareness. Quantitative analysis using t-tests revealed significant

improvements in most assessed areas, including scientific reasoning and knowledge retention (e.g., Question 1, $p = 0.012$; Question 3, $p < 0.0001$; Question 4, $p < 0.0001$). However, Question 2 ($p = 0.075$) showed no significant change, suggesting some curriculum areas require refinement. Thematic analysis indicated a shift from general themes to focused engagement with topics such as environmental stewardship, leadership, and collaborative problem-solving. Notably, Question 10 showed significant growth in environmental responsibility themes, with participants increasingly emphasizing "caring for the planet" and "collaboration." Despite limitations, such as variability in participant attendance and prior knowledge, the findings demonstrate the value of nontraditional educational settings in fostering curiosity, critical thinking, and environmental awareness. Future improvements could focus on addressing attendance challenges, refining curriculum delivery for less improved areas, and scaling the program to larger participant groups. Overall, the study highlights summer camps as effective informal learning environments that cultivate scientific knowledge, environmental responsibility, and a stronger scientific identity among participants.

10283 - A Microplastics Protocol that Minimizes Contamination and is Optimized for Fish Tissues

Lili McNulty, James Burgess, Ryan Saylor

Berry College, Mount Berry, GA

Microplastic contamination of fresh and saltwater ecosystems has increased dramatically over the last several decades. While microplastics research is becoming more common, there is a paucity of data investigating contamination of biological tissues, especially in freshwater fishes. Increased microplastics surveillance of freshwater fishes is needed, yet a budget friendly, time-effective procedure that minimizes sources of contamination remains untenable for many smaller research laboratories. Our goal was to examine current methodologies of microplastics analysis of fish tissues and develop a cost and time-efficient procedure with minimal barriers of entry. One of the most common challenges of microplastic research is contamination of samples with microplastics from the air, surfaces of glassware, and plastic storage devices for chemicals used throughout processing. We identified potassium hydroxide and hydrogen peroxide as the two most common methods used for biological sample processing; however, our procedure was a modified version of the hydrogen peroxide method. Quantifications of microplastics generally focus on using dissecting microscopes to analyze sizes and number, while newer methods involve staining with fluorescent dyes and counting via a dissecting microscope UV light attachment. Our protocol, therefore, also involved staining with Nile red and UV fluorescence. The use of RAMAN to identify the type of microplastics from our fish samples was also explored. Our samples were compared to pure RAMAN spectrographs of the most common types of microplastics, i.e., polyethylene (PE), polyethylene terephthalate (PET), polyvinylchloride (PVC), and nylon. We compared counts under white light to Nile red stain using UV light to determine if use of stain and UV fluorescence was a cost-effective way to increase count accuracy. During this talk, I will describe the development and results of our novel method for microplastics analysis that minimizes risk of contamination and optimizes quantification by using light microscopy and simple fluorescent staining techniques.

10284 - Sublethal Temperature Effects on North American Unionid Mussels: Exploring Thermal Vulnerabilities

Victoria Martin[1], Susan Fuller[1], Shannon Brewer[2,3], James Stoeckel[4], Dr. Kaelyn Fogelman, PhD[1]

[1]Troy University, Troy, AL, [2]School of Fisheries, Aquaculture, and Aquatic Sciences, Auburn University, Auburn, AL, [3]U.S. Geological Survey, Alabama Cooperative Fish and Wildlife Research Unit, Auburn, AL, [4]Auburn University, Auburn, AL

The Southeast United States is a freshwater biodiversity hotspot and is home to one of the richest assemblages of freshwater mussels in the world. However, freshwater mussels (Unionidae) are among the most imperiled taxa in North America with over 25 extinctions in the past century and approximately 65% of species considered endangered, threatened, or vulnerable. Threats such as connectivity barriers, habitat degradation, and climate change exacerbate the decline of these keystone species, which play critical roles in maintaining ecosystem health and water quality. Thermal variation is a particularly urgent stressor for aquatic ectotherms like mussels, as temperature regulates their behavior, physiology, and reproduction. Sublethal thermal stress – manifesting at cellular, tissue, organismal, and population levels – can serve as an early warning sign of vulnerability and it is critical to understand sublethal thresholds as knowledge of lethal tolerance limits alone are not protective. To inform conservation and management strategies for North American mussel fauna, we conducted a systematic literature review on sublethal temperature effects across the biological levels of organization, analyzing 114 studies encompassing 83 of the 302 North American species. Our findings highlight significant gaps in data for many species, including those endemic to the Southeast. Importantly, this study aims to link sublethal thermal stress response pathways which result in population level effects contributing to decline. By identifying trends and areas for future research, we aim to provide actionable insights for natural resources managers and conservation practitioners to mitigate climate-related impacts. Our ongoing work seeks to translate these findings into tools for predicting and managing the responses of the Southeast mussels to environmental change, ensuring the persistence of these ecologically and economically valuable species.

10291 - Searching for Novel Superhydrophobic Surface Structures in Tropical Plants

Katherine McDonald

High Point University, High Point, NC

Microscopic plant structures can repel water through physical interactions, as in the leaves of the sacred Lotus (*Nelumbo nucifera*). Mimicking such surface structures can potentially serve as a non-toxic alternative to modern waterproofing chemicals such as PFAS. Hydrophobic surface structures also reduce biofilm formation, giving them many applications in health and medicine. Discovering novel superhydrophobic patterns (i.e., those yielding contact angles >150°) is an active area of research. In the present study, we characterized surface structures and quantified hydrophobicity of leaves of a species of corpse flower (*Amorphophallus* sp.), and the petals of an epiphytic orchid (*Phaleonopsis* sp.). Plants were grown in the Caine Conservatory on the campus of High Point University. Species were chosen because they exhibited visible water repellency when water was applied to tissues using a dropper. Contact angles were measured using both the traditional projector method and a Biolin Scientific goniometer. A Phenom XL scanning electron microscope was used to visualize dried tissue surfaces. Results showed that both surfaces were hydrophobic (contact angles between 90-150°), but not super-hydrophobic. SEM imaging of leaf and petal surfaces revealed waxy clusters on the *Amorphophallus* leaf, but not on the *Phaleonopsis* petals. No dermal structures (e.g., papillae or trichomes) were observed in either species, although this may be due to drying. We are currently investigating additional species.

10299 - Microbial community contribution to oxidative stress defense in high-biomass forming harmful algal blooms

Chelsea Donovan, Louie Wurch, Morgan Steffen

James Madison University, Harrisonburg, VA

Cyanobacterial harmful algal blooms (cHABs) form on every continent except Antarctica and often include toxic species such as Microcystis aeruginosa, a potent hepatotoxin producer. Due to their ecological and public health impacts, understanding the drivers of cHABs is critical for protecting our freshwater resources. Cyanobacteria generate reactive oxygen species (ROS) through photosynthesis that need to be broken down to avoid damage from oxidative stress within cyanobacterial cells. Some cyanobacteria, such as M. aeruginosa, lack the genes necessary to detoxify ROS, relying instead upon members within the bacterioplankton to carry out this important detoxification process. To advance our understanding of the role of phycosphere bacteria in neutralizing cyanobacteria ROS stress, we performed an incubation experiment across multiple stages of bloom development during the 2023 Lake Erie bloom season. Bloom samples were incubated with 10 µM H2O2, with samples collected at 0 hr, 30 min, 8 hr, and 24 hr for cell abundance, fluorescence, microcystin concentration, and biomass for RNA-Seq. The RNA-Seq data were mined for bacterial activity related to ROS neutralization, targeting the oxidative stress defense genes: katG, sodB, and ahpC, marker genes for the enzymes catalase, superoxide dismutase, and alkyl hydroperoxide reductase, respectively. Bacterial genera likely responsible for ROS neutralization in bloom communities include members of the genera Exiguobacterium, which we have previously shown as a critical member of the Microcystis phycosphere. These findings will provide more insight into how microbial interactions contribute to the competitive success of M. aeruginosa in freshwater and brackish systems.

10302 - Diet of the harvestman *Leiobunum formosum* (Opiliones, Sclerosomatidae)

Victor Townsend,Jr., Maynard Schaus, Jacob Hofstetter

Virginia Wesleyan University, Virginia Beach, VA

The diet of the sclerosomatid harvestman *Leiobunum formosum* was investigated using field observations of foraging individuals, scanning electron microscopy of fecal samples, and the collection of stable isotope data. In the field, harvestmen were rarely observed feeding, but when provided different types of food, showed a significant preference for sliced fruit (peach or mango) over acorns (oak), pokeweed berries, or rocks (negative control). Over a two-year period, SEM examinations of 81 fecal pellets collected from adults revealed considerable variety in the diet including evidence of herbivory, fungivory, and carnivory, based upon the presence of fragments of exoskeleton and setae from arthropods, and the stiff bristles of annelids. The occurrence of identifiable remains of these food items in the feces indicate that these harvestmen lack the capacity to digest cellulose or chitin completely. Based upon a relatively modest sample size, the results of our stable isotope analyses also support the characterization of the diet of *L. formosum* as omnivorous. Adults had nitrogen isotope ratios that show considerable variation between individuals. These $\delta^{15}N$ signatures were much more variable and substantially lower than those obtained for syntopic species of spiders (carnivores) and the cosmetid harvestman *Vonones* sp.

10303 - A Herpetofaunal Inventory of the Wildsumaco Wildlife Sanctuary in Ecuador: Lessons from one of Earth's Richest Biodiversity Hotspots

Jeff Camper[1], Travis Knowles[1], Brian Arbogast[2], Natasha Vanderhoff[3]

[1]Francis Marion University, Florence, SC, [2]University of North Carolina Wilmington, Wilmington, NC, [3]Jacksonville University, Jacksonville, FL

Many scientists agree that we are in Earth's sixth mass extinction because of the effects humanity on the biosphere. Biodiversity hotspots are regions that are exceptionally high in species richness, endemism, and vulnerable to anthropogenic destruction. Starting in 2008 we began to monitor the amphibian and reptile fauna of the Wildsumaco Wildlife Sanctuary on the eastern slope of the Andes Mountains in central Ecuador. The preserve is located adjacent to the buffer zone of the Gran Sumaco National Park. The preserve consists of more than 500 ha of primary and secondary forest ranging from 1300 to 1500 m elevation in the foothills of Volcan Sumaco. This dormant volcano rises to an elevation of more than 3700 m and is approximately 50 km east of the Andes. To date we have documented 44 species of amphibians and 51 species of reptiles in this area. The South American rain frog genus (*Pristimantis*) appear to be particularly diverse at this site with at least 14 species documented so far. The amphibians also include two possible species of salamanders, two species of caecilians and 40 species of frogs. The reptiles include 15 species of lizards and 36 species of snakes. We still have one undescribed species of mushroom-tongued salamander, and one species of *Pristimantis* frog that are new to science that we need to describe.

10311 - Searching for novel superhydrophobic surface structures in tropical plants of the Caine Conservatory

Katie McDonald, Nicole Hughes

High Point University, High Point, NC

Microscopic plant structures can repel water through physical interactions, as in the leaves of the sacred Lotus (*Nelumbo nucifera*). Mimicking such surface structures can potentially serve as a non-toxic alternative to modern waterproofing chemicals such as PFAS. Hydrophobic surface structures also reduce biofilm formation, giving them many applications in health and medicine. Discovering novel superhydrophobic patterns (i.e., those yielding contact angles >150°) is an active area of research. In the present study, we characterized surface structures and quantified hydrophobicity of leaves of a species of corpse flower (*Amorphophallus* sp.), and the petals of an epiphytic orchid (*Phaleonopsis* sp.). Plants were grown in the Caine Conservatory on the campus of High Point University. Species were chosen because they exhibited visible water repellency when water was applied to tissues using a dropper. Contact angles were measured using both the traditional projector method and a Biolin Scientific goniometer. A Phenom XL scanning electron microscope was used to visualize air-dried tissue surfaces. Results showed that both surfaces were hydrophobic (contact angles between 90-150°), but not super-hydrophobic. SEM imaging of leaf and petal surfaces revealed waxy clusters on the *Amorphophallus* leaf, but not on the *Phaleonopsis* petals. No dermal structures (e.g., papillae or trichomes) were observed in either species, although this may be an artifact of air-drying. We are currently experimenting with critical point drying methods to better visualize surface structures. We are also in the process of testing hydrophobicity in additional species.

10317 - Using Wikipedia editing to improve research and communication skills in an undergraduate science writing course

Amber Rock

University of North Carolina at Pembroke, Pembroke, NC

Teaching writing in the biological sciences has traditionally focused on manuscript-style writing (Introduction, Methods, Results, Discussion) or other forms of structured research papers. However, only a small percentage of biology majors will continue to utilize these forms of writing in their future careers. Therefore, STEM writing courses should also include instruction in summarizing scientific information for a general audience, as students are much more likely to utilize this form of science communication after graduation. In this presentation, I will discuss my experience using Wikipedia editing as a tool for improving undergraduates' research, writing, and communication skills. With the support of Wiki Education, I have conducted a Wikipedia editing project in at least one of my courses for the past four years. To complete the project, each student must select a biology-related Wikipedia article that needs improvement, conduct a literature search to find information on the topic, and summarize the information in a way that can be understood by the general public. Along the way, Wiki Education tutorials teach students the technical aspects of editing Wikipedia articles, the types of references that are acceptable, and the importance of cultivating a more diverse community of Wikipedia editors. Students also improve their oral communication skills through classroom discussions and a short oral presentation about their selected topic. This presentation will outline the steps necessary to complete a course-based Wikipedia editing project, identify the pros and cons of Wikipedia editing, and evaluate the success of the project from both instructor and student perspectives.

10318 - The distribution of oak mistletoe [*Phoradendron leucarpum* (Raf.) Reveal & M. C. Johnst.] is more restricted with regards to habitat type than that of its avian frugivore dispersers.

Nicholas Flanders[1], Lytton Musselman[1], Christopher Randle[2], Daniel Barshis[1], Eric Walters[1]

[1]Old Dominion University, Norfolk, VA, [2]Sam Houston State University, Huntsville, TX

The dependence of many mistletoe species on highly visible avian frugivores for seed dispersal makes the study of mistletoe ecology especially illustrative of the importance of dispersal limitation in determining plant distributions. We sought to determine if dispersal limitation could explain a positive relationship between forested wetland habitat and oak mistletoe (*Phoradendron leucarpum*). Using stratified random sampling, we selected 96 circular plots with 25-m radii to survey repeatedly for avian frugivore species in winters (Dec–Mar) 2015–2020. Plots were in forested habitat in the Coastal Plain and Piedmont regions of Virginia and North Carolina, USA. We analyzed occurrence data using a community occupancy model to estimate species-specific relationships between forested habitat type and occupancy while accounting for imperfect detection. We did not find any relationship between occurrence and habitat for either of the two principal oak mistletoe dispersers. We also looked at correlations between oak mistletoe genetic structure and habitat type to examine evidence for cryptic disperser habitat relationships. Seven microsatellite markers were genotyped across 517 mistletoe samples from forested wetland and urban habitats. Analyses of the resulting fragment length data showed evidence for gene flow across habitats. Interestingly, there was a genetically distinct set of samples that were only associated with host trees of the genus *Nyssa*. These results, coupled with evidence from planting experiments, suggest that establishment limitations play a larger role in observed oak mistletoe habitat relationships than avian disperser behavior.

10324 - Presentation Withdrawn

10333 - The Effect of Temperature and Precipitation on Flowering Times and Germination in *Seymeria* (Orobanchaceae)

Ben Gahagen

Abraham Baldwin Agricultural College, Tifton, GA

Seymeria (Orobanchaceae) is a genus of approximately 19 root hemiparasitic plant species distributed throughout the Southern United States to Central Mexico. From the mid-1800s to present, surface temperatures have increased almost 2oF. Similarly, precipitation levels have also dramatically fluctuated. Plant phenology, specifically flower and fruiting times, is correlated to specific temperatures and precipitation levels and evidence implies as the climate shifts, so will the flowering and fruiting times. To assess potential flowering time changes due to climate change in Seymeria, digitized herbarium specimens of species with at least 50 specimens were recorded and assigned a phenophase – whether the collected plant was flowering, fruiting, or both. Results suggest that from the 1800s to present day, the two species distributed in the Southeastern United States have had a phenological shift while those species with a more western distribution show little change in flowering and fruiting times. Populations of S. cassioides are widely distributed throughout the Southeastern United States and are commonly found in ecosystems that rely on routine wildfires. To assess the impact fire and the heat generated from fire has on the germination of S. cassioides, a treatment group of seeds was subjected to a layer of burning pine needles. Control groups consisted of uncovered seeds and seeds covered with pine needles but not burned. Results suggest that fire has little impact on the germination rates of S. cassioides.

10338 - Effectiveness of Pulsed Gastric and Intestinal Lavage in Microplastic Research

Lilly Ibsen[1], Lili McNulty[2], Ryan Saylor[2]

[1]Berry College, Rome, GA, [2]Berry College, Mount Berry, GA

Microplastics are a global concern because they may impact freshwater, marine, and terrestrial animals, including humans. Threats from microplastics may include blockage of the digestive system to release of other noxious chemicals in the stomach. Currently, research on microplastics requires the sacrifice of live specimens followed by extraction of the entire gastrointestinal tract. We tested a non-lethal method, Pulsed Gastric and Intestinal Lavage (PGL/PIL; hereafter referred to as lavage), and compared the results to our lethal collection methods. Sample fish were collected from the Berry College campus because of potentially lower pollution levels in these streams. Fishes were collected using backpack electrofishing and all fish were euthanized using a clove oil solution (whole clove oil extract in 95% ethyl alcohol; 1:9) prior to administering lavage. Both lavage methods were performed by inserting a metal syringe into the stomach (through the mouth; PGL) or intestine (through the vent; PIL) to slowly pulse water into each organ, respectively, to empty the contents. Approximately 3 rinses of 60 milliliters of filtered deionized water were used during lavage and samples were collected/stored in glass jars. Following lavage, the entire gastrointestinal tract (esophagus to vent) was removed, and both (lavage and GI tract) were chemically digested using our hydrogen peroxide method. The microplastics were quantified using basic light microscopy and a novel staining procedure with UV fluorescence. Herein, we will describe the results of this pilot study and how it

compared to lethal collection and sampling methods. Our non-lethal method offers an alternative way to investigate microplastics in live animals without the need to sacrifice animals. Furthermore, reducing the use of lethal sampling is especially critical for endangered or threatened species, which are generally off-limits and represent knowledge gaps in our understanding of microplastic pollution.

10344 - Understanding how floral traits impact floral bacterial and yeast community composition in pollinator gardens

Grace Freundlich

Furman University, Greenville, SC

Plant-pollinator interactions are of vital importance to ecosystem functioning and a viable human civilization. To date, we've extensively studied how pollinators select for certain flowering plants and how these preferences shape floral morphology, display size, and color. However, we have failed to fully identify include how floral microbes influence plant-pollinator interactions. To understand how pollinators, plants, and microbes influence each other, my students and I investigated how these multiple variables act together to shape floral microbial communities in Upstate South Carolina. To begin addressing this question, we measured specific floral traits, such as the petal texture via scanning electron microscopy (SEM), to model how these features shape the resultant composition and diversity of floral microbe communities.

To date, we've discovered varying morphological features in the epithelial cells within the petals we sampled. The Asteraceae species we've sampled had more ridged surface features compared to the other species we sampled at the solar farm while the other families represented had unique morphological features in the petals. When we included this data with other morphological traits, we found significant species-specific effects that influenced the resultant bacterial communities we found residing in the flowers. In our future work, we will continue to survey additional flowering species and include a more nuanced approach to investigate how pollinators and flowers jointly select for microbial communities.

10349 - Investigating Missense Variants in γ-secretase Cleavage Site of Alzheimer's–related Amyloid Precursor Protein

Hanna Joy Jefcoat, Cynthia Stenger

University of North Alabama, Florence, AL

Alzheimer's Disease (AD) is the most common neurodegenerative disorder in the world and can be caused by aggregations of amyloid beta protein in the brain. Amyloid beta is a derivative of amyloid precursor protein, which is coded for by the APP gene. When APP is atypically cleaved, amyloid beta can be aggregated into longer chains, forming plaques. The oligomers and polymers that make up these plaques are toxic and illicit cascading reactions, causing neurotransmitter interruption and cell death. This bioinformatics project investigates missense amino acid swaps in the γ-secretase cleavage site of APP. Homology modeling and data gathered from pathogenicity predicting software were used to predict variant impact on protein structure.

10350 - A clustering approach to the study of bacteriophage genome mosaicism

Madison Bendele, Steven Cresawn

James Madison University, Harrisonburg, VA

Bacteriophages (phages), viruses that infect and kill bacteria, are the most abundant biological entity in the biosphere, with an estimated 1031 particles on Earth. Phages play key roles in the environment, advancements in biotechnology, and the ability to treat antibiotic-resistant infections. Their ubiquity and genomic diversity make their genomes the largest reservoir of unexplored genes and proteins in the biosphere, however, only approximately 30% of their proteins have been functionally annotated. Pervasive genome mosaicism among phages of a common host complicates any wholistic understanding of their genome organization or functional annotation of their genes, and there is a dearth of published transcriptomic data from phage-infected cells. To address this knowledge gap, we have taken a bioinformatics-based approach to describing genome organization of 4,516 phages infecting members of the Actinobacteria. This approach utilizes the principle of "guilty by association", wherein syntenic genome fragments containing two or more genes are quantified, clustered and visualized. Specific metrics for this approach include gap sizes between adjacent genes, relative transcriptional orientation, and frequency of genome co-occurrence relative to their background frequencies of occurrence individually. We hypothesize that phage protein "phamilies" that frequently are found in association with one another by these metrics are likely to be co-expressed and functionally related to one another. Future studies will focus on protein functional prediction using machine learning approaches and statistical modeling of patterns of co-occurrence.

10353 - Area-limited versus isolation-limited species: testing whether land vertebrates' differing responses to island area and isolation produce non-nested island communities in the Gulf of Maine

Grant Bowers, Gareth Russell

New Jersey Institute of Technology, Newark, NJ

An island's area and isolation affect whether any given mainland species can be found there. Species that have large area requirements and/or are good dispersers should be more area-limited, while species that have low area requirements and/or are bad dispersers should be more isolation-limited. It has been theorized that this should create non-nested island communities in which smaller nearshore islands have the isolation-limited species, larger remote islands have the area-limited species, and larger nearshore islands have both. Although this pattern has been anecdotally reported, no statistical test has been conducted to satisfactorily verify its existence. We set out to statistically analyze 1) whether there are interspecific differences in the relative importances of area versus isolation as predictors and 2) whether any species pairs show a non-nested pattern across island area and isolation. To do so, we used trail cameras to collect land animal presence/absence data from 24 small islands off the coast of Maine, USA. For the five terrestrial mammals and one terrestrial bird we analyzed, we modeled their presence/absence using a logistic equation, with area and isolation as predictors. For each species, we used a Markov Chain Monte-Carlo algorithm to generate a posterior distribution of the ratio between the area and isolation coefficients. We found that 1) differences between many of the species' ratios were strongly supported, and 2) the existence of the non-nested pattern itself was strongly supported for one pair of species: the more isolation-limited American red squirrel and the more area-limited wild turkey. This provides a counterexample to the usual nested pattern seen in island communities, showing how area and isolation alone might produce a mosaic of non-nested communities.

10354 - Extending SERNEC herbarium records with new functionality in Symbiota 3.1.

Andrea Weeks

George Mason University, Department of Biology and Ted R. Bradley Herbarium, Fairfax, VA

In late 2024, Symbiota 3.1 quietly rolled out to the Southeast Regional Network of Expertise and Collections (SERNEC) portal, which holds data from over 5.8 million herbarium records contributed by 134 southeastern US herbaria. Multiple improvements were included in this latest Symbiota database version but among the most potentially transformative is the new Extended Data Import Tool. This presentation will explain the purpose of this tool, how it ties to the emerging Extended Specimen Concept and how to use it as a data manager or researcher. Its use will be illustrated in a case study that links (e.g., extends) specimen records from the Lord Fairfax Community College herbarium with their digitized historical field notebook records using controlled vocabulary and archival universal resource locators.

10363 - Network Analysis of Plant-Microbe Interactions Influences Plant Fitness and Shows Overlap with Plant-Pollinator Interactions

Daniel Barker[1], Liedson Carneiro[1], Jessica Williams[2], Gerardo Arceo-Gomez[1]

[1]East Tennessee State University, Johnson City, TN, [2]Florida Atlantic University, Boca Raton, FL

Pollination is the exchange of floral rewards for the transport of pollen by animal pollinators, which facilitates plant reproduction. Recent studies reveal that nectar yeasts and bacteria play a significant role in shaping plant-pollinator interactions. These microbes metabolize nectar carbohydrates and amino acids, altering nectar chemistry and scent which alters floral attractiveness to pollinators. Furthermore, the overall effect these microbial groups have on plant-pollinator interactions is based on their identity and abundance. Using network theory, this research explores how nectar microbes affect male and female plant reproductive success, whether plants with similar nectar microbes share pollinators, and how plant-microbe network metrics correlate with plant-pollinator networks. Understanding these dynamics improves predictions of plant fitness and community interactions. This research was done by collecting nectar samples from multiple individuals across 16 plant species and which were cultured on YMA and TSA agar plates until isolated and identified by Sanger sequencing. In total, 21 bacterial and 9 yeast groups were found across 1396 flowers with 22,243 colonies counted from nectar cultures. Nectar microbiome specialization (degree and "d") significantly enhanced female reproductive success (pollen tube formation), while showing no effect on male success (conspecific pollen receipt or pollen dispersal). Also, nectar volume did not influence microbial colony abundance ($\chi^2 = 1.13$, df = 1, $p = 0.19$), suggesting that microbial presence may be strongly mediated by the plant host. Microbiome similarity between plant species was significantly correlated with pollinator composition ($r = 0.26$, $p = 0.02$), indicating overlap in pollinator sharing among plants with similar microbiomes. These results highlight the role of nectar microbiomes in shaping plant-pollinator interactions, particularly through their influence on female reproductive success, emphasizing the importance of incorporating microbial dynamics into pollination ecology studies.

10364 - Population Genetics of Three Mussel Species in the Genus *Elliptio*

Molli Newman, Mary Joy, Dr. Kaelyn Fogelman, PhD, Jonathan Miller, Brian Helms

Troy University, Troy, AL

The state of Alabama is home to 180 freshwater mussel species, 70% of which are imperiled. Mussels rely on their fish hosts for larval dispersal. However, due to fragmentation as a result of barriers to aquatic connectivity, fish movement can become limited, thus limiting mussel dispersal and gene flow. This project seeks to quantify the relationship between mussel genetic diversity and factors that could be influencing genetic connectivity of mussel populations within the Upper Chipola River Strategic Habitat Unit (SHU) located in southeastern Alabama. During summer 2024, a total of 15 sites were surveyed on Big and Cowarts Creeks, and mussel tissue samples were collected for 3 common mussel species, the inflated spike (*Elliptio purperella*), Gulf slabshell (*Elliptio fumata*), and Gulf spike (*Elliptio pullata*). Mussel population genetics were examined by extracting genomic DNA, amplifying the cytochrome oxidase I (COI) subunit gene, sequencing these amplicons, and then analyzing the sequences to examine population genetics within and among the various sampling sites for each mussel species. Patterns of population genetic diversity, structure, and connectivity will be related to geographic distance and measures of stream connectivity derived from Southeast Aquatic Resource Partnership road crossing assessments. This presentation will present the findings of this analysis and identify potential barriers to genetic connectivity for these common mussel species and other Endangered Species Act-listed Threatened and Endangered mussels within this critical habitat.

10371 - Vascular Flora of Paddy Mountain Plant Preserve, Ashe County, North Carolina

Christian Cline, Zack Murrell

Appalachian State University, Boone, NC

This study aims to document the flora of Paddy Mountain Plant Preserve in central Ashe County, North Carolina from Spring 2023—Summer 2025. Paddy Mountain lies within the Blue Ridge Range of the Southern Section of the Blue Ridge Physiographic Province. Additionally, Paddy Mountain is a part of the unique geological feature called the Amphibolite Mountains Macrosite. As amphibolite weathers it supports the development of rich soils with a high base content. This contributes to the high biodiversity found within the Amphibolite Mountains Macrosite. Paddy Mountain stands at a lower elevation than most of the other amphibolite mountains but includes a well-preserved High Elevation Rocky Summit plant community along its ridgeline. Known rare plants to Paddy Mountain include the North Carolina endemic *Liatris helleri* Porter and the southern Appalachian endemic *Houstonia montana* Small. In addition to specimen collection, photographs will be used to document species *in situ* on iNaturalist to provide living specimen data that can be cross-referenced with the herbarium vouchers. This study documents a new site for *Liatris helleri* and provides the first collection of *Capnoides sempervirens* in Ashe County. Over 190 taxa from 80 genera and 55 families have so far been documented. Voucher specimens collected in this study will provide the material necessary for genetic work and/or used for systematic analyses. This research will contribute to the floristic knowledge of the Amphibolite Mountains Macrosite by completing the first comprehensive inventory of the flora of Paddy Mountain Plant Preserve and guide future management decisions.

10375 - New Host Records for Nearctic Pincer Wasps (Hymenoptera: Dryinidae) through DNA Barcoding

Michael Rogers, Mackenzie Cooper, Aiden Starry, Alexander Shoemake, Grace Orewiler, Georgia Jinks, Danielle Lowe, Jacob Taylor, Jeremy Blaschke

Union University, Jackson, TN

Pincer wasps of the family Dryinidae (Order Hymenoptera) are ecologically beneficial parasitoids of planthoppers (Order Hemiptera: Suborder Auchenorrhyncha), many of whom are significant agricultural pests. However, little is known about the diversity of dryinids and their host use due to the difficulty in associating sexually dimorphic males with females and parasitoid larvae with adults. To generate novel data about the biology of these unusual wasps and to discover new host records, DNA barcoding was applied to freshly collected specimens of adult dryinids, their larvae, and their planthopper hosts collected from Cypress Grove Nature Park, Jackson, TN. In total, 53 planthopper hosts with attached larvae were collected, representing 19 species. 24 adult dryinids were collected. Planthoppers and adult dryinids were identified morphologically to species, and adult dryinids and larval dryinids were barcoded. The barcode for each larva was compared to adult barcodes to reveal the species identity of each larva. In this way, 3 new host records were found for the dryinid *Aphelopus*, including *Erasmoneura vulnerate*, *Alebra eburnea, and Erythroneura vitis*. These findings uncovered novel parasitic relationships within Dryinidae, thus contributing to a broader understanding of parasitoid-host dynamics in forest ecosystems.

10381 - Characterizing the *Mcoln1*$^{-/-}$ mouse as a model of early Age-related Macular Degeneration

Jonathan Miller

James Madison University, Harrisonburg, VA

Age-related macular degeneration (AMD) is a leading cause for vision loss across the world, as disease pathology remains irreversible. Better characterization of AMD will aid in early detection methods to combat disease development, as a proper animal model for studying this disease is not readily available. The Mcoln1-/- mouse may serve as a model for studying retinal degeneration in humans by comparative characterization of genomics data. Previous research has determined Mcoln1-/- mice suffer from retinal dysfunction, decreased expression and mis-localization of photoreceptor (PR)-specific proteins, and downregulation of phototransduction transcripts. Previous unpublished data in our lab demonstrates that human PR-specific genes have increased levels of DNA methylation and decreased transcription in AMD-affected tissues. The goal of this study was to determine if PR-specific genes and proteins are similarly dysregulated in Mcoln1-/- mice. Several key phototransduction proteins of older Mcoln1-/- mice exhibited distinct mis-localization in PRs, along with increased methylation of their genes promoter regions. Western blot experiments determined no significant loss in phototransduction proteins in Mcoln1-/- mice, suggesting overall dysfunction and dysregulation occuring in mutant mice to induce retinal dysfunction. These experiments suggest that the Mcoln1-/- mouse suffers from overall dysregulation of phototransduction components, rather than global cell loss as determined through H&E stained mutant retinas. The Mcoln1-/- mice that exhibit retinal dysfunction may serve as an effective tool for investigating early human retinal dysfunction, instead of traditional mouse models that exhibit global cell type loss.

10392 - Investigating the role of intrinsic foot muscles in modulating foot shape while performing asymmetric balance tasks and walking on banked surfaces.

Luke Lotsis

James Madison University Biology Department, Harrisonburg, VA

Background: Falls are the leading cause of injury, hospitalizations, and mortality among older individuals. 30% to 50% of falls occur due to environmental interferences such as structural obstacles and cross-slopes (inclined surface perpendicular to line of progression; Baltas et al., 2005), common features in our physical environment. Previous studies have supported the role of intrinsic foot muscles (IFM) in foot contact/manipulation during turning and balance on level uniform surfaces. Reeser et al. (1983) discovered complementary activation of IFM relative to center of pressure position in the foot, suggesting pedal muscle activity, specifically intrinsic abductors/adductors, might actively regulate medio-lateral load shift. The purpose of this study was to elucidate the role of IFM in modulating foot load when walking on banked substrates and performing asymmetric balance tasks

Methods: Synchronized wireless surface electromyography (EMG 3000Hz; Noraxon Telemyo), plantar pressure (100Hz; emed® Novel GmbH, Munich, Germany) and kinematics (Qualisys) were collected as 24 subjects walked on flat and banked, and granular substrates (5 randomized trials each). Raw EMG was filtered normalized, and smoothed. Plantar pressure (mean, peak) and contact time were calculated throughout stance in 12 anatomical masks (five toes, five metatarsal heads, mid/hind foot). Linear mixed effects models were used to compare integrated EMG for each muscle and forefoot plantar pressure across substrates.

Results: There was significantly higher activity* in the medial muscle group (ABDH, PDIO1) during upslope trials, correlating with increased T1/MTH1 pressure* compared to flat/downslope trials. Conversely, lateral muscle group (ABDM, PDIO3) activity was significantly higher* in downslope trials, correlating with increased T5/MTH5 pressures* compared to flat/upslope trials (* = $p<0.01$).

Interpretations: Results suggest IFM regulate foot-substrate interactions by modifying the relative position of the fore and rear parts of the foot to resist the tendency of the center of mass to “fall” down the cross-slope.

10394 - Team Terrapin: Impacts of Undergraduate Research Experiences, Participatory Science, and Strategic Partnerships

Jordan Gray

Turtle Survival Alliance, North Charleston, SC

In scientific research, the utilization of Undergraduate Research Experiences (URE), Participatory Science, and collaborative Partnerships has been a longstanding practice for data collection. A project focused on the Carolina Diamondback Terrapin (Malaclemys terrapin centrata) on an island in Northeast Florida initially involved undergraduates to assist in data collection, later transitioning under the auspices of Florida State Parks, which refined methods and expanded the project's scope. In 2016, Team

Terrapin was formed, marking a pivotal step forward for the project and its conservation efforts. A transformative partnership formed in 2022 with the Turtle Survival Alliance–North American Freshwater Turtle Research Group significantly strengthened these efforts, tripling volunteer participation that year and increasing it again by 50% in the following year. In 2024, volunteer participation rose again to 64 individuals, detecting well over 500 nests despite significant ecological changes on the island. The program also integrated a project to scientifically monitor nest temperatures, enhancing research on terrapin reproductive ecology and climate resilience. From 1997–2015, nest detections averaged 275 per year, increasing 93.09% to 536 per year from 2016–2021, and rising another 58.58% to 850 per year from 2022–2023. Nest predation detection increased from 193 annually (1997–2015) to 326 (2016–2021) and 616 (2022–2023). Adult turtle detections averaged 13 annually (1997–2015), dropped to 10 (2016–2021), then surged 370% to 47 annually (2022–2023). Volunteer participation rose dramatically, from 6 per year (1997–2015) to 10 (2016–2021) and 47 (2022–2023). This collaboration improved data collection, increased public awareness, boosted funding, and highlighted the power of integrating URE, Participatory Science, and Partnerships in ecological research. These efforts have significantly advanced protections for the Carolina Diamondback Terrapin, fostered community engagement, and sparked new collaborations, solidifying the island as a critical site for terrapin research and conservation.

10398 - Effects of an invasive crayfish and impoundments on macroinvertebrate assemblages

Colin Nunn[1], Riley Egan[1], Zanethia C. Barnett[2], Brian Helms[1]

[1]Troy University, Troy, AL, [2]USDA Forest Service, Center for Bottomland Hardwoods Research, Clemson, SC

Impoundments and invasive crayfish are pervasive disturbances in aquatic systems and can have strong, often long-term effects on aquatic macroinvertebrates. In the Cahaba River drainage (CRD) of central Alabama, Faxonius virilis has been introduced and become the dominant crayfish species in many reaches. With over 117 small dams throughout the CRD, interactions between F. virilis and dams could be significant. The objective of this study is to examine relationships of dams and F. virilis on macroinvertebrate assemblages in the CRD. Macroinvertebrate assemblages and stream habitat were quantified using standard techniques on 2 reaches (immediately downstream of dam and ~1km downstream of dam) in 6 impounded streams and 4 unimpounded streams (10 streams, 20 reaches total) within the CRD. In each reach during summer 2022, Surber samples were used to quantify macroinvertebrate abundance, richness, and structure. Macroinvertebrates subsequently were stored in 75% ethanol, identified to genus, measured, and enumerated. Preliminary results suggest that impounded reaches richness (mean 40.3, range 32-49) and density (mean 3423/m2, range 1188 – 9018 / m2) was similar to unimpounded reach richness (mean 38.4, range 25-46) and density (3003/m2, range 600 – 8574 / m2). Similarly, reaches with invasive crayfish had similar macroinvertebrate richness (mean 38.4, range 25-46) as reaches with only native crayfish (mean 40.3, range 34-49). However, reaches with invasive crayfish have slightly higher macroinvertebrate density (mean 4064 / m2, range 1622 – 9018 /m2) than reaches with only native crayfish (mean 2594 / m2, range 600 – 7137 /m2). These results, along with refined taxonomic resolution and further analyses, will help elucidate synergistic effects of dams and F. virilis on macroinvertebrate assemblages.

10404 - Testing the monophyly of Neotropical Palo Santo trees (*Bursera graveolens*; Burseraceae) using ddRADseq data

Elizabeth Collins[1], Dr. Andrea Weeks[2]

[1]George Mason University, Department of Biology and Ted R. Bradley Herbarium, Fairfax, VA, [2]George Mason University, Fairfax, VA

Bursera graveolens (Kunth) Triana & Planch. (Burseraceae), or palo santo, is an economically and ecologically important tree species found throughout the seasonally dry tropical forests (SDTF) of southern Mexico south to Peru. No study to date has evaluated the relationship among the many disparate island and continental populations of *B. graveolens*, which are among the most widespread in the genus and rivaled only by those of *B. simaruba*, a distantly related species of *Bursera.* subg. *Bursera*. My research examines the population genetics and phylogeography of palo santo to test biogeographic hypotheses regarding the formation of the SDTF on a continental scale and population genetic variation across its range. I am also completing a taxonomic revision using morphological and phylogenetic data to determine if palo santo as currently described comprises a single, widespread lineage or segregate taxa. In this presentation I will share the outcomes of my phylogenetic analyses testing the monophyly of the species.

10407 - Lowland River Valley Drives Patterns of Population Genetic Structure in Southern Appalachian Woodland Jumping Mice (*Napaeozapus insignis*)

Emma Watersmith, Stephanie Kamel, Brian Arbogast

University of North Carolina Wilmington, Wilmington, NC

At their southern edge-of-range, woodland jumping mice (*Napaeozapus insignis*) are associated with the high-elevation spruce-fir forests of the southern Appalachians, one of the most endangered ecosystems in North America. This ecosystem consists of a series

of Pleistocene relics, restricted to high elevations due to climate change. Consequently, gene flow is expected to be limited among sky island populations, which can result in these populations having strong geographic patterns of genetic structuring. To elucidate this relationship, we studied the population genetic structure of spruce-fir sky island associated woodland jumping mice. We sampled individuals from seven sites in western North Carolina (NC), the Allegheny Mountains in West Virginia (WV), and the White Mountains in New Hampshire (NH) and sequenced the control region of mitochondrial DNA and genotyped individuals at 13 microsatellite loci using novel primers. In using populations from both the central and northern Appalachians alongside our focal populations from the southern Appalachians, our study provides a comparative framework for understanding how genetic patterns vary across this species' range. Our results show distinct genetic clustering of WV and NC woodland jumping mouse populations, with minimal genetic overlap. Within NC, northern and southern sky island populations, separated geographically by the French Broad River, clustered separately. Importantly, the southernmost population is significantly differentiated from all other populations in NC. These results highlight the impacts of the geographic dispersal barriers posed by river gorges such as the French Broad River on the resultant population genetic structure of the woodland jumping mouse. Moreover, these data may be broadly informative to the conservation of other Appalachian sky island species.

10418 - Vegetative anatomy of *Physaria globosa* (Brassicaceae), with systematic and environmental considerations.

Shawn Krosnick, Windsor Kiefer, Sarah Elliott

Tennessee Tech University, Cookeville, TN

Physaria globosa, known as Short's Bladder Pod, is a Federally endangered plant species in the Brassicaceae. This species occurs in Tennessee, Kentucky, and Indiana and is limited to just 33 extant populations. Populations are typically found on limestone bluffs, either in full sun (Tennessee) or under tree cover (Kentucky and Indiana). There are only two species of *Physaria* found east of the Mississippi River. In the United States, ca. 25 species of *Physaria* are endemic to the Rocky Mountains on high elevation rock outcrops. *Physaria globosa* exhibits features that appear to be adaptive to xeric environments, including dense trichomes and stocky stem bases that die back annually. In order to better understand this species in relation to its environment, we completed an anatomical study using vegetative paraffin embedded tissues and differential staining, along with light microscopy. We present a full characterization of primary and secondary growth with the goal of identifying features unique to the genus *Physaria* and characteristics that may be environmentally adaptive.

10429 - Buzzed and Bothered: Investigating the Impact of Psychoactive Plant Alkaloids on Bumblebee Behavior

Skylar Mathieson, Joshua Foley, Melissa Whitaker

East Tennessee State University, Johnson City, TN

The relationship between plants and pollinators is often viewed as a strict food-for-service exchange in which plants provide nutritious rewards (nectar, pollen) for pollinators in exchange for the dispersal of plants' gametes (pollen). Yet in addition to provisioning key nutrients, the floral rewards of many plants contain diverse chemical compounds whose functions are mysterious or even puzzling. For example, many floral rewards contain plant secondary compounds that have are traditionally classified as defensive toxins. Some of these "toxins" include neuroactive alkaloids that affect pollinator cognitive functions such as learning and motivation, suggesting dual roles for these phytochemicals. We are investigating the behavioral and physiological responses of generalist pollinators (*Bombus impatiens* bumblebees) to three psychoactive plant alkaloids – caffeine, nicotine, and morphine – using robotic flowers. Pollinator preference and performance assays are coupled with pollen transfer experiments to identify potential tradeoffs or conflicts in alkaloid-mediated plant-pollinator interactions, and to assess the potential for hijacking of pollinator behaviors by plants. Investigations into plant manipulation of pollinator preference is particularly salient given that some pollinators have even found to exhibit addictive behaviors to neonicotinoid insecticides. With a better understanding of how floral reward chemistry affects pollinator cognition, behavior, and foraging decisions, we hope to work towards reconciling the seemingly contradictory forces that shape plant–insect coevolution and drive plant chemodiversity.

10466 - Can a variant of lamin A slow down the process of aging?

Aurora Arjmand, Jill Penn

Georgia Gwinnett College, Lawrenceville, GA

This study is investigating the possibility of slowing down the process of aging by looking into the Hutchinson-Gilford Progeria Syndrome. Progeria is a genetic disorder that causes rapid aging in children due to a point mutation in exon 11. A nine-nucleotide sequence in the wild type allele, CAG GTG GGC, differs from the consensus splice donor site by two nucleotides. The point mutation

that causes Progeria results in the stretch of nine nucleotides differing from the consensus sequence by only one nucleotide, CAG GTG GGT. In patients with progeria this cryptic splice site is used more often than in wildtype and results in a shorter mRNA and eventually a toxic protein called progerin that distorts the structure of the nuclear membrane. Study has shown that smaller amounts of progerin protein can be found in unaffected individuals, with increased amounts found in older individuals. By using bioinformatics software, it was found that the stretch of nine nucleotides in exon 11 is highly conserved among placental mammals. However, we found 8 species of mammals that differ from the consensus splice donor site by three nucleotides. We predict that in this subset of mammals, the cryptic splice will not be used, or will be used less often, compared to species with the evolutionarily conserved sequence. Absence of progerin might protect the species from the effects of aging.

10472 - Is Spring Break Coming Early? Effects of Climate Change on Alabama's Native Plant Phenology

Madisyn Barksdale[1], Tenzing Ingty[2]

[1]Jacksonville State University, AL, [2]Jacksonville State University, Jacksonville, AL

Climate change has significantly impacted biodiversity, prompting many species to adapt by altering their phenology—the timing of life cycle events. Shifts in plant phenology can have far-reaching ecological consequences, particularly for species that rely on these plants directly or indirectly. One critical consequence is the temporal mismatch between plants and their pollinators, a phenomenon observed in multiple species. Studies using satellite imagery have documented advances in spring phenology across the United States, but species-specific data remain limited, especially in the biodiverse and ecologically vulnerable Southeastern region. To address this gap, we analyzed historical records from herbarium specimens of native plant species in Alabama. Our dataset consisted of 1,304 specimens from 11 species, spanning 146 years. The analysis revealed that 10 of the 11 species exhibited advanced flowering phenology, with three showing statistically significant correlations ($p < 0.05$) between the day of year (DOY) of flowering and the collection year, as determined by Pearson's correlation. This study represents the first attempt to leverage herbarium specimens to investigate climate-driven changes in plant phenology in the Southeastern United States. The observed advancements in flowering phenology for most species align with global findings from previous studies. While satellite imagery has highlighted regional trends in spring phenology, its broad spatial scale cannot capture species-specific responses, underscoring the value of our specimen-based approach. Expanding this research to include more species and specimens would help address key limitations, including the small sample size for certain species.

10476 - Integrating Constructive Dialogue Pedagogy into the Genetics Classroom to Assess Potential Impacts on Students' Global Perspectives, Intercultural Competency, and Moral and Ethical Reasoning Skills

Elisabeth Javazon, Jill Penn, Mark Partridge, Thomas Lilly

Georgia Gwinnett College, Lawrenceville, GA

The Constructive Dialogue Institute defines constructive dialogue as "conversations in which people who have different values, beliefs, and perspectives seek to build new ways to understand and interact with each other, even as they sustain commitments to their own principles and perspectives." The ability to have constructive dialogue experiences between people with differing viewpoints or opinions is becoming more important in society. As future ambassadors of science, biology students will be tasked with communicating complex scientific concepts to people of varying cultures, beliefs, and perspectives. We integrated constructive dialogue curriculum as it relates to two of Georgia Gwinnett College's (GGC) core curriculum outcomes, the development of intercultural awareness and the demonstration of moral and ethical principles into the Introduction to Genetics course. The curriculum, called *Perspectives*, contained six to eight online modules, as well as, three in person peer-to-peer practice sessions. The impact of the constructive dialogue curriculum was assessed using three validated proprietary assessment tools.No statistical differences in global and cultural perspectives or moral and ethical reasoning skills were observed between the control and experimental sections of students taking genetics, however, positive trends were observed. A few challenges to this research project include small sample size and the limited in class exposure to constructive dialogue curriculum due to the large amount of biology content needed to be covered during the semester.Society benefits when there are more individuals in a society that can accept each other's differences and respectfully interact with people of differing opinions. The ability to see issues from different perspectives often results in finding solutions to difficult problems. Incorporating this type of pedagogy into collegewide curriculums may foster more welcoming campus and classroom environments and enhance social interactions outside of the college, particularly during this time of intense social discourse.

10509 - Comparative Analysis of Histone Modification Distribution in HepG2 cells in Response to HBV Infection and HCC Development

Abigail Hunninghake, Dr. Andrea Perreault, Mandi Lichtenstein

Elon University, Elon, NC

This research aims to identify and compare histone modification patterns in hepatocellular carcinoma (HCC) and Hepatitis B Virus (HBV)-infected cells. HBV is a small DNA virus that infects the liver, affecting over 296 million people worldwide. Chronic HBV infection is the leading cause of HCC, a form of liver cancer responsible for 70-85% of all liver cancer cases globally. HBV's replication relies on episomal covalently closed circular DNA (cccDNA), which serves as a template for viral mRNA transcription. Among HBV's viral proteins, Hbx is a critical regulator that alters the epigenetic landscape of host cells, particularly by modifying histones – proteins essential for DNA organization and gene regulation. Histone modifications, such as trimethylation (H3K27me3) and acetylation (H3K27ac) at lysine residue 27 on histone H3, play key roles in regulating gene expression by repressing or activating specific loci. This study will compare these histone modification patterns in HCC and HBV-infected cells with those in normal liver cells to identify loci associated with altered gene activity. Results are expected to reveal increased H3K27ac at oncogenic loci and increased H3K27me3 at tumor suppressor loci. These findings aim to enhance the understanding of HBV-induced epigenetic dysregulation and may inform the development of more targeted therapeutic strategies for HCC.

10530 - Recycling the biomass of marine fouling organisms into ceramic sculptures

Jennifer Zettler[1], Casey Schachner[2]

[1]Georgia Southern University, Armstrong Campus, Savannah, GA, [2]Department of Art, Georgia Southern University, Armstrong Campus, Savannah, GA

The Georgia coast has provided a rich source of natural materials that were creatively utilized by its earliest inhabitants. For thousands of years, Native American pottery was crafted using locally sourced clay, sand, and crushed oyster shells. Oysters were also used in early home construction as a coastal tabby concrete material. Georgia's salt marsh ecosystems continue to supply a variety of productive resources. Fueled by a dynamic exchange of tidal and freshwater flows, nutrients from both natural and human sources support primary productivity. However, excessive nutrient levels can lead to harmful algal blooms and overgrowth by biofouling organisms. One method for reducing nutrient overload is the use of Algal Turf Scrubbers (ATS), a simple system featuring a sloped flow-way with an attached substrate. Algal species colonize the substrate, absorbing and assimilating nutrients from the water into their biomass. One drawback to this technology is that the biofouling organisms that make up the biomass can become waste if not properly utilized. There is growing interest in repurposing ATS waste for biofuels, landfill covers, and compost, though the high salinity and ash content of marine biofouling organisms limits these applications. Paradoxically, the problematic salt and ash components of biofouling algal turf contribute to its suitability as clay for ceramics. Sculptures crafted from bio-clay are remarkably sturdy and can be fired at all kiln temperature ranges. Bisque-fired ceramics are porous and resemble terracotta clay pots and the low-fire pottery made by Native Americans. Bio-based ceramic sculptures have been showcased at public art venues and as habitat enrichment in aquaria for fish to create living-art educational displays.

10535 - A Vascular Flora of a Historically African American Recreation Area, Booker T. Washington State Park in Hamilton County, Tennessee

Julia Prins, Sevyn Brothers, Joey Shaw

University of Tennessee at Chattanooga, Chattanooga, TN

Booker T. Washington State Park is a 353-acre tract located on the Chickamauga Reservoir of the Tennessee River northwest of Chattanooga, Tennessee. The Tennessee Valley Authority developed it as the state's second African American recreation area and was formally deeded to the state in 1950. The park is characterized by dry-mesic calcareous forests and acidic sandstone ridges in the Southern Ridge and Valley. The most abundant plant community types within the park are "Appalachian Oak-Pine Forest and Woodland" and "Ruderal Forest," but all communities are heavily degraded.

The flora is represented by 96 families, 196 genera, and 279 species and lesser taxa. The three most represented families are Asteraceae, Poaceae, and Fabaceae, and the two most represented genera are *Quercus* and *Symphyotrichum*. Ninety-four percent of species are angiosperms, of which there are 217 eudicots and 48 monocots. Only 4% pteridophytes and 2% gymnosperms make up the remainder of the flora. Nonnative species make up 30% of the species, and much of the park's lower elevations are dominated by *Hedera helix*, *Ligustrum sinense*, and *Nandina domestica*. The dominance of nonnative species can be attributed to the minimal funding the park has historically received, most likely due to its history of being a predominantly African American recreation area. Other floras completed in the Valley and Ridge ecoregion have significantly fewer nonnative species and several other historically African American

recreation areas throughout the south show similar prevalence of nonnative species. A historic record of the federally endangered *Scutellaria montana* was recorded for the park in 1986 but attempts to relocate this species were unsuccessful. One reason for this baseline botanical survey is to finally provide baseline floristic data for the land managers and conservation workers who may seek funding and future projects to restore the ecological integrity of this old, historic state park.

10542 - A multi-pronged approach to understanding origins, relationships, and limiting factors of naturalized Floridian *Saccharum* populations

Indy Hughes[1], Scott Mangan[1], Santosh Rana Magar[1], Rima Lucardi[2], Travis Marsico[1]

[1]Arkansas State University, Jonesboro, AR, [2]USDA Forest Service, Southern Research Station, Athens, GA

Saccharum spontaneum L., wild sugarcane, is a well-documented aggressive invasive species and regulated by the USDA as a listed federal noxious weed (FNW). *Saccharum spontaneum* is currently used to create hardy, pest-resistant cultivars of *S. officinarum* L., domestic sugarcane. All modern cultivars have a small percentage of wild parentage, but the dosage is extremely low to lessen the chance of inheriting less of the undesirable traits. *Saccharum spontaneum's* naturalized presence in peninsular Florida has been reported since at least 1993, and likely escaped from regulated sugarcane breeding facilities. The proximity of *S. spontaneum* populations to modern cultivars, grown intensively in the state, could potentially increase the risk of invasion. It is typical of the genus to colonize favorable habitats and to interbreed. The Floridian populations exhibit wide phenotypic variation, even within species. They grow in different habitats, such as along hilly roadsides or submerged in canals. The exhibition of such diversity indicates high genetic diversity and adaptability, and we endeavor to delineate the relationships between potentially interbreeding populations. Such analysis is necessary to determine the overall risk of *Saccharum* invasion in Florida. We sampled a limited number of individuals from different populations, and produced biallelic SNPs from our multiallelic polyploid sequences, although this reduced our genetic diversity and total SNPs. We produced a maximum likelihood tree using IQ-TREE and a maximum likelihood ancestry estimation using ADMIXTURE/1.3.0 to determine relationships between individuals, and used a *k*-mer based approach to determine geographic origins. The genetic analyses revealed diverse, interwoven relationships between Floridian populations that can ultimately inform invasion risk assessments and policies moving forward regarding naturalizing *Saccharum*. In tandem with these genetic analyses, we conducted a greenhouse experiment in an attempt to quantify the effect that water availability, a potential limiting factor, had on individuals from different populations.

10543 - Change in abundance of native vs. introduced lady beetles over five decades

Carolina Trejo

Winthrop University, Rock Hill, SC

Many insect species have declined in recent decades, raising concerns due to their critical role in ecosystems. Non-native lady beetles, introduced for biological control, have been linked to declines in native species, though the impacts vary by region. Conflicting findings, particularly in the southeastern United States, highlight the need for further research. To investigate whether native coccinellid populations in the Southeast have experienced declines, and if so, whether introduced species are contributing to these declines, I analyzed 51 years of museum records (1966 to 2017) and modeled trends in population abundance over time. Introduced species—Coccinella septempunctata and Harmonia axyridis—increased annually by 5.2% and 10.2%, respectively, since ca. 2005 and 1995, while native species—Coleomegilla maculata, Hippodamia convergens, and Olla v-nigrum—declined by 5.1%, 6.9%, and 5.2% annually, with the last records in 2011 or 1997. This negative relationship between introduced and native species abundance supports the hypothesis that introduced lady beetles contributed to the decline of native species. However, establishing a causal relationship requires further investigation.

10545 - Taxonomy of the lepidote *Rhododendron* species (Ericaceae)

Charles Horn

Newberry College, Newberry, SC

Four species of lepidote Rhododendrons are currently recognized in the southeastern USA: *carolinianum*, *chapmanii*, *minus*, and *smokianum*. However additional taxa have been described and represent variation in floral color, floral tube length, leaf shape, and habitat. *Rhododendron minus* was first described by Michaux in 1792 from material he collected along the Savannah River in Georgia. Later, the species names *punctatum* and *cuthbertii* were recognized but based on material collected in the same area. These long-tubed, white to pink flowered forms (and sometimes purple) are found along the fall line from eastern South Carolina to Alabama. There does seem to be some variation over the distributional range, based on flower color and leaf shape. The shorter tubed, purple flowered forms of northwestern South Carolina, and northeastern Georgia have historically been lumped in with *minus*. The long-tubed, purple flowered form with revolute leaf margins from western Florida are of *chapmanii*. The short tubed, purple flowered forms of the Linville

Gorge area of North Carolina are known as *carolinianum*. Split away by some are the short tubed, white flowered forms of the Broad River watershed of North and South Carolina which are known as var. *margarettae*. The very short tubed purple flowered forms of the Smoky Mountain National Park are recognized as *smokianum*. Further field and laboratory work is needed to clarify if taxonomic revision is needed.

10546 - Species invasions as natural ecological and evolutionary experiments

Scott Harrison

Georgia Southern University, Statesboro, GA

Introduced species often generate ecological and economic costs. These species can also serve as interesting natural experiments as they are frequently exposed to new ecological conditions, undergo dramatic fluctuations in population size, and produce offspring that are interpopulation hybrids. Here, I will review insights gained from our studies of three recent and abundant introduced species to the southeastern US: the brown widow spider (*Latrodectus geometricus*), the titan acorn barnacle (*Megabalanus coccopoma*), and the kudzu bug (*Megacopta cribraria*). Some common patterns observed in these different species include significant bottlenecks and reductions in genetic variation do not inhibit the success of the species; despite low genetic variation, mechanisms to avoid inbreeding are common; alternative reproductive strategies may be used in introduced populations; and role of bacterial endosymbionts is often unknown.

10547 - Developing fully online Anatomy and Physiology courses on a limited budget that are comparable to face-to-face versions

Valarie Burnett

Newberry College, Newberry, SC

This study explores methods for teaching Anatomy and Physiology I & II online and how the online courses compare to face-to-face (FTF) courses. While biology lectures may be smoothly and cost-effectively adapted to online format, for labs, it is more challenging to adequately provide a remote learning experience that is comparable to a FTF lab. Lab kit options are limited to a small selection of biology courses and may cost more than the institution's standard lab fees. Virtual options are available for more courses but are typically expensive and may not be affordable for some institutions. In early 2020, a global pandemic forced a temporary transition to online learning. This prompted institutions to develop innovative methods for providing labs remotely. Newberry College is a small institution and could not support costly virtual options for this pivot. Some biology courses were able to utilize lab kits, but suitable kits were not available for most courses including anatomy and physiology (A & P), so I began developing online labs in A & P in 2019 as Covid-19 spread. By 2020, the College transitioned to remote learning for the next year, but for medical reasons, I was unable to return to campus when FTF learning resumed, so as the only A & P professor, it was essential to provide a comparable online lab experience long-term, and I had the rare opportunity to gather information from my online versions for 2.5 years and compare them to my FTF versions. While some students indicated they would prefer to have a more hands-on lab experience, many students enjoyed online labs and were impressed with their creativity and comparability to FTF labs. The results of lab assessments were also comparable. The development of online labs has also yielded many benefits to students, whether they're remote or FTF.

10548 - Presentation Withdrawn

10551 - Predicting 3D protein structure of gene fusions in AMKL patients using AlphaFold

Adam Parsons[1], Dr. Andrea Perreault[2]

[1]Elon University, Hendersonville, NC, [2]Elon University, Elon, NC

The organization of DNA in 3D space is important for gene regulation. Changes in DNA organization and resulting gene expression can have effects on cellular development and function, and have been linked with numerous diseases such as cancer. One way DNA organization may be altered is through binding of fusion proteins containing an intrinsically disordered region (IDR) and DNA binding domain. Fusion proteins form when two portions of independent genes fuse together – which occurs via structural rearrangements (predominantly translocations).

This project aims to help fill the gap that recent literature has highlighted regarding the structure of fusion proteins. This will be done using AlphaFold: an artificial intelligence program that uses amino acid sequences to predict 3D protein structure. This research project aims to predict the 3D structure of two gene fusions which were previously predicted by the Perreault lab to be found in Acute Megakaryoblastic Leukemia (AMKL) patients. ColabFold, a software within Google Colaboratory that makes use of AlphaFold, will allow the prediction of numerous proteins simultaneously. A program called ChimeraX will then be used to visualize and analyze the protein

structures. Uncovering the protein structure of genes linked with cancer is key for obtaining a clearer picture of tumorigenesis. Thorough analysis of predicted protein structure may illuminate features that may be useful for future drug development for AMKL. Preliminary results have shown that both fusions likely contain intrinsically disordered regions as well as DNA binding domains – possibly suggesting that these combined features play a role in AMKL development.

10554 - Bacteria on Paper Currency: A Direct Press Method, Survival and Implications

Robert Wolff

South University Columbia, Columbia, SC

Background: Paper-currency is probably the most handled fomite with the potential for transmission of pathogenic microbes among the general public. Because of very limited data on U.S. currency contamination this study was undertaken to examine the methods and biology used, including ten years of sampling dollar bills as a classroom project.

Methods: Sampling of currency, collected from many locations, includes directly pressing one-half of a folded bill onto the media surface of a plate. This method was compared to using a moistened swab for bacterial recovery. As only ¼ of a bill is sampled onto each type of media in surveillance studies, all four surfaces were sampled to determine efficiency. Bacterial survival was studied by spraying *E. coli* and *Staphylococcus aureus* onto bills and sampling over time.

Results: Direct contact was more effective than swabbing paper-currency, resulting in bacterial recovery from 100% greater numbers on Nutrient Agar to more than 1000%, with only 11% showing a lower recovery. When all four quarter surfaces were sampled, 42/45 (93.3%) had mannitol fermenters on one surface if they present on another surface. 10 bills had a surface where no MF grew, and all but one had only several total fermenters on the bill. All bills had non-mannitol fermenters. *E. coli* survival on dried bills was less than 48 hours while *Staphylococcus aureus* survived over 3 weeks. 300+ bacterial species were identified via 435 pyrosequencing.

Conclusions: Pressing dollar-bills onto agar media with direct contact is a simple and effective sampling procedure for microbes contaminating circulating banknotes. The method has demonstrated both seasonal and weather changes, allows monitoring of specific organisms, and longer term changes in abundance. This is an underutilized and underappreciated technique that could be highly valuable for Biosurveillance of disease causing organisms.

ASB Posters

1 - Survey of Free-roaming Cats *(Felis catus)* at Warren Wilson College

Ari Ypema

Warren Wilson College, Swannanoa, NC

Free-roaming domestic cat populations are subject to rapid growth. Control of these populations is necessary for the protection of native prey species including birds, rodents, and small reptiles. While Warren Wilson College has dealt with a significant community cat population in previous years, no monitoring program has ever been implemented to track changes in population size. Using camera traps, I surveyed central campus to estimate population size and catalog individuals for future monitoring. 10-11 individual cats were detected during the survey period, with detections occurring at 59.4% of total camera sites, and up to 3 different individuals being detected at a given camera site. This method of monitoring is an effective way to increase knowledge of cat populations and establish a baseline population estimate from which further research can be conducted.

2 - The Role of Sensory Cues in the Foraging Habits of *Manduca sexta* Moths Under Low-Illuminescent Conditions

Collin McClure[1], Austin Dunagan[1], Joaquin Goyret[2]

[1]University of Tennessee at Martin, Martin, TN, [2]The University of Tennessee at Martin, Martin, TN

It is widely acknowledged that pollinators heavily depend on visual and olfactory information when foraging. Historically, these moths innately prefer olfactory cues but have learned to associate food with various environmental signals, enabling them to track fluctuating nectar supplies in nature. Nocturnal hawkmoths rely more on olfactory signals, whereas diurnal moths favor visual ones. This suggests a possible evolutionary divergence of the diurnal, visually biased hawkmoths from the more ancestral, nocturnal, olfactory-biased hawkmoths. Alternatively, hawkmoths, in general, are flexible in using either depending on the situation and conditions. *Manduca sexta* is a nocturnal-crepuscular hawk moth species that forage in a wide range of illuminance from crepuscular to starlit environments. In an associative learning paradigm, we test *Manduca sexta* to better understand their capability of learning colors, odors, and/or both under crepuscular and nocturnal illumination. We train hawk moths with a rewarded yellow feeder scented with lavender oil, and an unrewarded blue feeder scented with bergamot oil. Then, we test each individually to find if they learned the color, odor, and/or both as a bimodal composite signal. Results thus far show that under crepuscular illumination, moths learn both the color and odor, and seemingly prefer the odor in contradictory tests (see Methods). We are now running the experiment under starlight illuminations.

3 - Effects of Manipulated Incubation Temperature on Baseline Corticosterone Levels in Eastern Bluebirds *(Sialia sialis)*

Cassidy Ferraro[1], Sarah Hill[1], Sarah Knutie[2], Lynn Siefferman[1]

[1]Appalachian State University, Boone, NC, [2]University Of Connecticut, Storrs, CT

Recent climate trends have increased the frequency and severity of aberrant weather. Extreme weather could disrupt homeostasis and negatively impact the likelihood that female songbirds complete the energetically expensive incubation stage. Indeed, historical data demonstrate that cold snaps and heat waves can cause females to abandon nests during incubation. Glucocorticoids are metabolic hormones that orchestrate plastic responses to environmental stimuli including temperature. Under extreme temperatures, baseline corticosterone levels help maintain energy balance so that birds continue with reproduction. We manipulated nest temperatures during incubation in a Southern Appalachian population of eastern bluebirds. Females were randomly assigned to either cold, control or heat treatments for 7 days. Next, we took a maternal blood sample to measure circulating baseline corticosterone levels. We also measured body condition and plumage color- traits associated with female reproductive effort and success in this species. Although hatching success did not differ with treatment, the heated clutches took longer to hatch- especially later in the breeding season. Yet, nestlings from heated clutches were also slightly more likely to fledge the nest. We expect females will have higher corticosterone after early season cold treatments and late season heat treatments. We also explore whether measures of female quality interact with treatment to influence corticosterone levels; high quality females may be less likely to elevate corticosterone in response to temperature stress.

4 - Nest Defense of Eastern Bluebirds (*Sialia sialis*) in Response to Competitors and Non-Competitors

Katalina Cunningham, Jonathan Pérez

University of South Alabama, Mobile, AL

Appropriate threat detection and response is essential for both survival of an animal, but also for maximizing fitness by avoiding unnecessary energy expenditure. Two strategies an animal can use to identify threats are specialization and generalization. With specialization, an animal is selective in what threats they respond to, while with generalization it responds broadly to a category of stimulus and without close discrimination. Both strategies come with benefits and drawbacks – when an animal uses generalization, they have a greater ability to respond to novel threats, but can also waste energy reacting to non-threats. Conversely, specialization minimizes the amount of energy wasted, but limits the animal's ability to respond to novel threats thus carrying a higher potential risk (loss of resources, offspring, and even death) in dynamic or rapidly changing environments. In this study we explore whether Eastern Bluebirds utilize a specialized or generalized approach to potential songbird threats to their nest. Using songbird models with corresponding audio for five minutes, we measure the difference in the defensive response of Eastern Bluebirds during incubation to a competitor (House Sparrow) and non-competitor (House Finch). Preliminary analysis of our data suggests that cavity nesting songbird threats elicit a stronger defensive response than do models of a non-cavity nester. This suggests that Eastern Bluebirds use a specialized approach to threat detection and response.

5 - Does nicotine state dependent learning require the ASER and ASEL neurons in *Caenorhabditis elegans*?

Jonathan Lindsay[1], Laura Mathies[2], Andrew Davies[2], Jill Bettinger[2]

[1]Emory & Henry University, Emory, VA, [2]Virginia Commonwealth University, Richmond, VA

Processing of external and internal stimuli allow organisms to form learned behaviors so that they might adapt to their environmental surroundings. One such behavior, called state dependent learning (SDL), occurs when effective learning and recall of a behavior takes place in the same internal state. This behavior has been demonstrated in a wide variety of model organisms, including Caenorhabdities elegans (C. elegans). Though investigations of this behavior have been performed over several decades, little is known of the molecular mechanism associated with SDL. Previously, we and others have demonstrated that ethanol and nicotine can confer SDL in C. elegans by combining these substances with a learning task called olfactory learning. Olfactory learning is a learned behavior that occurs when a diminished response to an odor is observed upon subsequent exposure to the same odor. When worms are kept in the same intoxicated state during learning and recall, no loss of olfactory learning occurs. Shifting state from learning with substance exposure to recall without substance exposure shows a loss in performance in olfactory learning. This loss in performance confirms SDL. Now, we are tasked with determining what molecular components are similar or different in the ethanol and nicotine SDL. For example, in a separate project we have investigated the role of genes encoding acetylcholine receptor subunits, acr-6 and acr-7, are required for ethanol and nicotine SDL. Here we will determine whether neurons required for ethanol SDL, are also required for nicotine SDL. The ASER neuron, which regulates responses to salts, is required for ethanol SDL. We have also shown the ASEL neuron, which expresses several of the same genes of the ASER neuron, is not required for ethanol SDL. Here we are testing if worms lacking ASER neurons or ASEL neurons are capable of nicotine SDL.

6 - Optimizing Passive Acoustic Monitoring: A Comparative Study of Sound Separation Techniques for Bird Identification

Caleigh Stivers, Dr. John Quinn

Furman University, Greenville, SC

Passive acoustic monitoring (PAM) is advancing avian diversity surveys, but accurately identifying species from complex soundscapes remains challenging. Existing automated tools, while improving, still produce errors, often due to overlapping vocalizations and background noise. This study explores the combined use of BirdNET, a deep learning algorithm for avian sound recognition, and Perch, an acoustic event detection model, to enhance the accuracy and efficiency of PAM data analysis. We focus on improving sound separation by incorporating Perch's ability to isolate avian vocalizations. Additionally, we investigate the potential of alternative sound separation models to further refine the accuracy of BirdNET predictions. We deployed PAM units in different ecosystem types and processed recordings using various combinations of BirdNET, Perch, and other sound separation techniques. We compared the performance of these approaches, assessing species identification accuracy, false positive rates, and processing time. Our results demonstrate the benefits of integrating sound separation models with machine learning tools, highlighting a promising avenue for automating PAM data analysis and increasing the reliability of avian research and conservation monitoring.

7 - Description of the Larva of the Caddisfly *Cernotina truncona* Ross, 1947 (Trichoptera: Polycentropodidae)

Truc Bui, Alexander Orfinger

Dalton State College, Dalton, GA

The caddisfly (Trichoptera) genus Cernotina is primarily Neotropical, with only three species recorded form the southeastern United States. Of the roughly 80 known species, the larva of only one has been described to date. The goal of this research is to describe, illustrate, and diagnose the larva of C. truncona using ecologically associated specimens. Also, we used publicly available mitochondrial DNA barcoding data to evaluate the genetic relationships of these species. The larvae of C. truncona can be distinguished from those of the previously described C. spicata by differences in setal placement and number on the meso- and metanota, mandibular morphology, head width, and distal setation of the tarsi. Using scanning electron microscopy, the ultrastructure of the anal claw is figured, highlighting the novel finding of small spines on the concave margin of a larva of Cernotina. The information provided herein enables the in-depth study of the ecology and life history of this diminutive caddisfly.

8 - Preliminary evaluation of a size-dependent bycatch exclusion device for insect UV light pan trapping

Hunter Smith, Alexander Orfinger

Dalton State College, Dalton, GA

A growing body of research indicates that global insect populations are declining worldwide, underscoring the ongoing anthropogenic threats to global biodiversity at large. Given this ongoing conservation concern, novel ideas to protect insects and other species vulnerable as bycatch to insect collecting techniques should be considered. These methods should ideally minimize bycatch while not impacting recovery of target taxa. In the field of aquatic entomology, the UV light pan trap is widely used. While effective, this method regularly incurs significant bycatch of unwanted arthropods and occasionally vertebrates which both compromises the sample and has conservation implications. The goal of this study was to develop and test a sized-based bycatch exclusion device deployed with UV light pan traps in the hopes of reducing non-target catches. This simple, cost-effective design does not require any modifications of the existing trap itself beyond adding a domed cage. “Caged” and “uncaged” traps were deployed simultaneously at the same locations across two streams in northwest Georgia, USA for a total of twelve trapping events over three months. To determine whether focal taxa were negatively impacted by the device, hydropsychid and hydroptilid caddisflies (Trichoptera) served as target taxa and total numbers of these were counted and compared between caged and uncaged traps. From this, it was determined that there was no significant difference in number of target taxa recovered between the two treatments. The data suggest that these exclusion devices do not negatively impact adult caddisfly sampling and should exclude undesired large insects e.g., dobsonflies, some saturniid moths, as well as many vertebrates. Though positive, these results are preliminary and additional questions must be addressed, which are discussed in the present study.

9 - Comparison of Joro Spider (*Trichonephila clavata*) Prey Capture and the Available Prey Diversity of their Nonnative Environment

Rindy Grubb, Rebecca Godwin

Piedmont University, Demorest, GA

The introduction of Joro spiders (*Trichonephila clavata*) into ecosystems alongside native orb weavers has presented concerns involving possible ecological consequences. The coexistence of these spider species may disrupt ecological dynamics, indicating potential resource competition and alternative patterns of capturing prey among native orb weavers. This study seeks to investigate the impact of Joro spiders on native orb weavers by comparing prey captured by Joro spiders to the available arthropod diversity in the area. This was assessed from early September to late October by collecting prey from a selected spider population and setting up sticky traps. All collected invertebrates were then identified to order. The data of the Joro web prey catches and the sticky trap prey catches were run through a Shannon Weiner species diversity index and those diversity values were use in a paired T-test. The results concluded that there was no significant difference in diversity index between the invertebrates that Joro spiders catch and what is caught or available to other species in the environment. However, a contingency analysis of the data indicated that the distribution of prey diversity was significantly different between the two groups.

10 - Unknown Natural Histories of the Folding Trapdoor Spider: Population Density, Distribution, and Burrowing Habits of *Antrodiaetus*

Jadon Gonzales, Rebecca Godwin

Piedmont University, Demorest, GA

Mygalomorphae is an infraorder of spiders that comprises funnel web spiders, tarantulas, and trapdoor spiders. As of right now, the infraorder contains more than 20 families and over 3000 species dating all the way back to the Middle Triassic era. During this study we looked closely at the burrowing tendencies of a genus in the family Antrodiaetidae, *Antrodiaetus*. *Antrodiaetus* are most commonly known as the folding door trapdoor spider because of their unique silk-lined burrow, which has a collar that folds inward to close. *Antrodiaetus* live a solitary lifestyle in burrows which tend to be clustered in suitable habitats that are mostly found on moist slopes in humid woodland habitats. As with many burrowing mygalomorphs, moisture is one of *Antrodiaetus'* biggest challenges, and to combat this problem they keep their door closed to prevent their burrows from drying out. We hypothesized that *Antrodiaetus* colonies (burrow clusters) located near water would have a higher number of tightly clustered burrows compared to those farther from water. Additionally, we predicted a positive relationship between burrow diameter and spider size, with larger spiders occupying larger burrows. Finally, we investigated the collar strength of different burrows to understand how structural integrity varies with different burrows. To test these hypotheses, we sampled burrows from eight different *Antrodiaetus* sites. Four of which were located on or near a stream bank and the other four were located farther from a water source. After analyzing the data, we found no significant relationship between nearest neighbor distance and habitat type. However, burrow diameter and carapace length were significantly correlated, and collar strength varied based on the presence of an anchoring structure.

11 - Invasive Pond Loach in Georgia: Exotic Fish with a Parasite Identity Crisis

Nicholas Bates, Riccardo Fiorillo, Peter Sakaris

Georgia Gwinnett College, Lawrenceville, GA

Invasive species pose significant ecological threats, including habitat disruption, competition with native species, and the introduction of novel parasites and diseases. This study investigates the parasite community and diet of the invasive Weather Loach (*Misgurnus anguillicaudatus*), collected from a small tributary of Sweetwater Creek in Gwinnett County, Georgia. Loaches were captured using electrofishing and minnow traps, and 30 individuals were necropsied to assess parasite loads and diet composition. Preliminary results revealed an underdeveloped parasite community characterized by low species richness and diversity, dominated by nematodes. The most prevalent parasitic nematodes were *Camallanus* sp. and *Contracaecum* sp. larvae, both of which utilize microcrustaceans as intermediate hosts. Dietary analysis showed that 60% of the loaches had full stomachs, with ostracods and chironomid larvae being the dominant prey items. Other food sources included other insect larvae and mollusks, primarily snails. These findings suggest that the loaches, having been recently introduced, have not yet been infected by other local parasites, likely because their diet is dominated by ostracods, limiting their exposure to other potential parasite-host species.

12 - Multiple Paternity of *Cambarid* crayfishes: A Surrogate Study for Propagation Methods of the Federally Threatened *Cambarus callainus*

Hannah N. Holbert[1], Zackary A. Graham[1], Drew T. Phipps[2], Brian T. Watson[3], Zachary J. Loughman[1]

[1]Department of Biological Sciences, West Liberty University, West Liberty, WV, [2]White Sulphur Springs National Fish Hatchery, White Sulphur Springs, WV, [3]Virginia Department of Wildlife Resources, Forest, VA

The Big Sandy Crayfish (*Cambarus callainus*) was described in 2014 after originally being thought to be the same species as the Guyandotte River Crayfish (*Cambarus veteranus*). Two years later in 2016, C. callainus was listed as Threatened by the Endangered Species Act by the U.S. Fish and Wildlife Service due to decreasing habitat availability. To aid in the recovery of the species, propagation efforts such as raising eggs or juveniles collected in the wild have been conducted. More advanced methods such as bringing adult individuals into captivity and allowing them to mate are not in use. In order to develop a better understanding of how to properly rear *C. callainus* in captivity, a genetic study of multiple paternity was conducted using surrogate species. *C. chasmodactylus, C. appalachiensis*, and *C. smilax* females and associated juveniles were collected in the field and brought in for nuclear genetic analysis of the paternal genes. The sequences collected will be used to analyze the number of fathers that contribute to each clutch, allowing replication of mating strategies in captivity to allow the most beneficial genetic diversity per produced clutch. Individuals produced through these methods once applied to *C. callainus* would be released to aid wild population diversity.

13 - The Effectiveness of Wildflower Habitat Enrichment in Boosting Wild Bee Abundance in the Coastal Plain of Georgia

Mark Schlueter

Georgia Gwinnett College, Lawrenceville, GA

Humans depend on honeybees for the pollination of their fruits and vegetables. Bees pollinate 1/3 of the human food supply. They pollinate nearly every fruit, nut, and vegetable. The main bee pollinator, the honeybee, has been in decline for several decades due to CCD. Finding alternative pollinators that could supplement or replace the declining honeybee would be a wise safeguard. Wild bees (including wasps) are already a source of sustainable pollination, contributing more than $3 billion in pollination services each year. Regional studies are essential in gathering accurate information on the wild bees present in each region to determine the types of wild bees and which habitat enrichments are most effective in recruiting and keeping target wild bee species in agricultural areas. In the current study, we focused on the poorly studied coastal plain areas of Central Georgia. Previous studies have indicated lower native bee diversity and abundance in the coastal plain areas of Georgia compared with the Piedmont region. A survey of native bee abundance was performed near Hephzibah Georgia (coastal plain soil type) to assess the wild bee community. The most common native bee pollinators observed were the sweat bees (*Lasioglossum* species), Southeastern blueberry bee (*Habropoda laboriosa*), mining bees (*Andrena* species), and carpenter bees (*Xylocopa virginica*). The most important wasp pollinators were the large hairy flower wasps (Scoliid species). To boost native pollinator populations, wildflower patches were planted next to several blueberry plots on a blueberry farm. A wildflower mix of several regional specific wildflowers were used. Several wildflower species consistently recruited the most bees to the blueberry plot. Spotted Beebalm (*Monarda* punctata) and Indian Blanket (Gaillardia pulchella) were the most effective wildflowers. Blueberry plots associated with wildflowers patches had larger abundance and diversity in each target pollinator group and recruited less common bee species (e.g. bumblebees).

14 - The Effect of Ethynylestradiol (EE2) Exposure on Rotifers (*Philodina acuticornis*) Egg Production in the Parental Generation

Savanah Koester, Naoma Nelsen

Erskine College, Due West, SC

17a-ethynylestradiol (EE2) is a common synthetic estrogen used in birth control but is also a known endocrine disruptor for aquatic vertebrates. Its' effects include impairment of reproduction, alteration to development, and change in growth mechanisms (3). There is little known knowledge on the effects EE2 has on rotifer's reproductive efficiency. It is known that some species of rotifers carry estrogenic receptors and produce ligand binding, but the known overall effect EE2 has on reproduction and hatch rates is limited (2). In most South Carolina runoff waterways, ranging levels of estradiol have been documented, with the highest known concentration reaching 133 ng/L. (1). In this experiment *Philodina acuticornis*, a freshwater asexual reproducing rotifer, was placed in diluted EE2 concentrations and the quantity of eggs and hatch rate of those eggs were each measured. It was determined that the adult rotifers transferred each day declined in number in all concentrations of EE2 except for the control. There was also an increase in all concentrations of EE2, compared to the control, in the amount of rotifer eggs per adult rotifer and an increase in the amount of rotifer hatchlings per adult rotifer compared to the control. The largest individual day of eggs per rotifer occurred on day 5 of the 100ng/L trial. The largest individual day of hatchling per rotifer occurred on day 5 of the 100ng/L trial.

15 - Benefits of using illustrations rather than digital photography to showcase morphology

Erin Kelly, Matthew Lehnert

Kent State University at Stark, North Canton, OH

Arguably, the most basic part of biology is what we can visualize and is why the field of morphology is integral to biology, providing means for species identification, biomechanics, phylogeny, and providing insight into physiology. Historically, morphology consisted of performing hand-drawn illustrations, but with improvements in technology (e.g., digital photography) the abundance of illustrations has become less common. The purpose of this project is to showcase some of the benefits of using hand-drawn illustrations when compared to the technology-driven imaging techniques. We show how illustrations of insect mouthparts can enhance publishable figures and remove artifacts from structures (e.g., food deposits on a mole cricket proventriculus). Although digital photography can produce high resolution and colorful images, the studied individuals might show artifacts or uncommon morphological variations. Illustrations, however, can show an individual without artifacts. Additionally, using hand-drawn illustrations provides opportunities for conversations between the illustrator and scientist to create illustrations that might have uncommon orientations or that represent the average morphology among different individuals of the same species.

16 - Preliminary Assessment of Eugenol's Teratogenic Effects in *Xenopus laevis* Embryos Using FETAX Assay

Ashley Brazier[1], James Rayburn[2]

[1]Jacksonville State Univeristy, Jacksonville, AL, [2]Jacksonville State University, Jacksonville, AL

Eugenol, a bioactive component of clove oil widely used in pharmaceuticals (e.g., toothache relief) and cosmetics (e.g., fragrances), has limited information available regarding its developmental toxicity. This study examines Eugenol's effects on *Xenopus laevis* embryos using the Frog Embryo Teratogenesis Assay-Xenopus (FETAX), assessing mortality, growth, and malformations. Adult frogs were injected with human chorionic gonadotropin and placed in a breeding chamber. Fertilized embryos were collected, dejellied, and sorted at the small-cell blastula stage to initiate the experiment. Groups of 20 embryos were incubated in 8 mL of FETAX solution at 24°C for four days, with daily solution changes and removal of dead embryos. At the conclusion, mortality, malformations, and embryo lengths were recorded. Statistical analyses (ANOVA, Bonferroni, and probit) were performed to determine LOEC, NOEC, LC50, and EC50 values. Preliminary findings show no significant impact on embryo length at the tested concentration. The LC50 for mortality was 6.4 mg/L (95% limits: 5.7–7.3 mg/L), while the EC50 for malformations was 2.9 mg/L (95% limits: 2.6–3.3 mg/L), yielding a Teratogenic Index of 2.2 (indicating increased teratogenic risk). Malformed embryos frequently exhibited facial abnormalities, edema, gut deformities, and stunted growth in a concentration-dependent manner. Based on these results, Eugenol may pose teratogenic risks, warranting further studies for confirmation.

17 - From the Top Down or Bottom Up: Thermal Behavior of *Hydrodynastes gigas* with Dorsal or Ventral Heat

Katherin Plate[1], Lauren Augustine[2,3], Peter DiGeronimo[2], Zachary J. Loughman[1]

[1]Department of Organismal Biology, Ecology, and Zoo Science, West Liberty University, West Liberty, WV, [2]Philadelphia Zoo, Philadelphia, PA, [3]Smithsonian National Zoological Park, Washington, DC

Reptiles need environmental heat to thermoregulate, allowing the body to perform a variety of biological functions. The inability for a reptile to obtain and sustain preferred body temperatures can result in extreme behavioral and physical risks. One-way reptiles achieve preferred temperatures by basking in heat such as sunlight; though the type of basking depends on the species. The objective of this study was to investigate potential differences in behavior between two groups of juvenile false water cobras, Hydrodynastes gigas, provided different heat sources. Thirty three H. gigas were housed individually in identical enclosures and were divided into two groups, each group receiving heat from a different source: ventral heat from heat tape or both ventral and dorsal heat from heat tape and a halogen bulb. Observational images were taken daily in three-hour intervals, between 8:00 and 17:00. The animals' behavior, physical position, and thermal body position was recorded from each image using an ethogram. There was a statistically significant difference in behavior, physical and thermal positions between the two groups. After data was collected for eight months, a Pearson's chi-squared analysis was run on all three observation sets which showed statistical significance among the groups. To determine where the significance lies, a Bonferroni post-hoc test was run to determine the statistical significance. Based on the findings of this study, it is recommended that captive juvenile H. gigas are offered both ventral and dorsal heat. Additional research should investigate the potential effects of thermal husbandry on growth rates and welfare of juvenile H. gigas.

18 - Diet of Three Co-Occurring Large *Plethodons* in Western North Carolina

Maxwell Ramey, Jon Davenport

Appalachian State University, Boone, NC

Three species of large *Plethodon* salamanders co-occur in northwestern NC; *Plethodon yonahlossee*, *Plethodon montanus*, and *Plethodon cylindraceus*. They occupy similar habitats so it has been hypothesized that dietary niches may differ to allow co-occurrence. We performed gastric lavages on >10 individuals of each species at three different sites. All regurgitated prey items were preserved for identification and enumeration. Out of the 170 samples collected thus far, we've processed 100. From those 100 samples, there is a high degree of overlap in diets of the three species. There is also high overlap among the most common prey items: ants, springtails, millipedes, mites, and beetle larvae.

19 - eDNA: A Powerful tool for Pine Snake *(Pituophis melanoleucus*) Conservation

Peyton Kinavey, Alan Jones, Michelle Barthet, Scott Parker

Coastal Carolina University, Conway, SC

Environmental DNA (eDNA) is a powerful tool for ecological research and conservation. It allows the detection of species that are

difficult to monitor through traditional methods. eDNA improves the ability to track rare and endangered species and map biodiversity in complex ecosystems using a non-invasive and highly sensitive approach. Cryptic species such as Pine Snakes (*Pituophis melanoleucus*) are elusive in the environment, prohibiting accurate assessment of location, population density, behavior, and other factors critical for conservation and ecological study. These challenges make it difficult to develop effective management plans for species like the Pine Snake, which is listed in the South Carolina Wildlife Action Plan as a "species of greatest conservation need." In this study, we developed novel eDNA primers targeting the *NADH dehydrogenase subunit 4 (ND4)* gene to detect Pine Snakes DNA. The primers were highly specific to *Pituophis*, effectively avoiding amplification of DNA from closely related species, while sensitivity tests determined a Limit of Detection (LOD) of 25 ng of *P. melanoleucus* DNA needed in a mixture of soil for detection. To assess field applicability of the new primers, we collected eDNA samples from three ~200-hectare sectors within a study site on the South Carolina Coastal Plain, home to a known Pine Snake population. This allowed us to evaluate the primers' effectiveness in detecting Pine Snake presence and mapping their distribution. The study successfully confirmed the presence or absence of Pine Snakes across the three environmental sectors, which demonstrated the effectiveness of the primers as a non-invasive, efficient tool for detecting Pine Snake populations.

20 - Assessing the impact of trade bans on invasive iguana populations in southern Florida through mathematical modeling

Blaklie Mitchell

Mississippi State University, Starkville, MS

The common green iguana, native to Central and South America, has remained one of the most-traded reptiles in the exotic pet industry since the 1960s. This trade has led to the species' widespread introduction across the tropics, with many iguanas escaping captivity or being released intentionally. In Florida, a major hub for exotic species, green iguanas were first reported in 1966. Initially considered established in southern Florida but not proliferating, the species' range and density have expanded dramatically over the past six decades. Anecdotal estimates suggest a current population size of roughly 20,000. However, this is likely to be an egregious underestimate due to their rapid proliferation in other regions, such as on the island of Grand Cayman. Currently, invasive iguana populations are managed in Florida through habitat modifications and capture-and-removal programs (i.e., culling). Eradication of established invasives is resource-intensive and often unsustainable in the long term. However, modeling different management strategies may help identify more feasible solutions. This study modeled the effects of Florida's 2021 ban on green iguana trade, implemented to curb invasive population growth. The primary goal was to assess whether this ban would significantly reduce wild iguana numbers compared to a model that permitted trade while incorporating a removal program. The model examined the dynamics between captive and wild iguana populations, influenced by trade-related factors such as supply and demand. Allowing trade led to increased wild iguana numbers through escapees and reproduction, but also facilitated the harvest of wild iguanas for the pet trade. Conversely, a trade ban halted new imports, which reduced immigration of captive iguanas, but also eliminated economic incentives for harvesting wild iguanas. Our investigation suggests that maintaining trade, with its associated harvesting incentives, is a more effective strategy for significantly reducing iguana densities at sustainable levels than implementing a trade ban.

21 - Evaluating potential climatic correlates in the range expansion Green Treefrog (*Hyla cinerea*) across the southeastern United States

Michelle White, Nyssa Hunt, Thomas Wilson

University of Tennessee at Chattanooga, Chattanooga, TN

Climate-driven trends of range expansion toward higher latitudes and elevations has been documented in a variety of plant and animal taxa. Range expansion has also been documented in the Green Treefrog (*Hyla cinerea*); however, little has been published about the ecological factors behind this phenomena. In this analysis, we aim to leverage historic and recent occupancy data of the Green Treefrog from the Global Biodiversity Information Facility (GBIF) as well as data on climatic factors from BioClim to better elucidate the spatiotemporal distribution of this species. We also plan to datamine this information to determine any notable changes that may be correlated to regional climate across different geographic scales. This project and its associated models can be used by stakeholders to develop adaptive conservation and management strategies for the Green Treefrog across the southeastern United States.

22 - Just Around the Riverbend: Population Genomics of Salamanders Influenced by River Capture in Northeastern Georgia

Tyler Brock[1], Todd W. Pierson[2], Brice Noonan[1]

[1]University of Mississippi, University, MS, [2]Department of Ecology, Evolution, and Organismal Biology, Kennesaw State University, Kennesaw, GA

River capture is an event where the flow of a river is diverted from its original channel into the channel of an adjacent river, typically one of a lower base level, upon their contact with one another. The modern Tugaloo River in northeastern Georgia is believed to be the result of such an event. Headwater erosion of the ancestral Tugaloo-Savannah River eventually resulted in the capture of both the Chattooga and Tallulah rivers, diverting their flow from the Gulf Coast (via the ancestral Chattahoochee-Apalachicola) to the Atlantic Coast. This hydrogeological phenomenon could have had untold impacts on the distribution and health of fauna in the affected areas, and evidence of these impacts may potentially be found in the genomes of extant populations still living in those areas.

I intend to use RADseq genomic data generated from 8 species of plethodontid salamanders native to northeastern Georgia and northwestern South Carolina in order to investigate these impacts. Multiple population genomic analyses will be performed to assess gene flow and population structure for each species, and divergence time estimation will be used to provide an approximate date for population divisions caused by the river capture event. The life-history strategy of each species (i.e., terrestrial direct-developing or aquatic biphasic) will also be taken into account to further inform the genetic impacts of shifting terrestrial and aquatic connectivity caused by the river capture.

23 - Differences in Larval Microhabitat between two Cryptic, Sympatric Salamander Species (*Desmognathus folkertsi* and *D. amphileucus*) in Northeastern Georgia

Erick Fortner, Carlos D. Camp

Piedmont University, Demorest, GA

Two related species living in sympatry often exhibit ecological differences that promote coexistence. Two cryptic salamander species, *Desmognathus folkertsi* and *D. amphileucus* (formerly *quadramaculatus*), live sympatrically across northeastern Georgia. The adults have been shown to exhibit different preferences in habitat with *D. folkertsi* predominating in smaller streams and *D. amphileucus* more abundant in larger streams. However, the question of differences in larval habitats remains. To test for possible differences in larval habitat, we chose a stream in Stephens County, Georgia, in which the two species are sympatric. We collected larvae from riffles and measured the following variables associated with each riffle: water speed, average rock size, riffle length, and stream width. Because the adults partially segregate by stream size, we noted the entry of a tributary that increased stream size. Contingency analysis showed a significant distribution of the two species above versus below the tributary with no *D. amphileucus* found above the tributary. We also found a significant correlation between water speed and stream width as well as a difference between species in water speed, suggesting that *D. folkertsi* prefers slower water flow. Notably, we found seven *D. folkertsi* nests above the tributary, suggesting that larval habitat may be influenced by the egg laying preference of females.

24 - Evaluating Eastern Newt (*Notophthalmus viridescens*) Road Mortality in Relation to Human Activity on High Knob, Virginia

Savanna Busick, Bryce Cheers, Walter Smith

The University of Virginia's College at Wise, Wise, VA

Roads present significant threats to amphibian populations, particularly when constructed through natural areas and near habitats critical to amphibian lifecycles. We investigated patterns of Eastern Newt (*Notophthalmus viridescens*) road mortality along a 2.25 km road segment in the Jefferson National Forest on High Knob, Virginia built in close proximity to several wetland habitats and maintained largely to provide access for recreational users. Our study aimed to quantify wildlife-vehicle collisions (WVCs) along this road segment involving Eastern Newts and identify factors influencing WVC rates. We analyzed two distinct sections of roadway: Location 1, a heavily-trafficked road segment leading to the High Knob Tower, and Location 2, a less-traveled road segment connecting the High Knob Tower and a nearby day use area. Data collection involved recording the number and location of newt WVCs, as well as the date, time, newt life stage, distance from road shoulder, canopy cover, and road features (e.g., road shape, ditch presence) for each WVC. Between August 2023 and August 2024, we documented more than 950 newt WVCs. Preliminary analyses revealed significant differences in WVC rates between the two locations (paired t-test, $p < 0.05$). Peaks in mortality were also observed on 25 September and 16 October 2023, coinciding with special events on High Knob that increased vehicle traffic. Higher mortality rates were associated with Location 1, suggesting traffic volume as a factor in shaping WVC rates. WVCs were also clustered near several artificial wetlands constructed close to the roadway as part of past habitat restoration efforts following timber harvests. Mitigation strategies, such as

temporary road closures during peak newt activity, may reduce the mortality rates observed in our study. More broadly, our findings highlight the importance of balancing recreational infrastructure with habitat conservation measures to protect vulnerable amphibian populations.

25 - A Preliminary Evaluation of Habitat Associations of *Plethodon pauleyi* Across Variable Rock Outcrop Substrate

Ninah Bamba, Savanna Busick, Jacob DeNeef, Walker Meade, Walter Smith

The University of Virginia's College at Wise, Wise, VA

Plethodon pauleyi is a recently-described plethodontid salamander found across portions of Appalachian Kentucky, Tennessee, West Virginia, and Virginia. Not much is known about the habitat requirements or geographic distribution of this species, other than its presence in and around crevices in rock outcrop substrate. In Virginia, only a few (n < 5) localities of *P. pauleyi* have been recorded to date, all from rock outcrops in the Wise Formation in Wise, Dickenson, and Buchanan Counties. By contrast, extensive long-term (10+ years) surveys in the nearby Lee Formation – a sandstone-dominated formation found to the south – have failed to uncover populations of *P. pauleyi*. These patterns suggest that *P. pauleyi* is constrained to outcrops in the Wise Formation in the Virginia coalfields, perhaps a consequence of the higher overall tolerance of xeric conditions reported in the literature for some members of the broader *P. wehrlei* complex. We performed a comparison of 12 habitat variables, including crevice dimensions, forest contexts, and crevice microclimate – at 16 localities across the Wise and Lee Formations to determine if microhabitat conditions differ between these rock types. We identified significant differences in crevice temperature, crevice moisture, and rock outcrop slope between the Wise and Lee Formations, with the Wise Formation possessing higher crevice temperatures, lower crevice moisture, and steeper slopes than nearby outcrops in the Lee Formation. These results support the hypothesis that different rock formations present variable microhabitat conditions for resident amphibian fauna and further indicate that *P. pauleyi* may indeed be constrained to warmer and drier rock outcrop substrate. Our preliminary results provide a foundation through which more intensive survey efforts for the species can be focused and serve as a hypothesis-generator for future work investigating how microhabitat preferences impact population dynamics and inform conservation strategies for outcrop-specialist plethodontids.

26 - Assessing the Osmoregulatory Capabilities of American Alligator Lingual Glands

Benjamin Angalet, Nicholas Green

Kennesaw State University, Kennesaw, GA

Crocodilians inhabit a wide variety of aquatic, marine, and estuarine habitats on 4 continents. Saltwater-adapted species and populations face considerable osmoregulatory challenges in maintaining homeostasis with respect to plasma salt [Na+ and Cl-] concentrations. In addition to the kidneys and cloaca found in all crocodilians, crocodiles possess a salt-secreting lingual gland whose presence and function is understudied in alligators. This study investigates the lingual gland anatomy, physiology, and potential function of American alligator (Alligator mississippiensis) populations exposed to varying salinity levels. At each of four sites (Jekyll Island, Sapelo Island, Okefenokee NWR, and Banks Lake NWR), we will capture 12 to 15 alligators and collect plasma ion concentrations and lingual tissue samples for histological analysis. Anatomical and histological assessments of tissue biopsies processed via microscopy will identify potential inter-population differences. Researcher safety will be ensured using a field-standard jaw prop device. This study will enrich our understanding of alligator physiology in estuarine habitats, which will become critical over the next 100 years as sea levels rise and many coastal alligator habitats are expected to become more saline. Findings will advance reptilian physiology research by clarifying the evolutionary novelty and significance of the crocodile (and perhaps alligator) lingual gland. As apex predators, the individual health and population viability of alligators is crucial to the conservation of ecosystems they inhabit. Additionally, the study's insights into alligator osmoregulatory mechanisms may inspire advancements in treating human conditions related to fluid and electrolyte imbalances, such as kidney disease, heart failure, and dehydration by revealing natural strategies for managing salt and water balance under extreme environmental stress.

27 - AlphaFold2 Analysis of Protein Point Mutations Within Conformational Landscape

Shreyash Singh[1], Richard Stein[2], Hassane Mchaourab[2]

[1]Vanderbilt University, Nashville, TN, [2]Vanderbilt University School of Medicine, Nashville, TN

Underpinning numerous biological functions, protein conformational changes are driven by various protein sequence mutations. This study explores the relationship between conformational shifts and specific mutations within biological proteins through a template protein of MhsT, which entails essential inward and outward conformations for its function. Utilizing machine learning, this study leveraged AlphaFold2's conformational predictions as an analytical tool to either repudiate or confirm our hypotheses of how mutations influence conformational landscapes.

Using SPEACH_AF, mutated multiple sequence alignments (MSAs) were generated, encoding each mutation into binary vector representations. The conformational states were quantified by extracting Cβ-Cβ distances between key residue pairs from AlphaFold2's generated protein structures. These extracted distances served as latent variables for mapping conformational shifts within MhsT's landscape.

From this dataset, a feed-forward neural network was developed to predict conformational outcomes. Particularly, disjointed encoder/decoder neural networks were constructed to coordinate MSAs to these latent space variables that correspond with specific conformations, thereby enabling robust modeling of mutation-induced conformational shifts. In these analyses, predictions were averaged across ten models that were optimized for the greatest performing parameters.

This analysis revealed that as the encoder correctly predicted moderate conformational shifts, it did struggle with more extreme values, particularly those that correspond to the outward conformation. Additionally, although this model's architecture did capture general trends, AlphaFold2's predictions did not exhibit the expected drift toward latent space extremes, suggesting a lack of sensitivity to certain outliers.

Overall, the study highlights the potential of combining computational tools with machine learning to investigate protein dynamics. However, limitations in modeling extreme conformational states indicate a need for alternative strategies, such as exploring phi/psi angle differences or employing architectures beyond neural networks. These insights pave the way for designing targeted mutations to manipulate protein conformations, with implications for understanding disease mechanisms and developing therapeutics.

28 - The Effect of Intermittent Fasting on Glucose Tolerance in Rats

Jordyn Deason, Timothy Maze

Lander University, Greenwood, SC

The prevalence of diabetes is rising at an alarming rate in the United States, with approximately 1 in 10 Americans currently living with diabetes and over 1 in 3 having prediabetes, according to the CDC. Caloric deficit diets are widely recommended for the prevention and management of prediabetes. Intermittent fasting is one way of achieving such caloric deficit. This study examines the effects of intermittent fasting on glucose tolerance in 23 age-paired rats. The rats were divided into two groups: fasted and fed ad libitum. Fasted rats underwent 24-hour fasting periods twice weekly. Rats underwent glucose tolerance tests between eight and ten weeks after beginning of treatment. Analysis of glucose tolerance test results provided insight into whether intermittent fasting improves glucose tolerance, and there was no significant difference in glucose tolerance between the two groups, suggesting that intermittent fasting does not significantly improve glucose tolerance or contribute to the prevention or management of prediabetes.

29 - Physiological Effects of Dual Environmental Stressors on Redear Sunfish (*Lepomis microlophus*)

Sam Williamson, Andrea Vega, Salvatore Blair

Winthrop University, Rock Hill, SC

Due to changing environmental conditions resulting from anthropogenic activities, it is valuable to understand how fish respond to changes in their environment. Freshwater fish can reversibly remodel their gill tissue in response to external stimuli. A compromise exists between the uptake of O2 and maintenance of osmotic balance, whereby the surface area of the gill tissue epithelium can be altered. Previous studies have shown that the interlamellar cell mass (ILCM) grows or is shed relative to environmental conditions. However, prior research does not make clear how gills respond to simultaneous competing stressors such as temperature and salinity. Therefore, the focus of this study was to use redear sunfish (*Lepomis microlophus*) as a model organism to compare ILCM levels between fresh (0 ppt) and elevated salinity water (17 ppt) and hot (26°C) and cold water (10°C) conditions, as well as to determine a potential cellular and molecular mechanism responsible for the observed gill remodeling. To test this, we created a matrix of varying combinations of the temperature and salinity conditions as different experimental 48-hour exposure treatments. The results thus far although complex indicate that there is a significant reduction in the interlamellar cell mass associated with the 26°C. Furthermore, exposure to elevated salinity only resulted in heightened plasma osmolality when fish were exposed to either extreme temperature, not while under control temperature conditions. These preliminary results indicate that temperature is likely a stronger environmental stressor on the redear sunfish capable of stimulating changes at the gill. We conclude that fish are at higher risk of osmotic stress when simultaneously exposed to changes in environmental temperatures.

30 - The impact of executive dysfunction on brain activity during postural control in older adults

Serene Alshalabi[1], Melike Kahya[1], Brad Manor[2]

[1]High Point University, High Point, NC, [2]Harvard Medical School, Boston, MA

Executive functioning is critical for maintaining physical performance in older adults, yet its impact on brain activity during postural control, particularly under dual-task conditions, remains underexplored. This study examined the relationship between executive dysfunction and brain activity during postural control in older adults under both normal and dual-task conditions. We hypothesized that older adults with impaired executive functioning would demonstrate decreased alpha power during dual-task standing, as alpha power is linked to executive function. Eighteen participants (age: 73.2 ± 4.5, 11 female) without executive dysfunction and six participants (age: 82.5 ± 7.3, 5 female) with executive dysfunction were recruited. Executive dysfunction was defined by a TMT B completion time exceeding 90 seconds. Electroencephalogram (EEG) assessed brain activity, while APDM inertial sensors recorded postural sway metrics during quiet and dual-task standing conditions. The Timed Up and Go (TUG) test assessed mobility. An Independent t-test compared EEG alpha power, mobility, and postural sway outcomes between these groups. The results indicated that individuals with executive dysfunction had significantly lower alpha power while standing quietly ($p=0.01$) and dual-task standing ($p=0.02$). Those with executive dysfunction took longer to complete the TUG test ($p < 0.001$) and had greater postural sway area during quiet standing ($p < 0.001$) and dual-task standing ($p = 0.03$). These findings suggest that executive dysfunction in older adults is associated with decreased alpha power and impaired postural control. Further research is needed to investigate the neurophysiological mechanisms underlying these observed relationships.

31 - Unveiling SFK Family Expression In *Danio rerio* (Zebrafish) Organs: Exploring BLK Modulation And It's Effects On Embryonic Development

Rida Hirani, Elyse Donaubauer

Lander University, Greenwood, SC

The SRC Family Kinases (SFKs) are proteins involved in regulating cell growth and mobility, with dysregulation often linked to cancer. This study focused on the expression of BLK, a lesser-studied SFK family member. BLK gene expression in adult zebrafish tissues revealed it is highly expressed in muscle, intestine, and liver tissues, suggesting roles in muscle function, intestinal physiology, and hepatic processes. Conversely, low BLK expression was observed in the eyes and gills, highlighting its tissue-specific significance compared to published results on other SFK members, which showed varying expression patterns across tissues. To investigate BLK's role in development, a BLK morpholino (BLK MO), which silences BLK expression, was injected at 4 hours post-fertilization. Observations at different time points revealed significant developmental disruptions. By 24 and 48 hours post fertilization, disrupted body structures and malformations were observed with BLK MO group, while control embryos exhibited normal development. At 96 hours, hatching rates were lower in the BLK MO group, with abnormalities persisting, compared to the normal development observed in all control embryos. Further research is needed to better understand the precise role of BLK in zebrafish development. However, these preliminary findings demonstrate that silencing BLK expression disrupts normal embryonic development and body structure. The observed developmental abnormalities and decreased hatching rates emphasize BLK's critical role in zebrafish development and implications.

32 - Frizzled 7-dependent regulation of planar polarity and cell migration in zebrafish gastrulation

Joy Harrison Creighton, Jason Jessen

Middle Tennessee State University, Murfreesboro, TN

Planar polarity is a context-dependent process vital for shaping the embryonic body plan. Key to planar polarity is the intercellular communication necessary for the uniform organization and orientation of actin-rich structures across a population of cells. In zebrafish (*Danio rerio*), loss of planar polarity during the gastrulation cell movements of convergence and extension produces severely misshapen embryos with defective dorsal-ventral and anterior-posterior body axes. Gastrula cells exhibit distinct planar polarity-dependent behaviors, including elongation and mediolateral alignment, as they engage in collective migration. Studies in the fly (*Drosophila melanogaster*) established that a core six-protein complex is required for planar polarity of actin structures in wing epithelia. Here, transmembrane proteins Frizzled and Van Gogh were identified as important regulators of planar polarity. In contrast to zebrafish Van Gogh (Vangl2), data is limited regarding the cellular requirements of Frizzled homologs for planar polarity in gastrulation. We have therefore undertaken a comprehensive analysis of Frizzled 7 (Fzd7) function during the establishment of planar polarity and the collective migration of zebrafish gastrula cells. We first confirmed Fzd7 was required for planar polarity-dependent cell behavior, identifying reduced cell orientation and impeded cell migration when Fzd7 was lost. Subcellular investigation found that Fzd7 promoted mediolateral polarization of large actin-rich membrane protrusions and stabilization of small filopodia-like protrusions. We also observed increased fibrillogenesis with the extracellular matrix (ECM) in *fzd7*-null embryos without increased expression of ECM-related proteins, which could be an indirect result of reduced RhoA expression. To better understand these findings, we are

currently investigating Fzd7 function in RhoA and JNK/c-Jun actin polymerization pathways. Preliminary results indicate increased expression of Rac1 during gastrulation, suggesting a shift to JNK/c-Jun actin polymerization activation. We therefore propose Fzd7 is essential to planar polarity, regulating actin for uniform cell orientation through protrusion modeling and promoting efficient migration through fibronectin assembly.

35 - Exploring the Therapeutic Potential of Targeting RRM2 with Osalmid Alone or in Combination

Zaw Bring, Chi-Wen Chen

Appalachian State University, Boone, NC

Osalmid, a resveratrol analog, inhibits the RRM2 subunit of ribonucleotide reductase, thereby disrupting DNA replication and repair by depleting dNTP availability. Given that RRM2 suppression has been shown to impede tumor growth in gastric cancer, our study investigates the therapeutic potential of targeting RRM2 using Osalmid. We analyzed RRM2 expression patterns at both the mRNA and protein levels in gastric cancer patients using TCGA datasets. Additionally, we explored the potential efficacy of RRM2 inhibition against gastric cancer cells through TCGA-based analyses.

36 - Synergistic Antitumor Effect of Combined ATM and Metabolic Pathways Inhibition in Ovarian Cancer Cells

Luiza Dias, Chi-Wei Chen

Appalachian State University, Boone, NC

ATM (Ataxia Telangiectasia Mutated) kinase is essential for repairing damaged DNA, and inhibiting it makes cancer cells more vulnerable to metabolic stress. ATM inhibition sensitizes cancer cells to metabolic stress. This project investigates the synergistic therapeutic potential of combining metabolic inhibitors with ATM inhibitors to enhance the treatment of ovarian cancer. This study employed bioinformatic analyses to explore the therapeutic potential of ATM as a target in ovarian cancer treatment by examining ATM gene expression patterns, mutation profiles, and survival outcomes using databases like KM Plotter and The Cancer Genome Atlas (TCGA). Analyses from the TCGA databases and KM Plotter revealed elevated ATM expression in ovarian cancer tissues, which correlates with poor survival outcomes. Furthermore, TCGA data indicated that ovarian cancer cells are highly sensitive to ATM and metabolic inhibitions, highlighting its potential as a therapeutic target. These results offer a bioinformatic basis for examining the combination of anticancer effects of blocking metabolic pathways and ATM as novel therapeutic strategies to improve cancer treatment outcomes by targeting both DNA repair and metabolic pathways. Ongoing research focuses on preclinical validation of ATM inhibitors and their combinatorial use with metabolic inhibitors to optimize therapeutic efficacy. Future work will establish the IC25 of ATM inhibitors to determine sublethal baseline concentrations for combination studies. Additionally, we will evaluate the synergistic effects of ATM inhibitors (KU60019 and AZD0156) with metabolic inhibitors (such as lactate and mitapivat) on cell viability and apoptosis to enhance anticancer efficacy. This research provides a foundation for innovative combination therapies targeting ovarian cancer, with the potential to significantly improve patient outcomes.

37 - RRM2 as a Key Therapeutic Target to Combat Chemoresistance in Ovarian Cancer

Gabriela Gonzalez Caquias[1], Daniel Chi-Wen Chen[2]

[1]Appalachian State University, Boone, NC, [2]Appalachian state university, Boone, NC

Ovarian cancer is one of the leading causes of cancer-related deaths among women, with poor outcomes often linked to chemoresistance and aggressive tumor progression. Ribonucleotide reductase subunit M2 (RRM2), a key enzyme in dNTP synthesis, is frequently overexpressed in ovarian cancer and correlates with worse survival rates and therapy resistance. Recent advances have highlighted RRM2 as a promising therapeutic target. Inhibitors such as osalmid, Didox, Triapine, COH29, and 4,4'-Dihydroxystilbene (DHS) disrupt RRM2 activity, impairing DNA synthesis and reducing tumor growth. Preclinical studies have demonstrated that these agents can overcome chemoresistance, particularly in ovarian cancer. Using data from the KM Plotter and The Cancer Genome Atlas (TCGA), we confirmed elevated RRM2 expression in ovarian cancer tissues, which is associated with poor survival outcomes. TCGA analysis further suggests that ovarian cancer cells are particularly susceptible to RRM2 inhibitors, supporting their therapeutic potential. Our findings establish RRM2 inhibition as a viable strategy for treating ovarian cancer. Ongoing studies will focus on the preclinical validation of these inhibitors and their combinatorial potential with standard chemotherapy to enhance therapeutic outcomes.

38 - The Effects of Eastern Diamondback Rattlesnake (*Crotalus adamanteus*) Venom on Human Triple-Negative Breast Cancer

Cassidy Lawrence[1], Dr. Lyndsay V. Rhodes, PhD[2]

[1]Florida Gulf Coast University, Naples, FL, [2]Florida Gulf Coast University, Fort Myers, FL

Breast cancer impacts approximately 13% of women in the United States. Although new treatments are allowing for longer lives, triple-negative breast cancer (TNBC) still remains difficult to treat due to its rapid progression and early metastasis. TNBC lacks estrogen receptors (ER), progesterone receptors (PR), and human epidermal growth factor 2 (HER2) protein expression which are all commonly targeted for breast cancer treatment. While certain advancements have been made, there is still a need for more effective treatments and better drug availability. Snake venoms have been explored as a potential cancer treatment for nearly 100 years as they are a complex mix of proteins and enzymes that cause cellular death. Eastern Diamondback Rattlesnake (EDR) venom samples were collected from four different regions around Florida and Georgia: Apalachicola National Forest (ANF), Sapelo Island (SAP), Caladesi Island (CAL), and Jekyll Island (JEK). Adult and juvenile samples were taken from ANF. All samples were screened for their anti-cancer abilities on three TNBC cell lines using cell viability assays. TNBC cells were treated with EDR venom at 10, 5, 2.5, 1.25, and 0.625 ug/mL concentrations then allowed to incubate for 72 hours. All EDR venom samples were able to inhibit cellular growth in MDA-MB-157, MDA-MB-231, and BT-549 cells in a dose-dependent manner. There were no major differences in cell viability due to region, however there was a slight reduction in potency with juvenile samples. Further analysis is needed to identify the proteins responsible for the anti-cancer activity.

39 - Cue-Driven Digestion: Molecular Insights into Prey Recognition in *Dionaea muscipula*

Niklas Plath[1], Jeremy Rentsch[2]

[1]Francis Marion University, Florence, SC, [2]Francis Marion University, FLORENCE, SC

The Venus flytrap (*Dionaea muscipula*) is capable of distinguishing between suitable prey and non-prey within 60 minutes of trap closure, initiating a complex digestive response dependent on mechanical and chemical cues. To investigate the molecular mechanisms underlying this decision-making process, we explore the expression profile of AKINß, a gene underlying nutrient uptake activity, under different feeding treatments. AKINß is known to be upregulated 60 minutes post trap closure, if suitable prey has been detected by the trap. Traps will be stimulated with seven treatments: falsely-triggered trap (no stimulus), a plastic bead, powdered chitin, a chitin-coated plastic bead, freeze-dried prey, and live prey. Using real-time PCR, we will quantify AKINß expression levels to determine which stimuli effectively trigger a continuation of the digestive response. This study will provide insights into the role of prey-associated cues in activating digestion and the specificity of the flytrap's prey recognition system.

40 - Histone H3 Colocalization with the ER: Insights into Mitochondrial Stress Responses

Edwin Guo, Claudia L. Rocha, Colleen Quaas, Kathy Zanin

The Citadel, Charleston, SC

It has been shown that under cellular stress, mitochondria interact with the endoplasmic reticulum (ER) via organelle membrane contact sites. Histone H3 localization in mitochondria in various species has been identified in our lab, and we hypothesize H3 may play a role in mitochondrial stress responses. If H3 enters mitochondria in response to cellular stress, then mitochondria containing histone H3 may also temporarily attach to ER. We utilize immunocytochemistry and confocal microscopy in IEC-18 cells to probe for the proteins histone H3 and prostaglandin G/H synthase 1 (PTGS1), an ER membrane protein. We have identified histone H3 with red fluorescence, PTGS1 with green fluorescence, and DNA with blue fluorescence (DAPI), with colocalization of H3 and PTGS1 resulting in a yellow fluorescence. Our results suggest colocalization of mitochondrial histone H3 with ER, which may provide new insights into the potential role of histone H3 in the intracellular activities that occur during cellular stress.

41 - Examining the Role of Adenovirus E411k Protein on Interferon-beta Expression

Odeya Atar, Lily Cox, Elizabeth Seidita, Kasey Karen

Georgia College & State University, Milledgeville, GA

Adenoviruses are double-stranded DNA viruses that cause illnesses, such as pink eye and the common cold. Early viral proteins, including E4 11k, will generate an ideal environment to promote viral replication. Specifically, E4 11k redistributes PML nuclear bodies and cytoplasmic p bodies, potentially altering their functions. Viral infections will induce a response in the cell via nucleic acid sensors that leads to inhibition of viral replication. RIG-I is a viral RNA sensor, which activates a signaling cascade to stimulate a type I interferon response. It has been demonstrated that the activation of type I interferon transcription is enhanced by the binding of RIG-

l to DEAD-box helicase (Ddx6). E4 11k has been shown to colocalize with and bind to Ddx6, causing Ddx6 to enter aggresomes. Influenza and EV71, single-stranded RNA viruses, have also been shown to interact with Ddx6, leading to the modulation of RIG-I. It is hypothesized that E4 11k binds to Ddx6 to modulate RIG-I, leading to a reduction in interferon-beta expression. Human lung carcinoma cells (A549) were infected with an Ad5 wildtype virus, a virus that only expresses E4 11k, and an E4 11k-deleted virus for 12, 24, 30, 36, and 48 hours. Reverse transcriptase q-PCR was performed to evaluate expression of RIG-I and interferon-beta. After normalizing to an internal control, biphasic expression of interferon-beta was observed during the wildtype adenovirus infection. In the presence of E4 11k expression, we observed interferon-beta peaks at 12-24 and 36 hours post infection (hpi) and decreases at 30 and 40 hpi. In the absence of E4 11k, the only difference in expression was at 36 hpi, where interferon-beta increased significantly. These data suggest that E4 11k is necessary in reducing interferon-beta expression at this late time point.

42 - Advancing Solid Tumor Diagnosis: Flow Cytometry Analysis of Formalin-Fixed Paraffin-Embedded Tissue

Kritika KC

Notre Dame of Maryland University, Baltimore, MD

Background - Histologic investigation of permanent formalin-fixed paraffin-embedded (FFPE) tissue is the current gold standard for the diagnosis of solid tumors. However, this method is limited by interobserver variability and limited sampling. Flow cytometry (FCM), has the potential to address this limitation. FCM is a technology that rapidly analyzes single cells or particles as they flow past single or multiple lasers while suspended in a buffered salt-based solution. While this method is routinely used for the diagnosis of hematologic malignancies, its utility for the diagnosis of solid tumors has not been fully realized.

Objective - Here, we aimed to use FFPE tissue dissociation and FCM to detect tumor cells in FFPE specimens.

Methods - The 25 um sections from FFPE breast tumor and astrocytoma specimens were dissociated into single cell suspensions using the Miltenyi Biotec FFPE dissociation kit. Single cell suspensions of the breast tumor and brain tumor were immunostained with fluorescently labeled antibodies to pan-cytokeratin or glial fibrillary acidic protein, respectively, and 4',6-diamidino-2-phenylindole (DAPI). DNA histograms and antibody labeling were evaluated with FCM. Flow cytometric results were confirmed with paired immunofluorescence results.

Results - In flow cytometric analysis, we observed aneuploidy in both the breast tumor and glioblastoma specimens. By gating pan-cytokeratin positive cells in the breast tumor sample, we observed an increase in the aneuploid G1 peak relative to the diploid G1 peak, including when gating GFAP positive cells in the glioblastoma sample. The fraction of cytokeratin positive cells in the breast tumor sample and GFAP positive cells in the glioblastoma sample were similar to the proportions observed microscopically of immunofluorescent labeled tissue of the same samples.

Conclusion - We demonstrated the ability to detect tumor cells in heterogeneous FFPE specimens using cell-specific antibodies and DNA ploidy. In future, FCM may serve as an adjunct diagnostic modality to standard of care histopathological diagnosis.

43 - The Effects of Intermittent Fasting on Leucine Rich Repeat Neuronal 3 Gene Expression and Gray Matter Thickness in 4-Month-Old Fischer (CDF) Rat Brains

Lila Bagley, Jennifer Maze

Lander University, Greenwood, SC

Intermittent fasting is a popular weight loss method many use, but it also has several other health benefits, including enhanced cognitive function. Leucine Rich Repeat Neuronal 3 (LRRN3) is a conserved gene expressed at high levels in the human brain and is associated with gray matter and cerebral cortex thickness. The gray matter and cerebral cortex are responsible for helping control movement, emotions, and memories. LRRN3 has been shown to decrease in expression during aging however, there is little research on how the LRRN3 gene is affected by fasting. In this study, a group of 2-month-old Fischer (CDF) rats were placed on a 24-hour feeding/fasting schedule for 10 weeks. Using quantitative RTPCR, changes in the expression of LRRN3 in the rat brains were observed. A two sample t-test showed the expression of the LRRN3 gene significantly increased in rats on fasting schedules compared to non-fasted rats. Additionally, whole brains were processed, embedded with paraffin wax, and sliced. The gray matter thickness was measured and a two sample t-test showed a significant increase in thickness in rats on fasting schedule compared to non-fasted rats. This study helps provide additional understanding of the cognitive benefits associated with intermittent fasting.

44 - APC and TP53 in Metastatic Colorectal Cancer Survivability

Jamison Darden, Jennifer Hurst-Kennedy

Agnes Scott College, Decatur, GA

This study aimed to discover whether alteration of either APC or TP53 genes best predicts survivability in metastatic colorectal cancer (CRC), using CRC patient genomic sequencing data from the 2020 Pan-Cancer Atlas. APC and TP53 were chosen because they have the highest rate of mutations in metastatic CRC. Both genes are tumor suppressors whose normal functions are to negatively regulate cell proliferation. The Oncoprints for CRC patient mutations showed truncated APC gene mutations were common in CRC, likely causing overstimulation of the Wnt signaling pathway resulting in uncontrolled Wnt-mediated gene expression and proliferation. Additionally, missense and truncated TP53 mutations were common in CRC, possibly contributing to metastatic CRC by allowing cells to bypass cell cycle checkpoints causing uncontrolled cell growth. Kaplan-Meier survivability graphs were generated to investigate APC and TP53 mutations in CRC patients. The experimental groups had one or more mutated genes (mutated TP53, mutated APC, or both mutated APC and TP53), and the unaltered group (wild-type APC and TP53) served as the control. Based on the data, APC has a higher survivability compared to TP53. A combination of mutated APC and TP53 has a value of survivability medial to two genes individually. The low p-value suggests statistical significance that APC mutations have a higher chance of survivability than a TP53 mutation. This suggests that for further diagnostic testing and treatment options, TP53 mutations should be targeted first in comparison to APC to increase survivability in patients.

45 - Utilizing DNA Sequencing to Identify and Confirm Species of Hairworm (Phylum Nematomorph) Samples

Denise Garcia Salas[1], Dr. Christina Anaya[1], Dr. Jennifer Boddicker[2]

[1]Florida Gulf Coast University, Fort Myers, FL, [2]University of Florida, Gainesville, FL

The phylum Nematomorpha, commonly known as hairworms, consists of Nectonematida, marine hairworms, and Gordiida, freshwater hairworms. Hairworms are parasites of arthropods with both aquatic and terrestrial life cycles. Most species of hairworms have similar morphological traits, making species determination difficult. Researchers have reported roughly 360 distinct species of hairworms worldwide. Due to the lack of morphological variation in hairworm species and recent studies that suggest hairworms contain cryptic species, identification based on traditional morphological-based identification is ineffective. Therefore, molecular barcoding is a necessary task in taxonomic investigations. DNA barcoding is a molecular method that can mediate the challenge of morphological-based identification. This study used DNA sequencing to assess the identity of six nematomorph samples from various donors worldwide. The Masterpure DNA extraction protocol was followed to extract DNA, and agarose gel electrophoresis was used to confirm that the samples contained DNA. A nanodrop spectrophotometer measured DNA concentration in nanograms per microliter. Next, all the samples underwent a polymerase chain reaction (PCR). Finally, the EXOSAP-IT protocol was followed for all PCR samples before sending for sequencing. Our analysis concluded that the universal primers LCO and HCO at an annealing temperature of 59° C worked best for our samples. Only 9.17% of the 360 hairworm species have DNA sequences on GenBank. As we continue to extract and report sequences, we can close the gap in this disparity and investigate additional incidences of cryptic species and morphological studies.

46 - HSP101 Dynamics in *Arabidopsis thaliana*: Stress Memory and Developmental Regulation

Teil Fuller[1], Jeremy Rentsch[2]

[1]Francis Marion University, Florence, SC, [2]Francis Marion University, FLORENCE, SC

Arabidopsis thaliana exhibits a dynamic response to heat stress through the regulation of HSP101 (ClpB), a molecular chaperone critical for protein disaggregation and refolding. While the rapid upregulation of HSP101 is well-documented during acute heat stress, we have identified an anomalous late-life cycle spike in HSP101 expression, even in the absence of proximal stress events. To investigate the temporal dynamics of HSP101 regulation, plants were subjected to a heat pretreatment (38C°) followed by exposure to otherwise fatal heat stress (45°C). Preliminary data suggest a pronounced modulation of HSP101 expression over time, with distinct peaks correlating to specific developmental stages and stress conditions. This study aims to further describe the interplay between developmental cues and stress memory in the regulation of HSP101, providing new insights into plant resilience under fluctuating temperatures.

47 - Comparative Analysis of Soil Microbial Diversity and Abundance in Grazed and Ungrazed Environments at Buck Island Ranch

Laura Froberg[1], Elik Esquilin[1], Tatiana Guerra[2], Dr. Tammy Laberge, Ph.D[1]

[1]Miami Dade College, Miami, FL, [2]Miami Dade college, Miami, FL

The mission of Archbold Station, which includes Buck Island Ranch, is to understand and identify the correlation of the ecological effects of ranching. Therefore, our study focused on identifying bacterial diversity and abundance in the soil samples collected from Buck Island Ranch. We compared two pastoral environments: grazed and ungrazed. Microbial environmental DNA samples were isolated from soil using QIAGEN DNeasy PowerSoil extraction kits. Bacterial species composition were identified by metabarcoding using the 16S rRNA gene, which is unique to each microbe. The top 10 bacteria per soil type were identified and compared across all samples using DNA Subway Purple Line. Each soil type was found to have similar microbes, but their abundance varied. Interestingly, the microbiota were found to have similar ecological functions that attribute to the overall sustainability of life found in these environments.

48 - *Dalea foliosa* management and conservation: Genotyping-by-sequencing of microsatellite loci (GBS-SSR)

Nicolette Monnier, Ashley Morris

Furman University, Greenville, SC

Based on previous genetic work evaluating the genetic status of *Dalea foliosa*, the leafy prairie clover, there is a significant need for high resolution genetic evaluation and conservation effort. This study compared the allele base pair size data from fragment-based simple sequence repeats (FB-SSR) with allele sequencing data from genotyping-by-sequencing simple sequence repeats (GBS-SSR) to further a range-wide evaluation of *D. foliosa,* using a limited but geographically representative sample. The variation found between the two methods indicates that while the FB-SSR microsatellite analysis provides a methodologically sound intermediary step, the GBS-SSR approach generates an additional, more comprehensive genetic profile, uncovering greater allele diversity and offering a finer resolution in assessing population dynamics compared the previous standard. The higher resolution of data achieved using GBS-SSR in capturing genetic diversity affirms its strength as a method for population genetics studies. These findings deepen our understanding of genetic variation between *D. foliosa* populations and have important implications for its conservation and management, demonstrating the continued need for and relevance of conservation research.

49 - Investigating plastid genome evolution across the Campanulaceae

Bryson Scoffield[1], Alfredo López-Camaal[2], Laura Galloway[2], Karen Banard-Kubow[3]

[1]James Madison University, VA, [2]University of Virginia, Charlottesville, VA, [3]James Madison University, Harrisonburg, VA

Understanding the process by which new species form (speciation) is a fundamental goal of evolutionary biology. Coevolution between the nuclear and organelle genomes and the incompatibility that can result when this is disrupted is an understudied, potentially significant mechanism of speciation. *Campanula americana*, an herbaceous species in the Campanulaceae, has been found to exhibit elevated rates of plastid genome evolution and cytonuclear incompatibility, suggesting that elevated rates of organelle evolution may drive cytonuclear incompatibility, and thus speciation. It is known that the Campanulaceae in general tend to have elevated rates of organelle evolution, but the extent to which this varies within the family and whether C. americana is an outlier is uncertain. To investigate these questions, we characterized patterns of plastid genome evolution across the Campanulaceae. Plastid gene sequences were extracted from annotated chloroplast genome assemblies for 18 species from across the Campanulaceae and then aligned in Geneious Prime. The alignments were manually curated and concatenated according to the functional group. The concatenated gene sequences were used to create a phylogenetic tree which we input into Paml along with the alignments to determine dN, dS, and dN/dS and examine how these values varied across species and genes. The dN/dS ratio varied across the Campanulaceae family indicating variation in selection on organelle genes and in rates of organelle evolution. Additionally, in line with previous work, dN/dS varied among genes, with elevated ratios observed for genes involved in regulation but not photosynthesis. These data provide the first step for investigating the link between rates of organelle evolution and cytonuclear incompatibility. Future work will focus on the nuclear-encoded gene counterparts to test for signatures of cytonuclear coevolution and eventually testing for cytonuclear incompatibility in candidate species. This work will inform whether cytonuclear coevolution and incompatibility is a significant driver of speciation.

50 - Pathogenicity analysis of single nucleotide polymorphisms in the prion protein gene

Casey Torgesen

University of North Georgia, Oakwood, GA

The PRNP gene encodes a lipid-anchored protein localized to the outer surface of cell membranes. The exact function of the protein (PrP^C) coded by this gene is not fully understood, but it may mediate neuron homeostasis, cell signaling, and brain tissue response to oxidative stress experienced during strokes. Mutations in the PRNP gene have been implicated in neurodegenerative diseases where a misfolded variant of the protein, incapable of being degraded by cells, aggregates within the brain and leads to the formation of tiny holes resulting in rapid onset dementia and death. The protein consists of distinct parts with unique biochemical and structural characteristics. A flexible, unstructured region projects outward from the cell into the immediate neuronal microenvironment, while a more structured region remains closer to the cell membrane. The current study examines a genetic mutation of the gene and analyzes the molecular consequences upon protein structure. Computational analysis of this mutated protein will generate significant data that elucidates some of the molecular interactions governing the protein's folding and help to predict pathologies. The relevance of this study is underscored by the fact that a protein's three-dimensional structure directly impacts its function, and misfolded proteins are involved in cellular aging and diseases such as Alzheimer's, type 2 diabetes mellitus, Tay Sach's, and Creutzfeldt-Jakob disease.

51 - Species diversity of honey bee (*Apis mellifera*) pollen at the UNCP Apiary

Shannon Lowry, Kaitlin Campbell, Lisa Kelly

University of North Carolina at Pembroke, Pembroke, NC

Honey bees (*Apis mellifera*) play a significant part in the pollination services of agriculture and their local environment, acting as highly effective pollinators of our food crops and wild plants. Bees perform the majority of pollination for our cultivated crops, with bee-pollinated crops contributing to one-third of the human dietary supply. The University of North Carolina at Pembroke (UNCP) Garden was created in 2014, and an apiary was later created for educational purposes. Honey bee pollen has been collected from the UNCP Apiary for several years. We will extract the DNA from pollen samples using a commercial kit with the hopes of discovering their botanical origin by sequencing the gene of interest, *rbcL*, which encodes for the large subunit of ribulose bisphosphate carboxylase, an enzyme that is in the chloroplast. Preliminary data from the Plant Systematics students of Spring 2024 found that pollen collected in the late winter was composed of *Camellia sinensis, Taraxacum officinale, Prunus virginiana, P. persica,* and *Rubus trivialis*, which is consistent with late winter flowering plants. In the continuation of this project, we will expand our study to include identifying and comparing the species richness in the pollen at two UNCP apiary sites, determining the honey bee's preferred plant species, and creating a pollen color chart for the apiary. With this research, we can provide insight into honey bee interactions with pollination gardens and their plant preferences.

53 - Searching for Antimicrobial Producing Microbes in the Cockroach Gut

Katie Skinner, Michelle Thomas

Campbell University, Buies Creek, NC

Cockroaches live in pathogen filled environments, ingesting trash and feces. As such, they ingest pathogens on a daily basis without contracting illness. In contrast, if these same pathogens were ingested by humans, it could cause serious illness. Therefore, the population of microbes in a cockroach gut may have certain adaptations to counteract harmful pathogenic infections. The goal of this experiment was to investigate the microbes present in the digestive tracts of wild cockroaches and test for antimicrobial production. First, cockroaches were obtained from various sources including a college campus, businesses, and a domestic residence. The cockroaches were identified, and their digestive tract was extracted by dissection with 7 extracted gut samples obtained. A "gut solution" was created and cultured on nutrient agar. Diverse microbial populations were observed, and 57 unique colonies were isolated. The colonies were assayed for antimicrobial production against Escherichia coli (E.coli), Enterococcus raffinosus (E.raffinosus), Pseudomonas putida (P. putida), Enterobacter aerogenes (E. aerogenes), Staphylococcus epidermidis (S.epidermidis), and Enterococcus faecalis (E. faecalis). The percentages of isolate production against the test pathogens included 7.0% production against E.coli., 7.25% against E. raffinosus, 3.5% against P. putida, 0% against E. aerogenes, 15.7% against S.epidermidis, and 0% against E. faecalis (E. faecalis). Data from this experiment will contribute to the future exploration and role of antimicrobial producing microbes in the cockroach gut post ingestion of intestinal pathogens.

54 - Impact of Regenerative Agriculture on Colony-Forming units (CFU) and Antibiotic-Producing Bacteria

Samuel Bohlen[1], Michelle Thomas[2]

[1]Campbell university, Buies Creek, NC, [2]Campbell University, Buies Creek, NC

Regenerative agriculture is an increasingly popular method of farming that recovers the ecosystem and has been linked to increased soil quality. Soil microbes are a key component of the soil health ecosystem. This study will be exploring links between farming practices and soil microbial counts as well as antibiotic producing isolates. Soil samples at a depth of 4" and 12" were collected from four farms with varying practices. Colony- forming units were counted following serial dilution and spread plating. There was a notable 85% increase in average CFU counts between the conventional farm and seasoned regenerative sites. Colonies were selected from spread plates and screened for antibiotic production against near-relatives of ESKAPE pathogens. Regenerative agriculture practices resulted in a 50% increase in antibiotic producing isolates, with six gram negative and three gram positive bacilli or coccobacilli shown between all sample locations. There was shown to be a positive correlation between regenerative agriculture and both soil microbial counts and antibiotic-producing isolates. This reinforces the common belief that regenerative agriculture has holistic benefits to the ecosystem.

55 - Targeting Biofilm Formation in Multi-Drug Resistance *Candida auris* Using Amino-Carboxyl Compounds for Enhanced Antifungal Therapy

Japhet Senyo Kamasah[1], Sahar Hasim[2], David Goode[3]

[1]PhD Microbiology Program at Alabama State University, Department of Biology, Montgomery, AL, [2]Alabama State University, Montgomery, AL, [3]Mercer University Department of Chemistry, Macon, GA

Biofilm formation is a critical virulence factor in *Candida auris (C. auris)*, enabling this multidrug-resistant (MDR) pathogen to evade antifungal agents and immune defenses. The Biofilm's protective extracellular matrix enhances drug resistance, making infections difficult to treat and increase morbidity and mortality rates. This study investigates the potential of amino-carboxyl synthetic compounds to inhibit C. auris biofilm formation by targeting key stages, including initiation, maturation, and dispersal. Four amino-carboxyl compounds were synthesized and evaluated for their biofilm-inhibitory activity against multiple *C. auris* clades, including MDR isolates. Biofilm formation and disruption were quantified using colony-forming unit (CFU) assays, minimum inhibitory concentration (MIC) determinations, and advanced imaging techniques. Additionally, the effects on extracellular polymeric substances (EPS), including polysaccharides and proteins, were assessed to elucidate the mechanisms of biofilm inhibition.

Preliminary results demonstrate that these compounds significantly inhibit biofilm formation at early stages. This study highlights the potential of amino-carboxyl synthetic compounds as novel biofilm inhibitors, addressing a critical gap in antifungal therapy. By targeting biofilm-associated resistance mechanisms, these compounds offer a promising strategy to combat the global threat of *C. auris* infections and overcoming the limitations of current antifungal treatments. Further development and optimization could lead to next-generation antifungal therapeutics.

56 - Abundance of Fecal Indicator Bacteria and Genetic Diversity of *Escherichia coli* in Streams Draining Residential Areas of Varying Socioeconomic Status

William Johnson, Morgan Soukhamneut, Owen Smith, Andrew La, Suresh Muthukrishnan, Min-Ken Liao, Gregory Lewis

Furman University, Greenville, SC

In urban areas, environmental quality can be lower in residential areas of lower socioeconomic status than in residential areas of higher socioeconomic status. The major goal of our study was to compare bacterial abundance in small streams draining from residential areas of lower and higher socioeconomic status. We hypothesized that the abundance of fecal indicator bacteria would be higher in streams draining areas of lower socioeconomic status. To test this hypothesis, during June-July 2024, we sampled 20 small streams in and near the City of Greenville in the Piedmont region of South Carolina. The watershed areas of these streams ranged from 0.26 to 2.23 km^2 and included residential areas of predominantly single-family homes. Of the 20 streams, 10 drained residential areas of low socioeconomic status and 10 drained residential areas of high socioeconomic status based on the socioeconomic status theme of the U.S. Centers for Disease Control and Prevention's Social Vulnerability Index. Water samples were collected under baseflow conditions and were analyzed for total coliforms, *Escherichia coli*, and enterococci. Individual *E. coli* isolates were identified and typed into phylogroups A, B1, B2, or D. Tetracycline-resistant *E. coli* strains were isolated using 20 µg/mL tetracycline. Contrary to our hypothesis, we found no statistically significant differences in the abundances of any bacterial group between watersheds of the two socioeconomic statuses. However, on at least one sample date at all 20 streams, *E. coli* and/or enterococci concentrations exceeded recreational water limits recommended by the US EPA. Additionally, the frequencies of *E. coli* of phylogroup D were greater and the frequencies of phylogroup A were lower in streams draining residential areas of higher socioeconomic status. Additional

research is needed to determine whether these differences in phylogroup frequencies result from different *E. coli* sources within the watersheds or from different conditions within the streams.

57 - Real-life Zombies: Cordyceps in our Backyard?

Dylan Cienfuegos, Daniel Ruiz, Alli Eudy, Christina Masika, Carmony Hartwig

Catawba College, Salisbury, NC

With a horror story that pushes the boundaries of nonfiction, Ophiocordyceps, a genus of parasitic fungi, infamously turns ants into 'zombies', manipulating the host's behavior to favor parasite survival and reproduction over host viability. Such behavior in *Ophiocordyceps unilateralis* is exhibited through phenotypic attributes displayed by *Camponotus* spp. hosts, such as a "death grip" induced by chemical manipulation of the host to the underside of a twig. Recently, *Camponotus* spp. ants have been observed in Catawba College's Fred Stanback Jr. Ecological Preserve (FSJEP) with demonstrated infection by suspected Ophiocordyceps. We hypothesized that the fungus infecting ants in our preserve is related to *O. unilateralis kimflemingae*, a newly described parasitic species from neighboring South Carolina. We used a three-pronged approach to characterize this new FSJEP fungal parasite, through morphological, behavioral, and molecular attributes. Morphologically, the FSJEP species is similar in size and lifecycle forms to *O. u. kimflemingae,* as determined through light microscopy. Behavioral characterization of the FSJEP species suggests an optimal 'fungal zone' distance of 143.8 ± 7.4 cm, as well as a potential relationship (R^2 = 0.0399; p = 0.088) between host head mandible width (2.12 ± 0.05 mm) and twig diameter (2.67 ± 0.14 mm). Barcoding analysis demonstrates the FSJEP species has a unique ITS gene sequence, with fragmented coverage to the *O. u. kimflemingae* (89-93% homology). Future work will focus on whole genome sequencing of the FSJEP species, as well as investigating the presence of this phenomenon in surrounding localities.

58 - Examining the effects of 29 unique exogenous fatty acids on growth and membrane permeability in *Vibrio cholerae*

Carli Todd, Lydia Byerly, David Giles

The University of Tennessee at Chattanooga, Chattanooga, TN

Many Gram-negative bacteria possess the intriguing ability to utilize exogenous fatty acids from their environment for physiological and behavioral purposes. Specifically, *Vibrio cholerae* has been shown to scavenge an array of polyunsaturated fatty acids for incorporation into membrane phospholipids, thereby affecting permeability and antimicrobial resistance. *V. cholerae* encodes several homologs of proteins involved in the uptake and assimilation of fatty acids into phospholipids. This study conducted an initial survey of saturated fatty acid responses in *V. cholerae* by performing growth curves and permeability assays with a library of commercially available fatty acids. Assessment of growth over 12 hours involved both i) normal minimal media with 300 micromolar fatty acid and ii) carbon-deficient minimal media with 1 millimolar fatty acid. Compared to the control, most fatty acids slowed the growth of *V. cholerae* when monitored in minimal media. Preliminary findings suggest that *V. cholerae* is capable of utilizing over a dozen fatty acids as sole carbon sources. Using the hydrophobic dye crystal violet, we determined the membrane permeability impact of fatty acids, ranging from 18 to 4 carbon lengths and 0-6 unsaturation(s). Of 7 linolenic acids (18:3), only one caused a decrease in permeability. 20-carbon fatty acids followed a pattern of increased permeability with each added unsaturation. Longer carbon lengths generally led to more significant changes in permeability. Regardless of carbon length, polyunsaturation typically resulted in significant changes to permeability. Up to 20-30% fluctuations in permeability were observed compared to the control. Collectively, data suggests a wide repertoire of fatty acids can alter growth and membrane permeability in *V. cholerae*. These effects on growth and membrane changes highlight *V. cholerae*'s ability to scavenge a multitude of fatty acids from its environments, as well as the potential for these fatty acids to alter lipid homeostasis.

59 - An Examination of the Microbial Communities Associated with the WV Exhibition Coal Mine (Beckley, WV): A Pilot Study

Katelyn Hall, Brooklyn Gibson, Thomas Saladyga, Darla Wise

Concord University, Athens, WV

The microbial composition in soil from coal mines is a current topic of interest. This study will examine the impact of sulfur concentrations affecting the diversity and abundance of bacteria in topsoil. Soils from coal mines in China were reported to have a high concentration of sulfur had a bacterial prevalence of *Proteobacteria* and *Gemmatimonadetes*. As a negative control, soil was collected from nearby farmland. In the control area, the sulfur concentrations were lower, with the most dominant bacteria being *Actinobacteria*.

Soil samples were collected throughout the Exhibition Coal Mine, DNA was extracted from the soil, and the DNA samples analyzed using MinION sequencing to determine the profile of the microbiome. As a negative control, soil samples were obtained from nearby fields. A soluble reactive phosphorus test will be used to determine the amount of sulfur in each of the soil samples. The expected results of this study are anticipated to correlate with previously conducted studies; with the soil coal mine containing higher amounts of sulfur content than the control and the most prevalent bacteria would be *Proteobacteria* and *Gemmatimonadetes*. The control soils are expected to have lower sulfur levels and a prevalence of *Actinobacteria*.

60 - Oral Probiotics: Looking for Changes.

Miles Lester, Meredith Marchetti, Alejandro Alvarez, Nourhan Ali, Jairus Johnson, Hunter Sheppard, Erin Witalison, Francisco Camacho, John Turner

Catawba College, Salisbury, NC

Understanding the human microbiome is critical to understanding human health. More and more companies are promoting live microbial supplements (probiotics) to promote human health. This research focuses on probiotic lozenges containing the M18 strain of *Streptococcus salivarius*. *S. salivarius* has been shown to decrease the likelihood of dental caries, which is possibly the most prevalent human disease. There are a few proposed mechanisms for the effects of S. Salivarius on dental caries, including the production of bacteriocins. This research examines the changes in the bacterial community with the introduction of *S. salivarius*. 14 volunteers participated in the study of which only 10 completed it. The baseline sampling was buccal swabs, Participants were randomized for the treatment, and after 14 days a final buccal swab was taken. DNA from the oral microbiomes was isolated, followed by the PCR amplification of the 16S rRNA gene. Oxford Nanopore libraries were created from the 16S amplicon. Libraries are being run on the Oxford Nanopore MinION with a Flongle Flow cell. Data is being analyzed in EPI2ME.

61 - Characterizing the bacterial community of copepods in James Madison University's retention pond

Vanessa Rollins, Karen Banard-Kubow, Jordan Heydt

James Madison University, Harrisonburg, VA

Zooplankton, particularly copepods, play a vital role in aquatic ecosystems and serve as potential carriers of pathogenic bacteria. This study investigated the bacterial communities associated with copepods in a retention pond at JMU's East Campus. By combining water and copepod samples collected at multiple time points, we aimed to identify microbial communities through 16S rRNA gene sequencing. The methodology included DNA extraction, PCR amplification, and sequencing via Illumina MiSeq, followed by comparative analysis between microbial communities on copepods and in the water column. Our focus was to assess the prevalence of pathogens or other bacterial species, exploring variation across copepod species and across time. Some taxa found across the samples were proteobacteria, cyanobacteria and gammaproteobacteria. A group of particular interest were the Burkholderiales, which were more abundant in copepods compared to water samples, and the dominant species within this group changed in abundance over time. These findings will offer insights into the ecological dynamics of copepod-associated bacteria and their potential risks to public health.

62 - Isolation and Preliminary Characterization of Phosphorus Solubilizing Microbiota From a Monoculture Cotton Field in Hartsville, SC

Manav Harikumar, Bennett Brockman, Valeria Avanzato

South Carolina Governor's School for Science and Mathematics, Hartsville, SC

Phosphorus is the second most common limiting element affecting crop growth and development. Soil contains an average of 0.05% phosphorus, with only 0.1% available as soluble phosphorus, leading to inadequate phosphorus availability for crops. Fertilizers are commonly used to supplement minerals and enhance crop yield. However, most of the phosphorus in fertilizers remains insoluble, which results in low phytoavailability and environmental issues such as groundwater pollution and eutrophication. Sustainable practices, including compost/manure supplementation, crop rotation, and no-till farming, have been effective in mitigating over-fertilization. Recently, the application of naturally occurring phosphorus-solubilizing microbes —fungi (PSF) and bacteria (PSB)—has shown promise in enhancing plant nutrient acquisition through enzymatic solubilization of insoluble phosphorus. Rhizospheric soil samples were collected from a monoculture cotton field in Hartsville, SC, during February-March 2024. Fungal colonies were isolated using the soil dilution method and Rose Bengal and chloramphenicol as the selective culture medium. After 5-10 days of incubation, individual colonies were transferred to PVK (5% $Ca_3(PO^4)_2$) medium to identify phosphorus-solubilizing strains. Positive isolates were recognized by halo formation on the PVK medium. Phosphate solubilization was assessed using the Solubilization Index (SI). Cultural and morphological characteristics were used to identify isolates at the genus level. Out of 76 fungal isolates, 10 (13%) showed phosphorus solubilization ability 'in vitro', with *Penicillium* species being the dominant genus. The phosphorus-solubilizing efficacy of

microbiota from the local cotton field suggests the potential use of endemic PSF as sustainable alternatives to commercial fertilizers. Future research should include: (a) molecular characterization of fungal isolates, (b) increased field coverage sampling to optimize PSF isolation and, (c) 'in planta' experiments to evaluate the impact of local PSF isolates on seed development and plant growth. This study aimed to isolate and characterize PSF strains from a heavily fertilized cotton field in Hartsville, SC.

63 - Polyunsaturated fatty acids (PUFAs) can alter the killing effects of antimicrobial peptides in *Vibrio cholerae*

Meredith Grant, David Giles

The University of Tennessee at Chattanooga, Chattanooga, TN

One of the top global threats to public health is antimicrobial resistance. There is an urgent need for development of novel therapeutic regimens that can bypass existing microbial mechanisms of antibiotic resistance. Previous research has established that exogenous polyunsaturated fatty acids (PUFAs) are assimilated into the membrane phospholipids of Gram-negative bacteria, altering membrane permeability and susceptibility to antimicrobials. Introducing membrane vulnerability may create opportunities for antimicrobials to diffuse through the outer and inner membranes of Gram-negative bacteria. In this study, combinatorial treatment of the human pathogen *Vibrio cholerae* with three physiologically relevant PUFAs (linoleic acid [18:2], arachidonic acid [20:4], and docosahexaenoic acid [22:6]) and 12 antimicrobial peptides (cecropin A, cecropin B, LL-37, melittin, SMAP29, TET20, temporin L, CRAMP, NRC-16, PMAP-23, apidaecin 1B, and protegrin 1) was evaluated using broth dilution minimum inhibitory concentration (MIC) assays. Significant changes in MIC (> 8-fold) were observed, particularly when 20:4 was paired with SMAP29, protegrin 1 and melittin. Minimal changes to MIC were observed for LL-37 and temporin L, while the MIC of some peptides (CRAMP, PMAP-23) could not be determined due to limiting concentrations. Collectively, this data highlights not only PUFA-mediated biomembrane effects, but also the potential for PUFAs and membrane-attacking antimicrobials to synergistically target Gram-negative infections. Conversely, availability of these physiologically relevant PUFAs may allow bacterial membrane adaptation that facilitates innate immune evasion, thereby contributing to pathogenesis in *Vibrio* species.

64 - Pseudomonadota Dynamics in *Clostridiodes difficile Infection* (CDI): A Focus on *Klebsiella pneumoniae* and *Escherichia coli*

Loraye Smith

Notre Dame of Maryland University, Baltimore, MD

Clostridiodes difficile infection (CDI) is a prevalent hospital and community acquired infection characterized by the colonization of endospore-forming Clostriodies difficile. CDI arises following antibiotic exposure and concurrent dysbiosis of the gut microbiome, leading to severe gastrointestinal symptoms. In 20-30% of patients, CDI may recur following initial treatment (rCDI), which is a testament to C. difficile's capability to persist in the host. How this persistence occurs is still a largely unexplored area in the field. One existing observation is that patients with CDI or rCDI have a higher prevalence of Pseudomonadota in the dysbiotic gut compared to healthy or non-recurrent controls. Thus, we hypothesize that Pseudomonadota may play a role in C. difficile persistence. The goal of this study was to confirm the observations of previous studies that there is an increased Pseudomonadota prevalence in our patients with recurrent versus non-recurrent CDI. Serial fecal samples of CDI patients from cohorts at Johns Hopkins Hospital were collected and DNA was extracted for analysis. Polymerase Chain Reaction (PCR) was employed to detect C. difficile and Pseudomonadota, specifically KP and EC which are common Pseudomonadota in the gut microbiome. Preliminary data suggest KP prevalence in our CD-positive rCDI patients after 6 months in comparison to our non-recurrent patients. Confirming the presence and or correlation of these Pseudomonadota in our patient cohorts between recurrent and non-recurrent CDI patients will enable us to further explore these associations, potentially leading to new study approaches and therapeutic methods for rCDI patients.

65 - Genetic and Physical Characterization of an Unknown Bacteriophage from a Commercially-Available Sample of *Bacillus thuringiensis*

Caroline Paccione, Dinene Crater

High Point University, High Point, NC

Bacillus thuringiensis (*Bt*) is a common soil bacterium that is used as a natural insecticide since its spores are toxic to insects when ingested. Previous research in our laboratory isolated an unknown phage from a commercially available sample of *Bt*. Bacteriophages, also known as phages, are viruses that specifically infect bacteria and are harmless to animal and plant cells. The purpose of our research is to perform structural and genetic characterization of this unknown *Bt* phage. DNA was isolated from the phage and subjected for RAPD-PCR analysis to produce a PCR fragment. Preliminary DNA sequence analysis of the 644 bp PCR fragment showed a 99.2% identity to other *Bt* and *Bacillus cereus* lysogenic phage over only 17% of the DNA. From this data, we hypothesize

that we have isolated an uncharacterized *Bt* phage. To differentiate this *Bt* phage from known samples, we subjected the purified *Bt* phage genomic DNA to whole-genome sequencing. This yielded a more complete genome sequence than a small PCR product for a BLAST sequence analysis, with analysis still needing to be performed to confirm our hypothesis. We will also attempt transmission electron microscopy from a high titer of purified *Bt* phage. This will allow for a structural comparison with other known *Bacillus* phage. Combining genetic and structural analyses will help to determine if we have isolated a previously uncharacterized *Bt* phage.

66 - Detecting Snake Fungal Disease in GA Waterways Using eDNA Analysis

Hanna Busche, Jiselle Gonzalez, Jeanelle Morgan, Swapna Bhat, Margi Flood

University of North Georgia, Oakwood, GA

Snake Fungal Disease (SFD) is a severe to fatal skin infection affecting wild snake populations in the Eastern United States. The fungus Ophidiomyces ophiodiicola (Oo) causes SFD, which can be detected by analyzing eDNA. eDNA is environmental DNA that is free-floating within the environment due to behavior, such as snake shedding, and can be sampled noninvasively. This research began with developing a protocol for collecting and analyzing eDNA to determine the presence of Oo in Georgia waterways. The protocol's validity was initially tested on waterways surrounding the University of North Georgia (UNG) Gainesville campus. Oo was positively detected in the UNG pond and local creeks. Although the protocol is proficient, whether the fungus is present in Georgia waterways with larger snake populations is unknown. However, we predict Oo is present outside of the Gainesville area. By applying the same protocol and extending the sampling area, we can further determine the Oo range and understand how its widespread distribution impacts snake populations. We are expanding our sampling locations to focus on areas with higher snake populations, such as the North Georgia mountains and the Atlantic coast. We are considering sampling from lakes, the Etowah River, and the Amicalola area. Once the samples are collected using sterile 1L bottles, they will be vacuum filtered using 0.45µm mixed cellulose ester filters. Genomic DNA will be extracted using Qiagen Dneasy PowerWater Kit, and a qPCR analysis will be utilized to amplify the DNA and analyze it for the presence of Oo. Our qPCR analysis results will inform if Oo is observed in our samples, providing implications for the role of SFD in decreasing snake populations, guiding future mitigation efforts, and expanding future research to include soil and time variation.

67 - Diurnal Ecophysiological Patterns on Cloudy and Sunny Days for the invasive C4 Grass *Microstegium vimineum* Growing Beneath a Closed Pine Canopy

Rebekah Davis, Ethan Smith, Howard Neufeld

Department of Biology, Appalachian State University, Boone, NC

Microstegium vimineum is an exotic, invasive, C4 grass found throughout the eastern United States that dominates understories of deciduous and evergreen pine forests. C4 photosynthesis requires additional ATP compared to C3, which is why most C4 plants inhabit sunny environments. *Microstegium* is unusual by being shade-tolerant, which raises questions about how it dominates in forest understories. We wanted to understand how this species was able to gain carbon over the course of a day when growing in the shade beneath a pine overstory in Boone, NC. Using a Li-6800 gas exchange system, we measured gas exchange and water potentials (ψ_w) over the course of a cloudy day with only diffuse light and over a sunny day with periods of high light sunflecks. Light levels (PAR) ranged from 8 to 42 µmol m^{-2} s^{-1} while temperature remained constant at 22°C. Photosynthesis (A) and stomatal conductance (g_s) reached maxima of only 2.2 µmol m^{-2} s^{-1}, and 0.085 mol m^{-2} s^{-1} by early afternoon and ψ_w never dropped below -0.16 MPa, indicating lack of water stress. On the sunny day, shade PAR ranged between 6 and 20 µmol m^{-2} s^{-1} and A never exceeded 0.5 µmol m^{-2} s^{-1} while g_s decreased from a morning maximum of 0.071 to 0.040 mol m^{-2} s^{-1}. ψ_w were lower than on the cloudy day and reached -0.48 MPa by late afternoon. During sunflecks, PAR averaged 579 to 879 µmol m^{-2} s^{-1}, and A and g_s rose to 11.3 µmol m^{-2} s^{-1} and 0.103 mol m^{-2} s^{-1}, respectively, while ψ_w dropped as low as -0.87 MPa. Mv is able to achieve net carbon uptake at PAR as low as 1% full sunlight (~20 µmol m^{-2} s^{-1}) but gains much more carbon (~100X more) during sunflecks, demonstrating that sunflecks are important for Mv to dominate in shady forest understories.

68 - The Long and the Short of It: Dynamic Gas Exchange Responses to Sunflecks of Varying Duration by the C4 Invasive Grass *Microstegium vimineum*

Ethan Smith, Rebekah Davis, Howard Neufeld

Department of Biology, Appalachian State University, Boone, NC

Microstegium vimineum (Mv) is an exotic, invasive, C4 grass species that dominates forest understories in the eastern United States. Due to its C4 photosynthetic pathway one would expect Mv to thrive in high light environments, but this species is unusual by being shade-tolerant. Our research focused on a population of Mv growing beneath a white pine canopy in Boone, NC. We hypothesized that Mv may utilize sunflecks to gain carbon in this light-limited environment, but there are few studies of how C4 grasses respond to

sunflecks in the field. Studies suggest C4 species induce slower than C3 species due to anatomical and physiological differences between the two photosynthetic pathways. We created sunflecks in the field using the Li-6800 gas exchange system and measured responses of leaves to long (5 min) and short (2 min) sunflecks. For long sunflecks, we exposed leaves to 5 minutes of low light (PAR) at 30 µmols m^{-2} s^{-1} and then raised PAR to 650 µmols m^{-2} s^{-1} for 5 mins, monitoring photosynthesis (A) and stomatal conductance (g_s) every 5 seconds. For our short sunflecks we acclimated leaves at low PAR of 30 µmols m^{-2} s^{-1} for 2 minutes and then raised it to 650 µmols m^{-2} s^{-1} for 2 minutes, measuring every 5 seconds, and repeating this for a total of 6 sunflecks. A averaged 9.4 µmols m^{-2} s^{-1} during the long sunflecks and leaves required nearly 5 mins to reach their maximum rate (A_{max}). For repeated short sunflecks leaves achieved progressively higher A and g_s with each sunfleck and induction was complete by the 4th sunfleck, and of similar magnitude to the long sunfleck (8.6 µmols m^{-2} s^{-1}). Mv requires multiple sunflecks to achieve A_{max} when sunflecks are short but can reach near full induction in ~5 mins when exposed to constant high light.

69 - The Effects of Cobalt on the Symbiotic Relationship between *Exaiptasia diaphana* Sea Anemones and *Breviolum minutum* Algae

Jonathan Daniel[1], Alison Roark[2]

[1]Furman University, SC, [2]Furman University, Greenville, SC

Corals and anemones often exist in a symbiotic relationship with intracellular dinoflagellate algae. This fragile relationship is susceptible to disruption by environmental stressors that cause the loss of symbiotic algae, or bleaching, which often kills the host cnidarian unless it can be recolonized. Such stressors may include heavy metals like cobalt, which are increasingly used in producing lithium-ion batteries and other electronics. Little is known about the effects of cobalt on the symbiotic relationship between cnidarians and algae. In this study, I tested the effects of cobalt on this relationship by exposing Exaiptasia diaphana sea anemones and their native symbiotic algae (Breviolum minutum) to cobalt and then measuring the extent of bleaching and recolonization of the host and the size and photosynthetic efficiency of the algae. I hypothesized that symbiotic anemones exposed to cobalt would experience a loss of algae indicative of bleaching, that aposymbiotic (or bleached) anemones exposed to cobalt would demonstrate decreased recolonization, and that the photosynthetic efficiency and size of cultured algae exposed to cobalt would be reduced compared to untreated controls. Anemones and algae were exposed separately to cobalt for multiple weeks. Algal density was quantified as percent algal cover of tentacles using fluorescent microscopy, and algal cell size and photosynthetic efficiency were measured using flow cytometry and pulse amplitude-modulated fluorometry. As predicted, anemones exposed to 2.5 µM cobalt demonstrated bleaching and decreased recolonization compared to untreated controls; however, algae exposed to cobalt did not differ in size or photosynthetic efficiency compared to untreated controls. Because cobalt did not affect cultured algae but caused bleaching and impaired recolonization in host anemones, the detrimental impacts of cobalt on the symbiosis likely result from its influences on host-initiated processes. Future studies should focus on elucidating these processes.

70 - Mitochondrial copy number dynamics during development and stress in the brown widow spider

Victoria Vining, Scott Harrison

Georgia Southern University, Statesboro, GA

Although commonly referred to as the powerhouse of the cell, mitochondrial function is not limited to aerobic energy production. Mitochondria are involved in many important processes, including apoptosis regulation, calcium uptake and signaling, immune response, and embryonic development. Mitochondrial copy number (MCN) contributes to health and disease and can change in response to environmental or cellular conditions. The dynamics of mitochondrial copy number may provide insight into mechanisms of mitochondrial health, with higher numbers associated with greater mitochondrial membrane potential, respiratory enzyme functioning, and energy reserves. However, limited information is known about the use of mitochondria in Arthropods during development within the egg. In this study, we quantify mitochondrial copy number changes in the brown widow spider (*Latrodectus geometricus*) during development and in response to stress using Quantitative Polymerase Chain Reaction (qPCR). Preliminary results indicate MCN decreases continuously from egg to hatching, with the most significant drop occurring late in development (hatching). In addition, low-temperature stress induced a significant MCN increase early in development. Adult spiders also increased MCN under low-temperature stress conditions.

71 - Winter light stress effects on leaf pigmentation in females, males, and juveniles of the dioecious *Juniperus virginiana*

Jonathan Moore[1], Morgan Cunningham[2]

[1]Campbellsville University, Campbellsville, KY, [2]Campbellsville University, CAMPBELLSVILLE, KY

Reproductive allocation often trades off with other traits such as growth or stress tolerance. In dioecious plants, females generally

have higher total sexual reproductive investment than males, which can lead to lower stress tolerance for females compared to males. In evergreen plants, often the greatest light stress comes during winter due to cold limitation of photosynthesis. Thus, we expected that females of evergreen dioecious species, due to tradeoffs with their higher reproductive investment, would have lower photoprotective carotenoids per dry mass or carotenoids/chlorophyll ratios in their leaves. We also investigated chlorophyll content and chlorophyll *a/b* ratio. We used a natural population of eastern redcedar (*Juniperus virginiana*) to test our hypothesis. We assessed late winter pigmentation (total carotenoids, carotenoid/chlorophyll ratio, total chlorophyll, and chlorophyll *a/b* ratio) of female, male, and juvenile individuals in mid-March. Individual leaves were separated from branch tips and extracted in methanol. We correlated pigmentation with total winter light estimated using hemispherical canopy photographs near each sampled branch. We found no sex-specific differences in pigmentation, but juveniles had greater carotenoids and carotenoid/chlorophyll ratios than adults. Across sexes and life history stages, chlorophyll was negatively correlated with light, while chlorophyll *a/b* and carotenoid/chlorophyll ratio were positively correlated with light. Carotenoids did not significantly change with light. We suggest that, while reproductive allocation does not appear to trade off with winter pigmentation differently between the sexes, juveniles may have relatively higher carbon to invest in winter protection (carotenoids) than sexually reproductive adults. When chlorophyll is reduced due to winter light stress, juveniles maintain a larger pool of carotenoids, which increases their carotenoid/chlorophyll ratios relative to adults. Alternatively, winter light stress might be more pronounced for juveniles than adults.

72 - Temperature Tolerance, and Metabolic Physiology of Asian Swamp Eel within the Chattahoochee Nature Center near Atlanta, Georgia

Olivia Sato[1], Ryan Saylor[2]

[1]Berry College, Rome, GA, [2]Berry College, Mount Berry, GA

The Asian swamp eel (*Monopterus albus/javanensis*) is a non-native fish with an established population in the Chattahoochee Nature Center near Roswell, Georgia. Asian swamp eels have unique physiology that allow them to survive extreme environmental conditions like droughts by aestivating. Some studies are available to describe its tolerance of high and low temperatures, but no one has investigated this population and its ability to survive conditions indicative of winter in north Georgia. Our first objective was to determine the most effective method to catch Asian swamp eels in the Chattahoochee Nature Center. Traps were deployed for at least one week and then sampled for swamp eels twice from 12 sites (36 total traps) in July and September 2024. We also aimed to establish a baseline temperature profile from which we can design thermal challenge trials. To that end, we deployed iButton temperature loggers to collect air and water temperature data every hour starting in June of 2024. Loggers were placed inside weatherproof holders and secured roughly 60 cm above (air) and below (water) the water surface on a piece of PVC embedded in the substrate. Leaf-litter traps were confirmed to be the most effective method of capturing neonate and juvenile eels, which live in the thick layer of decaying organic matter found along the bottom of the pond. We also aim to collect adults using backpack electrofishing and seining to sample shoreline habitat since leaf litter traps did not successfully trap adults. Our second objective will be to use cessation of feeding trials to assess the lowest possible acclimation temperature of this swamp eel population compared to another established in south Florida. Ultimately, we hope to use these data to investigate potential brumation in Asian swamp eels that may experience water temperatures near 0°C during winter cold fronts.

73 - Investigating the Impact of Roundup Exposure on Hearing in Channel Catfish (*Ictalurus punctatus*)

Joshua Adams, Daniel Holt

Columbus State University, Columbus, GA

Pesticides are applied to U.S. agricultural crops at a rate of approximately 225 million kg of active ingredient per year. While the acute effects of pesticide exposure on humans are well-documented, their impact on fish sensory systems remains poorly understood despite evidence of adverse effects from pesticide runoff in aquatic ecosystems. Anecdotal reports suggest that prolonged exposure to glyphosate, the active ingredient in Roundup, may cause hearing loss in humans. This research investigates the impact of acute exposure to the common agricultural herbicide Roundup (glyphosate-based formulation) on hearing sensitivity in farm-raised Channel catfish (Ictalurus punctatus). We conducted a randomized controlled trial in which catfish were exposed to 3 mg/L Roundup for 96 hours, with auditory function assessed using the auditory brainstem response (ABR) technique. Hearing thresholds at frequencies ranging from 100 to 2000 Hz were measured and compared to a control group subjected to identical conditions without Roundup exposure. A two-way ANOVA was used to analyze threshold differences between groups. Preliminary findings indicate that a 96-hour exposure to this concentration of Roundup does not significantly affect auditory sensitivity in Channel catfish. While these results suggest resilience of the auditory system to short-term, low-dose Roundup exposure, we plan to conduct further studies to determine potential long-term impacts and effects on other sensory modalities such as olfaction, where the sensory epithelia is more exposed to the external environment.

74 - Snails in the Diet of *Exoglossum maxillingua*, Cutlip Minnow

Tess Taloumis, Steven Powers

Roanoke College, Salem, VA

Tess Taloumis and Steven L. Powers

The Cutlip Minnow, *Exoglossum maxillingua,* is an important component of the stream fish fauna of Virgnia and has a very unusual lower jaw. Some of the earliest hypotheses of the function of this bizarre jaw included dislodging snails from their shells, but numerous studies of the diet of this species have never documented snails as food items. Recent snorkel observations revealed *E. maxillingua* carrying snails in their mouths in the Roanoke River. Preliminary examination of the gut contents of preserved *E. maxillingua* from Virginia revealed snail parts in many specimens. An in-depth examination of the diet of this species was conducted examining the gut contents of specimens from across most months of the year. Standard length (SL) and mass of each specimen was recorded. Gut contents of each specimen were weighed and identified to the lowest practical taxonomic category. Digital images of gut contents were captured to aid in identification. Text and web resources were utilized to identify items identified as opercula from snails in the family Pleuroceridae. A total of 57 of 145 specimens examined contained snail parts. Mass of gut contents increased with SL. Specimens containing snail parts were larger than those lacking snail parts. No shells of snails were found indicating *E. maxillingua* remove snails from their shells before ingesting them. These results suggest the unique lower jaw of this species does indeed play a role in removing snails from their shells making them an important food source for this charismatic minnow.

75 - Post-fire size recovery of sourwood (*Oxydendrum arboreum*) and sassafras (*Sassafras albidum*)

Kerrington Norman, Nicholas Stalford, Jennifer Schafer

Winthrop University, Rock Hill, SC

Species characteristics, such as growth rate, and habitat characteristics, such as resource availability and fire return interval, can influence plant species resilience after fire. We compared post-fire recovery of resprouting sourwood (Oxydendrum arboreum) and sassafras (Sassafras albidum) individuals in a temperate deciduous forest. We also compared post-fire recovery of sassafras in temperate deciduous forest and longleaf pine sandhills, which differ in fire return interval, soil resource availability, and topography. We haphazardly selected sourwood and sassafras individuals in a temperate deciduous forest site six months post-fire in Kings Mountain National Military Park in South Carolina. We counted the number of resprouts and dead (pre-fire) shoots and measured the height and basal diameter of the largest resprout and dead stem of each individual. We found that the ratio of resprouts to pre-fire shoots was higher in sourwood than sassafras. Resprout basal diameter was positively correlated with pre-fire stem basal diameter in both species and was greater in sourwood than sassafras. Both species recovered their diameter after fire at a similar rate. We measured height and basal diameter of sassafras resprouts and pre-fire shoots approximately six months post-fire at the Carolina Sandhills National Wildlife Refuge in South Carolina. We found little difference in post-fire recovery of height and diameter in sassafras between temperate deciduous forest and longleaf pine sandhills habitats. Overall, sourwood and sassafras recovered diameter at similar rates six months post-fire, but sourwood had larger diameters and neither species fully recovered their pre-fire basal diameter. We did not compare height recovery between species because the top of many sourwood resprouts had been removed by deer, which suggests that vertebrate herbivores can limit post-fire recovery of sourwood. For sassafras, post-fire recovery was not affected by habitat, indicating that sassafras is similarly resilient in temperate deciduous forests and longleaf pine sandhills.

76 - Dolphin abundance and distribution in the lower St. Johns River basin, Jacksonville, Florida

Ellie Maus, Francesca Vasic

Jacksonville University, Jacksonville, FL

The St. Johns River is a unique environment, as its south to north flow contains large variances in salinity changing due to tides, seasonal and human influence. This greatly impacts the distribution of the river's ecosystem, including organisms at the top of the food chain, like the Tamanend's dolphins (*Tursiops erebennus)*, a year-round resident of the northern parts of the river.

Since 2012, Jacksonville University has been involved in a dolphin photo identification (ID) program to monitor the presence and abundance of the dolphins in specific sections of the river, in Duval County. Photo ID data have been collected monthly at each sighting along with coordinates, depth, and water quality data, such as temperature and salinity.

Over the past decade, average sighting of dolphins varied with years (max, 2012, n=7,4 dolphins/sighting, d/s; min, 2020, n=4 d/s) and seasons (max, summer-fall 2022, n=8.2 d/s; winter-spring 2012 n=10.75; min, summer-fall 2020 n=3; winter-spring 2020 n=5). Water salinity measured in the same locations has seen fluctuations with the highest values during winter (8.57±6.21 ppt vs summer

5.88±2.71 ppt). The behavior and abundance of the dolphins was correlated to salinity values. As expected, dolphins were more abundant during times of higher salinity and mild temperature (2012, 12.06 ppm, 23.15°C, n=10.75 d/s). However, the dolphin population remains stable despite a trend in lower salinity values in the area examined. While dolphins were expected to be more elusive during times of lower salinity, that was mostly observed mostly in correlation with low temperatures when they are believed to travel north to the mouth of the river. This potential new adaptivity showed to lower salinity raise many questions about distribution shifts and the long-term effects of low salinity on dolphin health and the conservation of the dolphin population inhabiting the river.

77 - Snorkelwort occupancy in granite outcrop pools is driven by soil depth: A comprehensive approach incorporating detection rates

Anna Wyngaarden, Megan DeMarche

University of Georgia, Athens, GA

Estimates of a species' area of occupancy rely largely on presence-absence data and are underestimated if the species' true presence in an area is detected imperfectly. Incorporating a species' detection rate into estimates of its area of occupancy yields more accurate estimates and has long been standard practice in animal systems yet remains underutilized for plants. Ephemeral, annual plants are uniquely prone to imperfect detection because of their short life span and dormant seed bank, which can lead to falsely detecting the species absent when truly present. *Gratiola amphiantha*, or snorkelwort, is an ephemeral, federally threatened annual plant endemic to granite outcrop pools. Pools vary in soil depth, area, and competitive vegetation cover. These habitat features have been manipulated in pools to directly manage for the species, however it remains unclear how they drive the rare species' occupancy. Here, we repeated presence-absence surveys of snorkelwort multiple times throughout the growing season in 2023 and 2024 at two sites, to determine the detection rate of the species. We then estimated the probability of snorkelwort occupancy in suitable pools, directly incorporating the rate of detection, and ultimately determined which habitat characteristics best explained pool occupancy. We found that snorkelwort has a relatively high mean detection rate of 0.91 across sites and seasons. Pool soil depth was the strongest predictor of occupancy and was positively correlated with occupancy. Despite snorkelwort's relatively high detection rate, omitting it from occupancy estimates led to decreased estimates of total pool occupancy, further highlighting the need to include detection rates in plant species' occupancy estimates, particularly for species of conservation concern. This work provides some of the first evidence for habitat characteristics that drive the occupancy for the federally threatened species which can be utilized for pool management efforts.

78 - Spartina Super Seeders: Linking Seedling Production to Plant and Soil Characteristics in Coastal Georgia Salt Marshes

Annabelle Mayes, Heather Joesting

Georgia Southern University, Savannah, GA

Spartina alterniflora is a dominant salt marsh plant species along the East and Gulf Coasts of the United States, where it plays a vital role in marsh stabilization and ecosystem function. *S. alterniflora* individuals have been shown to have significant variation in fecundity and fertility within populations, with most plants producing few to no seedlings and few individuals producing a large number of seedlings, which have been nicknamed Super Seeders. The aim of this research was to investigate the relationship among plant characteristics, soil characteristics, and seed viability and germination to determine potential influences on Super Seeders. To this end, ten random individuals in a natural population in Chatham County, GA, were measured at three time points during the reproductive season. Measurements were taken of the plant height, stem diameter, and leaf chlorophyll content, and leaves were collected for measurement of tissue nitrogen. Soil samples from around the stem were taken for analysis of soil characteristics, including soil salinity, pH, nutrients, and texture. Spikelets (reproductive stems) containing seeds were collected and returned to the lab to count the number of seeds, after which seeds were placed in cold, wet conditions for winter stratification. Starting in Spring 2025, seed viability tests will be conducted on a subset of collected seeds using the tetrazolium-chloride test, after which seeds will be placed in germination trials. Once all data has been collected, a series of linear regressions will be conducted to determine any relationships between seed viability and germination and soil and plant characteristics.

79 - Defining the preferred substrates of Louisiana Freshwater Sponge Species

Geremiah Perkins, Rose Dawes, Sarah Darst, Chris Hill, Mary Miller

Baton Rouge Community College, Baton Rouge, LA

The Louisiana Freshwater Sponge Project investigates what substrates contribute to the growth and development of different freshwater sponge species. Freshwater sponges are understudied, environmental health indicators. These organisms are filter feeders that assist in cleaning freshwater ecosystems. To further understand the driving factors of freshwater sponges, the Louisiana

Freshwater Sponge Project has prioritized identifying and tracking these organisms' species richness. Previous studies show that freshwater sponge survival depends on water quality and availability of substrates. However, the literature provides little research on the preferred substrates that contribute to sponge growth and development. This study analyzed the substrate specificity of 1242 collected sponge samples from over 290 water systems in Louisiana. During sampling, sponges were photographed and attached to their substrates. In the lab, the sponges were identified using sponge morphology and/or DNA sequencing of the COX-1 gene. Substrates were classified as logs, rocks, tree roots, trash, plant roots, and bricks. Using Excel, substrates were documented for fourteen species in Louisiana. The analysis of this data collection has found rocks and logs to be the most abundant substrates. However, some species are limited to root systems. This information contributes to the environmental parameters that support sponge growth.

80 - The Louisiana Freshwater Sponge Project: Examining Changes in Species Richness through a Comparison of two Ecological Studies

Chris Hill[1], Juliana Coletti[1], Rose Dawes[1], Abhi Mehrotra[1], Stephanie Archer[2], Mary Miller[1]

[1]Baton Rouge Community College, Baton Rouge, LA, [2]Louisiana Universities Marine Consortium, Chauvin, LA

Beginning in 2019, the Louisiana Freshwater Sponge Project (LFSP) is a longitudinal study focused on describing freshwater sponge species richness in Louisiana water systems. While very understudied, freshwater sponges have been reported to be environmental health indicators. Tracking any change in species richness over time provides a picture of the overall health of water systems as well as indicates the effects that changes in environmental conditions have on freshwater sponges. The LFSP ecological survey compares the current freshwater sponge species richness with a previous survey conducted in 1969. In addition to comparing these previously surveyed water systems, this study includes an additional 200 new sites and has identified over 1,400 sponge samples. Thus far, LFSP has revisited 146 out of the 152 sites included in the original survey, or over 95%, though 58 of these sites have been made inaccessible due to land development and other geographical changes. Utilizing the same sampling methods from the 1969 survey, submerged substrates within six feet of the shoreline were retrieved and examined for sponges. Freshwater sponge samples were identified through phenotypic spicule analysis and COX-1 sequencing. Comparison of results between the two studies indicates some consistencies and variances. Consistent with the previous study, the most prevalent species in Louisiana are still *Trochospongilla horrida* and *Eunapius fragilis*. The most significant variation observed between the two studies is an overall decline in species richness across Louisiana.

81 - Can Sediment Analysis be used to Further Describe Species Richness of Freshwater Sponges?

Destiny Marvel, Marquis McQuirter, Geremiah Perkins, Lisa DiMaggio, Rose Dawes, Mary Miller

Baton Rouge Community College, Baton Rouge, LA

This study explores the role of sediment analysis as a contribution in defining freshwater sponge species richness in Louisiana. Freshwater sponges serve as vital indicators of environmental health, yet they remain largely under-researched. The Louisiana Freshwater Sponge Project (LFSP) is a longitudinal study aimed at documenting sponge diversity within Louisiana's freshwater systems. Sponges are collected and identified through spicule morphology of the sponge body and gemmules. If gemmules are not present, sponges are identified through COX-1 gene sequencing. This identification relies solely on the observation of sponges within a 10 meter length of area at 6 feet of reach within the water system. To test the research question of this study, sediment was randomly collected from the surveyed sites. The sediment samples were dried and processed through a series of chemical reactions to remove inorganic and organic matter, leaving only silica-based particles, including sponge spicules. The prepared sediment was then observed with light microscopy. Findings from 47 different sites indicate that sponges may be present in areas where they were not observed and collected. In such cases, sediment analysis provides evidence of additional sponge species, suggesting a broader species richness than documented solely on sponge collection. This method not only confirms the presence of observed sponge species but also expands known species richness for specific locations. Sediment analysis therefore provides a comprehensive view of species richness, allowing species verification at sites without directly observing and sampling sponges.

82 - Gene Flow of Peanut snails (*Cerion*) in the Florida Keys

Charlyce Mitchell, John Philips

Valdosta State University, Valdosta, GA

The Florida Keys are an island system running southeast of Florida that provides a diverse ecosystem in support of a wide variety of biodiversity. We are using these islands that provide an isolated environment to study evolutionary change in Cerion land snails. We will use genome-scale sequence data from Cerion across the Florida Keys to examine dynamics and patterns of gene flow and test how these patterns relate to the geography of the archipelago and ocean currents. We will also test patterns of dispersal relative to biotic and abiotic factors that may influence the gene flow of Cerion. These samples were collected from all known keys when Cerion

populations exist, primarily from the endemic species C. incanum, but also other introduced Cerion species. The inclusion of these non-native taxa will allow us to analyze rates of hybridization and introgression in these snails.

83 - A Decade of Puma (*Puma concolor)* Population Dynamics in southwestern New Mexico

Sarah Darrah[1], Travis Perry[1,2]

[1]Furman University, Greenville, SC, [2]Natural Curiosity, Hillsboro, NM

Puma lack uniquely identifying coat patterns, occur at low population densities, and are usually found in remote areas with rugged terrain, making population density estimates rare and studies of long-term population dynamics, even more uncommon still. Understanding puma population densities and how dramatically those densities fluctuate over time is critical to long-term planning in puma conservation and management efforts. We examined puma (*Puma concolor*) population dynamics over a 10 year period in southwestern New Mexico from 2012 to 2022. We used photos of puma collected from 25 remote cameras, distributed over 100 km^2, and operated continuously over this 10 year period. We used the photo data software Photogofer to record, archive, query, and export data from these photos. These data included individual puma ID's based on unique ear tags and GPS collars fitted to these puma to address other research questions. We used the package SECR in R to perform spatially explicit sight-resight population density estimates during 40, 90-day sampling periods (i.e., sessions) corresponding to climatic seasons. For those sessions where the number of marked puma or the number of resights were too low to calculate a population density estimate using SECR, we used random encounter modeling (REM), using the package RandEM in R. We found puma population density estimates ranged from 0.15 to 3.43/100 km^2 with an average of 1.18/100 km^2 across the 10 year period, with no longitudinal trend or cyclical pattern. These results support previous, "snap shot" population density estimates obtained using different methods. The most striking aspect of puma population density over this period is the relative stability, despite significant fluctuations in precipitation, prey abundance, two large wildfires, and variable hunting pressure.

84 - Bobcat (*Lynx rufus*) population density dynamics and correlations with precipitation in southwest New Mexico

Paige Estes[1], Travis Perry[1,2]

[1]Furman University, Greenville, SC, [2]Natural Curiosity, Hillsboro, NM

For much of the planet, climate change forecasts predict higher temperatures and decreased precipitation/water availability. These climatic changes will significantly affect the abundance and distribution of many species, especially in semi-arid regions, like the southwestern U.S. We examined bobcat (*Lynx rufus*) population dynamics and correlations between bobcat population density and precipitation over a 4 year period in southwestern New Mexico. We used photos of bobcats collected from 25 remote cameras, distributed over 100sq Km, and operated continuously from 2014 to 2017. We used the photo data capture program Photogofer to record, archive, query, and export data from these photos, including individual bobcat ID's based on unique spotting patterns. We used the SECR package in R to perform spatially explicit sight-resight population density estimates during16, 90-day sampling periods corresponding to climatic seasons. We then performed a one-tailed, cross-correlation analysis between bobcat population density estimates for each season and the total precipitation for seasons, collected from the nearest NOAA weather station. We found a range of 1.08 bobcats to 8.35 bobcats per100km^2, with an average density of 3.31 bobcats/100km^2 over the four year study period. We found a positive, but not statistically significant ($p=0.16$) correlation between total seasonal precipitation and bobcat density, with a lag time of seven seasons, or 21 months. These results suggest that bobcat populations in the more arid regions of the Southwest will be severely impacted, perhaps eliminated, with predicted climate change.

85 - Climate Change and a Decade of Black bear (*Ursus americanus)* Population Dynamics in Southwestern New Mexico

Jacob Cooper[1], Travis Perry[1,2]

[1]Furman University, Greenville, SC, [2]Natural Curiosity, Hillsboro, NM

The American Black Bear (*Ursus americanus*), a species native to the Southwest, is particularly sensitive to seasonal temperature variation. Understanding how black bear populations respond to changing climate is critical to their conservation. We examined the correlation between seasonal minimum and maximum temperatures and black bear (*Ursus americanus*) population density dynamics over a 10 year period in southwestern New Mexico from 2008 through 2017. We used temperature data from the closest NOAA weather station to our study site. We used photos of black bear collected from 25 remote cameras, distributed over 100 km^2, and operated continuously over this 10 year period. We used the photo data software Photogofer to record, archive, query, and export data from these photos. used random encounter modeling (REM), using the package RandEM in R to generate population density estimates during 40, 90-day sampling periods corresponding to climatic seasons. We found that average, daily, minimum and

maximum temperatures for all seasons have been increasing in our study area since 1956. We found black bear population density estimates ranged from 0.01 to 3.0/100 km^2 for males and 0.03 to 8.3/100 km^2 for females over the 10 year period. Finally, we found that black bear density estimates have remained constant during the spring season, but have declined over the last 10 years in summer and fall. We hypothesize that bears are moving to adjacent, higher elevation areas, and cooler temperatures, as temperatures at our study site have increased.

86 - Talking Turtles

Alvin R. Diamond[1], Fisher Parrish[2], Ethan Jones[2], Elizabeth Kobs[2]

[1]Troy University, Troy, AL, [2]Dept. of Biological and Environmental Sciences, Troy University, Troy, AL

Successful wildlife management requires basic demographic information on species present and the dimensions and dynamics of population change within those species. We initiated a mark–recapture survey of freshwater turtles in an isolated urban pond on the campus of Troy University in Pike County, Alabama to establish a long-term monitoring program. Mullis Pond is a 1 ha manmade impoundment constructed in the 1950's that is spring fed and receives significant urban runoff. We sampled from April -November 2024 using both small and large funnel traps baited alternately with cat food and peanut butter, as well as basking floating traps. Carapace length and width, plastron length, weight, sex, and species were recorded for each individual as well as trap type, and capture date. Each individual was marked for future identification by notching the marginal scutes on the carapace following the protocols of the North American Code, and photographed. Our study documented three species from the pond that correspond to observations on iNaturalist, while 2 species reported on that database have not thus far been documented by trapping.

87 - Allocation to carnivory and prey trapping in pink sundew (*Drosera capillaris*) in seasonal ponds in Florida

Nicholas Stalford, Sabrina Rocha, Amber Mercer, Jennifer Schafer

Winthrop University, Rock Hill, SC

Carnivorous plants capture prey to supplement the low availability of nutrients in the soil. The goal of our research was to investigate the effects of time since fire and resource availability on allocation to carnivory and prey trapping in pink sundew (*Drosera capillaris*), which uses sticky glandular trichomes to capture prey. We conducted our research in the Florida scrub ecosystem at Archbold Biological Station, where they manage the ecosystem with prescribed fire. Pink sundew occurs in seasonal ponds in the Florida scrub ecosystem. We haphazardly searched for pink sundews in seasonal ponds 1 to 16 years post-fire. When pink sundews were located, we established a plot and selected focal individuals in and near the plot. We measured the length and width of the pink sundews then collected the individuals. In the lab, we counted the number of leaves and the number of trapped arthropods. We also assessed light availability and soil resources in each plot. There was a negative relationship between time since fire and the total number of leaves and pink sundew area. The number of live leaves was positively correlated with soil moisture. There was no relationship between time since fire and the number of arthropods trapped on pink sundew, but there was a positive relationship between pink sundew area and the number of arthropods trapped. We were able to identify 68 of the 201 trapped arthropods. Of these, over 75% were in the order Diptera or Hymenoptera. Less commonly trapped arthropods included collembolans, ephemeropterans, and lepidopterans. Our results suggest that allocation to carnivory in pink sundew is influenced by time since fire and resource availability. Prey trapping by pink sundew could be related to arthropod abundance in addition to plant characteristics.

88 - Leaf it to the herbivores: Effect of species identity and time since fire on insect herbivory in two resprouting plant species

Amber Mercer, Sabrina Rocha, Nicholas Stalford, Jennifer Schafer

Winthrop University, Rock Hill, SC

Plant characteristics, including physical defenses and nutrient content, and fire, which affects plant growth and nutrient content, can influence insect feeding behaviors. The objective of our research was to investigate the effect of species identity and time since fire (TSF) on insect herbivory in gopher apple (*Licania michauxii*) and Feay's Palafox (*Palafoxia feayi*), which are resprouting plant species that occur in Florida scrubby flatwoods. *Licania* grows as a ground cover and has waxy leaves. *Palafoxia* shoots typically reach greater heights than surrounding vegetation and its leaves are covered with trichomes. We haphazardly selected individuals of both species in scrubby flatwoods sites with different times since fire. To assess plant characteristics and herbivory, we measured the leaf area, leaf mass per area (LMA), foliar nitrogen concentration, percent of leaves damaged by herbivores, and percent of leaf area lost to herbivory of each individual. In recently burned sites, *Licania* had higher LMA, while *Palafoxia* had higher foliar percent nitrogen; however, there was no difference in the percent of leaves damaged or the percent of leaf area herbivorized between *Licania* and *Palafoxia*. There was a significant relationship between TSF and LMA for *Palafoxia*, but not *Licania*. Foliar nitrogen concentration was

not related to TSF for either species. There was a positive relationship between TSF and percent of leaf area herbivorized for *Licania*, but the percent of leaf area herbivorized was not related to TSF for *Palafoxia*. *Licania* and *Palafoxia* do not differ in herbivory rates in recently burned areas, which suggests that their different physical defenses, LMA, and foliar nitrogen do not influence insect feeing behavior. Our results also suggest that TSF has minimal effects on leaf characteristics and that species identity mediates the effect of TSF on herbivory.

89 - Microhabitat Factors Influencing Shrub Encroachment into Coastal Grasslands

Giselle Ponce-Bautista[1], Julie Zinnert[2], Natasha Woods[1]

[1]Moravian University, Bethlehem, PA, [2]Virginia Commonwealth University, Richmond, VA

Shrub encroachment into grasslands is a worldwide phenomenon. Encroaching shrubs can shift ecosystems from being dominated by grasses, with ecosystem-level consequences such as available wildlife habitat, plant species richness, ecosystem structure, and carbon dynamics. This transition of plant dominance from grass to shrub has occurred rapidly on the U.S. mid-Atlantic and Gulf coasts. On Hog Island, Virginia, a Long-Term Ecological Research site, warmer winter temperatures contribute to the expansion of native shrub, *Morella cerifera* into grasslands. However, there are areas within the grassland where shrubs do not establish. The purpose of this study was to compare differences in microhabitats that may contribute to shrub presence in newly encroached grassland and un-encroached grassland. Understanding these differences can allow researchers to anticipate which conditions favor shrub encroachment and allow scientists to model future expansion. The study established plots in grass-dominant areas (grassland plots) and shrub-dominant areas (transition plots) (n = 5). Within these plots differences in woody plant cover, soil relative water content, and soil chlorides were examined during the summer. No differences occurred in total vegetation cover between the two sites. In the grassland plots, woody species make up 1% of the plant cover, whereas in the transition plots, woody species make up 41%. Soil relative water content (12%) and soil chlorides did not differ between grassland and transition plots Although there are stark differences between woody plant cover in the grassland and transition plots, summer soil water content and chlorides do not appear to explain plant structure Ongoing research will examine seasonal changes in soil salinity and water availability to help identify limitations to shrub establishment.

90 - Does human infrastructure affect the composition of mammal communities?

Kaitlyn Thompson, Lisa McDonald, Emily Prince

Lander University, Greenwood, SC

Humans are the ultimate predators, and studies have shown that they pose the greatest threat to large carnivores. Other trophic groups may benefit from human infrastructure both because the predation threat from carnivores is reduced and because they may utilize human resources such as trash. To better understand how humans affect mammal communities, we investigated whether human infrastructure had different effects on different trophic groups. We hypothesized that high human infrastructure would negatively impact large carnivores and large omnivores while benefiting other trophic groups. To test this hypothesis, we utilized our network of 25 camera stations in three counties across South Carolina to observe mammal presence. For each station, we used GIS to calculate a human infrastructure score based on the density of roads and buildings nearby. To determine if human infrastructure affects trophic groups differently, we calculated the proportion of observations of each trophic group at high and low human infrastructure stations. We then compared the proportion of large carnivores at high infrastructure stations to the proportions of each of the other trophic groups at these stations and found a significant difference between each comparison. There were 2.4 times as many observations of large carnivores at low as compared to high human infrastructure stations. Large omnivores were never found at high human infrastructure stations suggesting that they are significantly more sensitive to human disturbance. In contrast, all other trophic groups were between 1.4 and 2.9 times more common at high as compared to low human infrastructure stations suggesting that they may benefit from human disturbance. Overall, we found that human infrastructure changes the composition of mammal communities, reducing the number of sensitive large omnivores and large carnivores, while potentially benefiting other trophic groups.

91 - Living in the shadow of human infrastructure: The effects of artificial lighting on nocturnal mammals

Keegan Finnerty, Lilliane O'Dell, Lisa McDonald, Emily Prince

Lander University, Greenwood, SC

Mammals have varying sensitivities to human disturbances. In Upstate South Carolina, raccoons are frequently found in areas with high human infrastructure while wary animals like rabbits, coyotes, armadillos, and opossums are less common in these areas. Artificial light at night (ALAN) is an aspect of human infrastructure reported to change the migration patterns, foraging behavior, and diel activity of mammals. We sought to determine whether a mammal's tolerance to human infrastructure was related to its response to artificial lighting. To test this, we altered ALAN levels at 18 camera trap stations around Upstate South Carolina. Each site was illuminated with white light, red light, or no light. We hypothesized that wary nocturnal mammals would be observed less frequently than tolerant

mammals at red and white stations. When they were detected at red and white stations, we hypothesized that they would be farther from the camera than at control stations. We identified species captured in images from August 2022 to January 2023 and compared the proportion of observations of tolerant and wary species at each station. For each species, we calculated the proportion of observations in which the animal was close to the camera at each station type. For some species the proportion of observations close to the camera was higher at certain station types, however, no clear association between proximity to the camera and wariness was found. As hypothesized, we found that observations of tolerant species were more common at white than red or control stations, but fewer wary species were observed at white than red or control stations. Overall, this suggests that mammals more tolerant of human infrastructure are less impacted by ALAN and red lighting is less disruptive to wary mammals than white lighting.

92 - Impact of Burial and Salinity on Seedling and Juvenile Growth of *Morella cerifera* in Coastal Ecosystems

Brianna Whalen[1], Julie Zinnert[2], Natasha Woods[1]

[1]Moravian University, Bethlehem, PA, [2]Virginia Commonwealth University, Richmond, VA

Barrier islands act as essential shields to mainland cities and ecosystems during major storm events. *Morella cerifera*, hereafter *Morella,* is a native shrub occuring on barrier islands of the US mid-Atlantic and Gulf coasts. Warmer winter temperatures have caused *Morella* to encroach into neighboring grasslands, resulting in large expansive thickets across islands. Dunes can shield *Morella* from overwash and other disturbance events that deposit sediment and introduce salt spray. However, if dunes are destroyed by storms before they can be rebuilt, *Morella* may experience increased burial from storms and increased salinity from salt spray. The impact of the frequency of burial and salinity on *Morella* is currently unknown; however, seedling age may impact the tolerance to these stressors. The experiment investigates the extent to which the growth of *Morella* at two life stages (seedling–7 week old–and juvenile–1 year old) are differentially impacted by salinity, burial, and the combination of burial and salinity. The combination treatment simulates natural overwash events in the field. In order to simulate the natural microenvironment, each pot contained a single *Morella* surrounded by three *Sporobolus pumilus* grasses, and they were buried in sand obtained from Hog Island, Virgina. Seedlings (7 weeks old) treated with both salinity and burial were the least successful, with 25% survival and no growth of those that survived. Juveniles in the combination treatment increased growth (111%). These results suggest that the resilience of *Morella* to overwash stress conditions is partially dependent on the age of the seedling. Therefore, *Morella* must have time to establish and grow before it is able to withstand stress from overwash events.

93 - A Comparative Analysis of Two *Astragalus* Congeners: Phenology and Reproductive Success

Matthew Stout

Middle Tennessee State University, Murfreesboro, TN

Differences in pollination ecology and reproductive output may, in part, help explain the abundance and geographical ranges of closely related species. *Astragalus bibullatus* is a federally endangered legume endemic to the limestone cedar glades in Rutherford County, TN. It co-occurs with *Astragalus tennesseensis*, which is more widespread and abundant throughout its range in Tennessee. This study compared flowering phenology, pollinator visitation rates, pollen viability and morphology, fruit production, and seed viability between the two species at three study sites. Flowering time overlapped by about 2 weeks. *A. tennesseensis* produced significantly more flowers per raceme across all sites than *A. bibullatus*. However, *A. bibullatus* produced more racemes than *A. tennesseensis*. Overall visitation rates were not significantly different between *A. bibullatus* and *A. tennesseensis*, and pollen morphology did not significantly differ between them. Fruit counts varied significantly between sites and species. Although mean number of fruits per raceme was 2.2 for *A. bibullatus* and 1.1 for *A. tennesseensis*, *A. tennesseensis* produced more total fruit than *A. bibullatus*. The Airport site had the highest mean fruit count per raceme throughout the 2024 field season, suggesting that site-specific environmental factors could play a role in the reproductive output in both *Astragalus* species. Seed counts differed significantly between site and species, and a significant interaction was found between site, species, and viable versus aborted seeds. *A. tennesseensis* produced more total seeds and significantly more viable seeds than *A. bibullatus*, and *A. bibullatus* produced significantly more aborted seeds at every site. Results thus far indicate *A. bibullatus* produces fewer flowers per raceme and viable seeds which may help explain its lower reproductive output and narrow geographic range compared to *A. tennesseensis*. Further work should aim to compare pollen counts, viability, and pollinator taxa between the two species.

94 - Puma, Mule Deer, Elk and the Landscape of Fear in Southwestern New Mexico

Parker Marshall[1], Travis Perry[1,2]

[1]Furman University, Greenville, SC, [2]Natural Curiosity, Hillsboro, NM

Landscape of fear is a term that describes how prey species view the physical landscape in terms of predation risk, avoiding high risk areas and selecting low risk areas. Thus, prey distributions are determined by predators as a function of both mortality and behavior.

In this context, we examined a puma-elk-mule deer predator-prey system in southwestern New Mexico and asked four questions: 1. Do elk and mule deer spend the majority of their time in different habitats? 2. Are the habitats where elk spend the majority of their time different from the habitats where elk are killed by puma, i.e. do elk avoid high risk habitat? 3. Are habitats where mule deer spend the majority of their time different from the habitats where mule deer are killed by puma, i.e. do mule deer avoid high risk habitat? And, 4. Is there a difference between the habitats where elk are killed and the habitats where mule deer are killed, i.e. do mule deer and elk experience the same landscape of fear? We used data from pellet plots to determine mule deer and elk habitat selection. We used data from prey cache investigations, made possible by puma wearing GPS collars, to determine habitat associations with mule deer and elk kill sites. We obtained habitat data by intersecting pellet plot and kills site coordinates with raster files for elevation, aspect, solar gain, vegetation type, slope, distance to drainage, and topographic ruggedness at multiple scales in ArcGIS. We used logistic regressions to examine habitat differences in each of the pairwise comparisons outlined in questions 1 to 4. We found mule deer and elk spend the majority of their time in different habitats. Both species avoid high risk habitat. For both species, high risk habitat is the same.

95 - Prey Switching in a Puma, Mule Deer, and Elk Predator-Prey System.

Anna Cheek[1], Travis Perry[1,2]

[1]Furman University, Greenville, SC, [2]Natural Curiosity, Hillsboro, NM

Prey switching is a behavioral phenomenon where predators adjust their foraging preferences based on the relative availability or abundance of different prey species. In the context of optimal foraging theory, this behavior is explained as a strategy to maximize the predator's energy intake per unit of time, while minimizing the costs associated with searching for and handling prey. As part of our long-term study of puma ecology in southwestern New Mexico, we asked if puma switched the dominant prey in their diet based on changes in the relative abundance of those prey. We used 12 years of data collected from 2008 to 2020: data from prey cache investigations, found by fitting puma with GPS collars, to determine the relative proportion of mule deer and elk in their diet; and, photo rates of mule deer and elk collected from 25 remote cameras, distributed over 100 km^2, as a measure of their relative abundance. We used the photo data software Photogofer to record, archive, query, and export data from these photos. We found that photo rates of mule deer and elk, individually, fluctuated significantly over the study period, with elk replacing mule deer as the species with the higher photo rate after 2014. Further, using a Chi-Square test of independence, we found that the relative proportions of mule deer and elk in puma diet also reversed position of dominance before and after 2014 – mule deer before and elk after ($p < 0.05$). Finally, using a general linear model we found that, after accounting for puma sex as a covariate, relative predation rates on mule deer decreased significantly as a function of elk photo rates, and visa versa. These results provide strong evidence of prey switching in puma, with important implications for protected or vulnerable prey species such as desert bighorn sheep.

96 - Regional Analysis of Medical Apartheids in Spartanburg County

Anthony Tarulli, Jennifer Bradham

Wofford College, Spartanburg, SC

Medical Deserts are a widely understood phenomena in societal structure, yet this classification seemingly ignores the deep-rooted discriminatory nature and carefully calculated infrastructure of the healthcare system in the United States. A relabeling of these regions as Medical Apartheids therefore was done for this study to further address outside factors that can contribute to the formation and prevalence of these regions. Aims of this study were to build upon existing collaborations with South Carolina non-profit organizations to aid these groups in focusing on areas within the state where access to healthcare facilities has been and still presently is needed. This was done through (i) clarifying where Medical Apartheids were found throughout Spartanburg County and (ii) quantifying correlations between spatial (e.g. rural, urban, residential, commercial, etc.) and socio-demographic factors (e.g. income, race, etc.). Methodology such as geolocation of licensee locations for preliminary identification of patterns within Spartanburg County and statistical analysis (e.g. hot spot analysis, buffer analysis, k-means clustering) allowed for a further understanding of how these Medical Apartheid regions were dispersed. Preliminary results have shown there to be a pattern of absence in healthcare facilities on a spatial and socio-demographic scale, however, research was limited to certain facilities. Current work aims to focus on a wider scope of healthcare facilities to generate reports outlining Medical Apartheids and will be shared with non-profit organizations in Spartanburg County to support their efforts in assessing regions of need.

97 - Untangling the Influence of Competition and Microbial Interactions on *Saccharum spontaneum*, *Imperata cylindrica*, and *Andropogon glomeratus* in South Florida

Joshua Poland, Travis Marsico, Scott Mangan

Arkansas State University, Jonesboro, AR

Invasive graminoids (e.g., grasses, sedges, and rushes) are often classified as “rapid colonizers” and can be ecologically harmful

organisms that promote loss of a variety of plant, insect, bird, and fish species through increased litter deposition, alteration of habitat suitability, and shifts in soil chemistry. These plants tend to outcompete native species through a combination of escape from native pathogens and rapid growth rate, leading to success in highly disturbed areas. In addition to direct competition, interactions among plants and soil microbes are major drivers of biodiversity and productivity in a variety of ecosystems. The influence of soil microbial communities on plants can include altered root development, pathogen infection, protection from pathogen infection, and altered access to limiting soil resources, all of which can influence individual plant success and community dynamics. The enemy-release hypothesis states that the absence of native microbial communities and competitors will bolster the success and distribution of the invading species as the novel organisms offer a release from co-evolved biotic stressors. Plant-microbial interactions and competition are both important for structuring communities; however, the relative importance of how each influence plant invasions is less clear. Targeting these two mechanisms for invasion independently will offer insight into specific evolutionary strategies that make invasive plant species successful. We selected two target C4 invasive/federal noxious weeds (wild sugarcane; *Saccharum spontaneum* L. and cogon grass*; Imperata cylindrica* (L.) P. Beauv.), and one native C4 grass (bushy bluestem*; Andropogon glomeratus var. tenuis*pathius (Walt.) Swallen.) for a full-factorial study comparing native vs. foreign rhizospheres as well as differing degrees of competitive pressure. Conclusions from this study will be linked with other research that relates phylogenetic relatedness and phenotypic plasticity to invasion by wild sugarcane.

98 - Shrub encroachment in coastal ecosystems: the role of grass root interactions

Natasha Woods[1], Helaena Holjes[1], Emma Philip[1], Julie Zinnert[2]

[1]Moravian University, Bethlehem, PA, [2]Virginia Commonwealth University, Richmond, VA

Shrub encroachment is occurring in ecosystems worldwide but provides unique ecological scenarios in barrier island systems as extensive shrub canopies disrupt the natural island response to sea-level rise by reducing sediment flux to the interior. Warming winter temperatures are a primary driver of coastal woody encroachment by reducing freezing induced embolism. However, the potential for grassland species to influence the encroachment process through belowground interactions (i.e., competition, mycorrhizal fungi facilitation) in these nutrient poor environments is limited. A hoop house experiment was set up to determine the extent to which belowground biotic interactions with grasses influence the growth of *Morella cerifera* seedlings (a native, evergreen shrub) by allowing or excluding root interactions with the dominant grass, *Sporobolus pumilus* (also known as *Spartina patens*) (n = 15). Shrub growth metrics included plant height, canopy area, above and belowground biomass, mycorrhizal root infections, and root length and surface area. After twelve weeks, *M. cerifera* height and canopy area were enhanced when roots were interacting with *S. pumilis.* There were no significant differences between mycorrhizal root infection rates, biomass, or root traits in the control versus root exclusion group. These results suggest that belowground interactions with the dominant grass provide faster canopy growth for *M. cerifera* seedlings to grow and ultimately exclude grass species, but belowground interactions access to grass roots do not enhance root growth or the rate of mycorrhizal root infections.

99 - Rooted in Stress: Understanding the role of Salinity and Burial in *Morella cerifera* Establishment

Jacob Donmoyer[1], Natasha Woods[2], Julia Lapinska[2], Julie Zinnert[3]

[1]Undergraduate Student, Bethlehem, PA, [2]Moravian University, Bethlehem, PA, [3]Virginia Commonwealth University, Richmond, VA

Accelerated shrub encroachment into grasslands on barrier islands is impacted by many factors (e.g., warmer winter temperatures, dune elevation); however, the role of storms in affecting seedling shrub growth and persistence is unknown. Plants are most vulnerable to changes in the environment at early stages of development and salinity often affects germination rates of woody species. Salinity and burial may inversely impact seedling survival and growth (aboveground and belowground), slowing the encroachment process. On Hog Island, Virginia, *Morella cerifera*, (here after *Morella*) is rapidly encroaching into grasslands. The goal of this study was to examine the independent influences of salinity, burial, and the combination of both on the aboveground and belowground growth of *Morella*. The experiment took place in a light and temperature-controlled environment. A single pot contained one *Morella* seedling with grasses to simulate the natural microhabitat. Treatments consisted of no burial or salinity (control), salinity only, burial only, and salinity x burial (n = 7). To mimic a massive storm disturbance, seedlings were treated with 35 ppm salinity one time and/or burial to 75% of plant height. Shrub growth (i.e., plant height, canopy area, root length, surface area and biomass) was monitored for 3 months. Burial had no effect on *Morella* seedlings height or canopy growth rates, but salinity and salinity x burial induced significant reductions in both height and canopy area growth rates ($p < 0.01$ for both). There were no effects of any of the treatment groups on root length and biomass; however the salinity treatment reduced the surface area of *Morella* ($p<0.05$). A reduction in surface area could lead to a reduction in nutrient uptake and decrease the growth of *Morella* in coastal grasslands. With projected increases in storms and sea-level rise, salinity exposure will be an important control on encroachment.

100 - Container Mosquito Oviposition Activity as a Function of Urbanization in Guilford County, NC

Tyler Wright[1], Maggie Garr[1], Bella Perez[2], Daniel Greene[1]

[1]High Point University, High Point, NC, [2]Northwest Guilford High School, Greensboro, NC

Mosquitoes such as Aedes aegypti (Linnaeus) and Ae. albopictus (Skuse) breed in containers, and an increased amount of refuse associated with increased urbanization has been associated with the creation of novel oviposition habitats for container-breeding mosquitoes. To assess the effect of urbanization on mosquito oviposition activity in Guilford County, NC, we conducted weekly (4 weeks) oviposition sampling events across 20 sampling sites from 12 June-10 July 2024. Each sampling site featured two 473 ml black 'ovitraps' (one at 1 m in height, one at 0 m in height [ground level]) and belonged to one of two grids (Grid A, 6.71km ²; Grid B, 5.62km²) that differed in their level of urbanization. Ovitraps were filled with water and lined with brown kraft cardstock ("ovistrip") to provide an oviposition substrate for mosquitoes. During each sampling event, ovistrips were removed and replaced in each ovitrap, and ovitraps were refilled with water. The number of viable, desiccated, and hatched eggs were then counted under a stereomicroscope. Enviromental data (e.g., temperature, humidity, eCO2, VOC, etc.) was also collected at multiple sampling sites with a BirdWeather Portable Universe Codec (PUC). The total number of eggs were separately analyzed via generalized linear mixed modeling using land cover, collection date, and ovicup trap height as predictor variables. As human expansion continues to increase, the identification of environmental and land-use variables associated with increased mosquito activity/abundance is of paramount importance as we seek to reduce the transmission of mosquito-borne diseases.

101 - Evaluating impacts of foot-traffic intensity on ecosystem function of sand dunes on Tybee Island, Georgia

Kaylee Braddy, Skyler Fox, Lissa Leege

Georgia Southern University, Statesboro, GA

Due to climate change, coastal areas are becoming increasingly vulnerable to storm surge, erosion, and sea level rise. Sand dunes play a vital role in protecting inland areas from these effects, however climate change is not the only disturbance coasts face. Tybee Island, Georgia, USA hosts 1.9 million visitors annually, creating human disturbance, especially via footpath access to the beach. This study determined relationships between foot-traffic intensity and sand movement, vegetation cover, and species diversity on the sand dunes of Tybee Island. The response of dune habitat (toe, crest, heel, interdune) to foot-traffic intensity was evaluated, and Placer.ai, location intelligence software, was assessed for its utility in tracking foot-traffic. To determine these relationships, researchers tallied the number of people using each footpath (12) and their adjacent crossovers (9) over ~70 daylight hours for the period of May 10 - June 19, 2024. These tallies were used to determine pedestrians per hour, and compared to those extracted from placer.ai data to calculate correction factors. We measured sand movement against a dowel and estimated vegetation cover and identified species in replicate 1x1m plots adjacent to footpaths. Our study showed that foot-traffic was negatively correlated with vegetation cover at the heel and species abundance in the interdune, and positively correlated with species abundance at the crest. There was no relationship between foot-traffic intensity and sand movement. Wooden crosswalks were used up to 47 times more frequently by pedestrians accessing the beach compared to footpaths. Our model showed that Placer.ai consistently and severely underestimated visitorship. These findings are consistent with the literature in that they show the effect of anthropogenic disturbance on sand dunes. These results could be used to advocate for improvements in limiting dune disturbance on coastal regions.

102 - Examining decomposition in suburban woodlot across seasons using the tea bag index

Rebekah Young, Rachel Collins

Roanoke College, Salem, VA

Soils serve as a major carbon reservoir, holding over three times the amount of carbon currently in the Earth's atmosphere. Soil carbon storage is greatly influenced by decomposition dynamics. Furthermore, it is important to study decomposition in suburban woodlots because urban soil is exposed to outward stress factors such as soil compaction and toxic pollutants. We examined soil decomposition rates using the Tea Bag Index (TBI) in a suburban woodlot in at the Roanoke College, Salem, Virginia (37.289°N, -80.043°W). The forested site is closed canopy dominated by invasive and ornamental tree species. TBI was developed by Keuskamp et al. (2013) uses commercially available tea bags as a standardized protocol in measuring decomposition. TBI uses Lipton brand rooibos and green tea in plastic tea bags which are not longer available. Our goals were to find suitable alternative tea bags currently available and to compare the rate of soil decomposition in an suburban woodlot across seasons (spring & summer). We used four kinds of tea from Tealyra™. We recored pre-treatment masses for each tea bag and attached number metal tags to each bag. We buried three sets of tea bags to a depth of 10 cm in four locations in the woodlot. Every 30 days for 90 days we dug up sets and recorded dry mass. We found that rooibos had the lowest biomass lost (10.4%), mint biomass loss was intermediate (25.1%), and green teas had the most biomass lost (60.6% & 48.2%). These results paralleled the original TBI method. Decomposition was higher in the spring than summer; likely due to moderate temperatures and higher soil moisture, which is ideal of microbial activity. Understanding how

seasonal factors affect decomposition in urban woodlots is important for managing ecosystem functions in urban green spaces.

103 - Accuracy Assessment of a Coastal Vegetation Map in South Carolina, US

Zak Bartholomew[1], Cody Goodson[1], John Holloway[2], Kyle Palmquist[1]

[1]Marshall University, Huntington, WV, [2]Department of Natural Resources, The Marine Corps Recruit Depot Parris Island, Parris Island, SC

The effects of climate change on accelerating sea-level rise and increasing storm surge events pose a substantial threat to coastal vegetation communities. Classifying vegetation types and mapping their current extent is a critical step in identifying potentially vulnerable communities. For this research, we conducted an accuracy assessment to evaluate a vegetation map of Marine Corps Recruit Depot Parris Island (MCRDPI), a sea island in South Carolina, USA generated by supervised deep learning classification. Previous research efforts established permanent vegetation plots within major coastal vegetation types on the island and used cluster analysis and ordination to delineate vegetation types. A supervised deep learning classification using these data produced a 2022 map of 23 land cover types on the island. Field surveys for the accuracy assessment were conducted in December 2023 and during summer 2024, and a total of 525 validation points were sampled. At each validation point, we recorded the coarse and fine scale land cover type, the homogeneity of the plot, physiognomy, and dominant vegetation cover by strata. To determine the accuracy of the vegetation map we compared the vegetation classification map's expected land cover type against the field surveys recorded land cover type using a confusion matrix. The accuracy assessment yielded an overall accuracy of 62% and a Kappa statistic of 0.6. The most extensive vegetation type on MCRDPI (soft marsh, covering 41.4%) had a producer's and user's accuracy of 84% and 58%, respectively. Results from this research demonstrate the potential utility of the classification method while also highlighting areas for improvement. This map will facilitate future monitoring on MCRDPI including quantifying changes in salt marsh cover and extent that result from sea-level rise and more intense storm events, providing valuable data on how these changes are impacting coastal ecosystem stability and health.

104 - Range Variability of Species Across North Carolina Found with BioBlitz Data

Madeline Helt, Annkatrin Rose

Appalachian State University, Boone, NC

This project looks at the correlation between geographical location and species presence in various regions of North Carolina through various BioBlitz projects done on college campuses across the state. Participating campuses include Appalachian State University, UNC Wilmington, and UNC Greensboro. This is done using the site iNaturalist, a platform designed to record biodiversity on Earth using identification and social tools to help identify organisms at specific locations. The BioBlitz project is meant to encourage many to go out and record all the species found in a particular area in a specific time frame. These findings were then posted into iNaturalist to create a data set to analyze biodiversity in particular areas.

This research involves the analysis of data collected from previously recorded BioBlitz project data on iNaturalist. This site provides a multitude of informative takeaways from each organism's observations and therefore provides a great and easy to access way to analyze data on biodiversity. Looking at specific location parameters such as elevation, habitat, and climate when analyzing this data is important to understanding why particular species live in specific areas. Looking at these features provides clues into why species are often found in specific locations and how urbanization and human developments have affected their possible living locations.

105 - Examining Storm Water Infiltration in a Meadow Restoration Site: Where does the rain go?

Abbigail Reed, Rachel Collins

Roanoke College, Salem, VA

The soil plays an important role in stormwater absorption, run-off, and ponding. The quality and characteristics of soil are drivers in determining how much stormwater infiltrates into and replenishes ground water, as well as how well it mitigates flash flooding. Soil, highly degraded by human activities such as fill sites, is especially prone to disrupting storm water absorption. We examined storm water infiltration rates at a recently restored fill site in Salem, Virginia. To do this we used HOBO©net multi-depth soil moisture sensors in both the fill site and in a nearby rain garden. Our goals were to examine the stormwater infiltration patterns in the fill site, and to analyze the peak percent increase in soil moisture at different depths after rain events. We found that the patterns of rain infiltration were inconsistent in the fill site. Soil moisture increased at the deepest depth for the large rain events, but not small rain events. In the rain garden, rainwater was quickly and consistently absorbed to the deepest depth. Understanding how storm water infiltrates in recently restored sites offers a baseline to compare changes in infiltration as the native grassland species take hold and increase in biomass over time.

106 - Native Tree Species Success in Riparian Restoration Zones in Rockingham County, Virginia

Ireland Lewis[1], Erin Naman[1], Heather Griscom[2]

[1]James Madison University, Biology, Harrisonburg, VA, [2]James Madison University, Harrisonburg, VA

The Conservation Reserve Enhancement Program (CREP) incentivizes landowners to regenerate riparian buffers previously degraded by agricultural and anthropogenic uses. Planting native species along streams is important for long-term ecosystem health and restoration. However, factors influencing survival and success of several native tree species are unclear. We monitored species growth and survival on two farms, Harpine for six years and Green Hill for three. Both farms enrolled in CREP in Rockingham County, Virginia. Height, basal diameter, and survival were recorded at the time of planting in early spring. At the end of each growing season (late fall), we recorded growth, survival, and evidence of deer browse to determine the success of 24 species. Survival of the 539 plantings at Harpine Farm was 68.2% after five years and 73.7% of the 444 plantings survived at Green Hill Farm after two years. Growth rate will be calculated after six years at Harpine Farm and three at Green Hill Farm. There was a significant difference between species across both farms in past years and we expect to see the same outcome from the recent growing season (2024). The best-performing species at both farms were recorded to report back to the landowners as recommendations for best results. New data collected this growing season should support the best-performing species in recent years, consistently outperforming other woody species.We conducted analyses on the relationship between survival and deer browse and determined that dogwood is the most resistant to deer browse. On the other hand, redbud and cherry are recommended only when deer browse pressure is low, while sycamore is recommended regardless of deer pressure. We will conduct further analyses to see if trends remain consistent after another growing season. These conclusions will hopefully be supported by the 2024 growing season data.

107 - Top-Down Effects of Large Mammal Herbivores in Tropical Forest Ecosystems

Kathryn Garner[1], Catherine Stewart[1], Jennifer Bradham[1], Malu Jorge[2]

[1]Wofford College, Spartanburg, SC, [2]Vanderbilt University, Nashville, TN

Tropical forests offer many ecosystem services, such as carbon sequestration, and contain high levels of biodiversity. The provision of these ecosystem services relies directly upon ecosystem's large mammal herbivores. However, much of what we know about the impacts of LMHs on ecosystems comes from temperate forests and tropical savannas, with a notable lack of research documenting the effects of LMHs on aboveground and belowground dynamics in tropical forests. This research focuses on LMHs impacts on forest rejuvenation measured via seedling growth and diversity. In the summers of 2023 and 2024, a total of 14 paired exclosure plots were constructed in the Brazilian Pantanal, the world's largest tropical wetland ecosystem. These sites consisted of two 5 x 7 m plots, one allowing for complete movement through and the other restricting any movement through and each with a motion sensor camera to record animal presence and behavior (or lack thereof). These plots were further divided into 1 by 1 m subplots in which each seedling was measured, photographed, tagged with a unique number, and identified to the lowest taxonomic level. The initial measurements, taken in 2023, show that there were no differences between the plant seedling density or species richness, acting as a good baseline for the following years, as the project is intended to last for 10 years. This presentation will show the results of any changes between 2023 and 2024, as well as preliminary data relating to the first year of collected images of animal presence and behavior. This is the first time that LMH impacts will be directly quantified through a controlled experiment for pristine tropical forests, allowing for a more complete understanding of plant-mammal interactions within this ecosystem and having broader implications for all Neotropical forests.

108 - Characterizing and Mapping Coastal Vegetation on a Sea Island in the Southeastern USA

Cody Goodson[1], John Holloway[2], Anne Axel[1], Zak Bartholomew[1], Pamela Puppo[1], Peyton Debowsky[1], Kyle Palmquist[1]

[1]Marshall University, Huntington, WV, [2]Department of Natural Resources, The Marine Corps Recruit Depot Parris Island, Parris Island, SC

Coastal ecosystems are among the most functionally important habitats, are structured by abrupt transitions in salinity, elevation, and tidal exposure, and are sensitive to climate change. Our objectives were to classify and map coastal vegetation types present on Marine Corps Recruit Depot Parris Island (MCRDPI), a sea island in South Carolina, and to investigate potential impacts of sea-level rise (SLR) on these types. MCRDPI is dominated by tidal salt marshes with large, inland areas of forested habitat and developed areas supporting Marine Corps training activities. We established 57 permanent vegetation plots within all of the major coastal vegetation types present on the island, made detailed plant community measurements and characterized the main environmental variables associated with each vegetation type. We employed cluster analysis and ordination to delineate these types based on vegetation plot data and then mapped those types onto existing Associations within the United States National Vegetation Classification (USNVC). Supervised deep learning classification was employed on 0.5 m RBG imagery to map the distribution of vegetation types and other land cover types. We identified four salt marsh Associations and eight forest or woodland Associations. The distributions of these vegetation types were primarily driven by salinity and elevation gradients. These vegetation types as well as additional land cover types not captured by the vegetation surveys were mapped as 23 distinct classes. The marsh types dominated

the landscape, covering ~57% of the classified area, while forest types covered ~13%. Accuracy assessment of the map yielded an overall accuracy of 62% and a Kappa statistic of 0.6. We successfully identified 12 existing USNVC vegetation types and mapped their spatial distribution on MCRDPI. The permanent vegetation plots and vegetation map will enhance monitoring efforts on the effects of climate change on coastal habitats and facilitate decision-making by the MCRDPI natural resources department.

109 - *Centaurea cyanus* (Cornflower) Distribution in Developed Wetlands

Desiree Berry, Michelle Barthet

Coastal Carolina University, Conway, SC

Centaurea cyanus is a temperate Europe native flower that is commonly referred to as the cornflower or bachelor's button. The cornflower is identified as medium to tall with usually blue petals (sometimes purple, pink, or white) and white hairs on the stem. The plant has many medicinal, culinary, perfumery, and other uses, but the most commonly known use is as a decorative plant. Now known as an invasive weed in North America, the cornflower is known to grow in habitats of full sun, disturbed but not moist soil substrates, on roadsides, and in gardens and fields. In South Carolina many areas of wetland and moist habitats make the cornflower difficult to grow in, but the Coastal Carolina University Herbarium has identified two samples of *Centaurea cyanus* in the 1980s: one in Horry County on the side of the road, and the other in Marion county in a fallow field. Since the samples were collected, the development of highways, housing, infrastructure, etc. has increased. In 2023 it was determined that 27% of the wetland habitats in South Carolina have decreased, creating the potential for more suitable habitats for cornflower growth to increase. Highways 90, 701, and 905 have undergone construction for highways, bridges, etc. with potential wetland habitat loss. There is no previous data to confirm the invasiveness of the cornflower in the areas of interest, but the changes to the wetlands can support the invasive growth of the non-native cornflower. It is believed that the distribution of *Centaurea cyanus* will positively correlate with the presence of developed areas along Highways 90, 701, and 905, meaning *Centaurea cyanus* density will increase with more developed areas and out-compete the native plants, becoming an invasive species.

110 - Temperature Analysis of Seasonal Stratification in Small Farm Ponds

Ma'Lon Lane, Clifton Ruehl

Columbus State University, Columbus, GA

Seasonal stratification of pond ecosystems affects a variety of abiotic processes including nutrient and oxygen distributions and biological processes like the distribution of organisms that are responding to abiotic processes. Temperature is the primary driver of seasonal stratification. For example, in the winter low density ice forms over the surface of water preventing mixing resulting in colder water at the surface and slightly warmer water at depth, while in the summer water temperature is warmer near the surface (Berquowitz 2023). Mixing occurs in the fall and spring when the pond becomes isothermal and wind facilitates mixing that redistributes nutrients and oxygen (Buttle, Frost, Marsalek, et.al 2013). I tested for seasonal stratification in a small farm pond characterized by low nutrient, cloudy water during the spring of 2024 using continuously recording thermometers (HOBOs) arranged in a logarithmic series on a PVC pipe. The pipe was driven into the pond floor so that the top HOBO was just below the surface. I used temperature data recorded at 3pm every ten days between 18 February 29 March to examine evidence for thermal stratification to occur with the onset of spring. Water temperature declined with depth as expected. The surface of the pond gradually warmed over time while temperature did not increase much at depth. Therefore, this pond is likely a monomictic pond that mixes each winter in the deeper section near the dam. in the deepest sections of the pond may not be accessible to organisms most of the spring summer and fall as it likely is anoxic. This feature of the pond may contribute to the seemingly low nutrient levels in the pond as organic material collects in the this deep section where little decomposition occurs.

112 - Comparing Parasitism and Resistance to Flow in Two Populations of the Freshwater Snail *Elimia virginica*

Morgan Hicok[1], Abbie M. Tomba[2]

[1]University of Mary Washington, Fredericksburg, VA, [2]University of Mary Washington, Department of Biology, Fredericksburg, VA

Trematodes are parasitic flatworms that infect freshwater snails and can cause changes in metabolic function and growth. Flow rates and water levels are now more variable due to climate change, increasing stress and dislodgment in the snail population. This study investigates how parasites, shell morphology and native flow environment influence resistance to disturbance. Elimia populations were sampled for differences in parasitism, shell morphology, and ability to withstand high flow environments in two different rivers. Sample sites at the Potomac River were tidal with low flow, while sites at the Rappahannock River were higher flow with pools and riffles. Approximately 10 square foot quadrats were randomly selected for sampling per sample location. The Rappahannock was sampled four times at three locations, while the Potomac was sampled five times at two locations. Snails were dissected and measured for shell morphological features, looking specifically at width and aperture. Shell width in Potomac was significantly larger than in the

Rappahannock (Wilcoxon p<0.0001). Shell widths and apertures were both significantly larger in infected snails than non-infected snails (Wilcoxon p<0.0001). Prevalence of parasitism did not statistically differ between rivers, 7.3% to 6.4% in the Rappahannock and Potomac respectively (X2 p=0.65). To measure snails' response to high flow, approximately 300 snails were collected per sample location and were subjected to a high flow environment (0.7 m/s) for 10 minutes to determine time of dislodgment. Excluding un-dislodged snails, the Potomac snails were able to hold on for longer than Rappahannock snails in the high flow treatment (Wilcoxon p=0.001). Infected Elimia in both populations have larger shell widths and apertures, this increase in size does not influence the snail's ability to resist dislodgment in high flow.

114 - Revisiting Freshwater Sponge History: A review of the Michael Poirrier Collection

Nicholas Teegarden, Sydney Gemeinhardt, Lisa DiMaggio, Mary Miller

Baton Rouge Community College, Baton Rouge, LA

The late Michael Poirrier, PhD, was a zoologist who focused his research on benthic restoration ecology. His doctoral dissertation, in 1965, focused on the Louisiana freshwater sponge populations; this study led to many consulting opportunities during his academic career. In 2019, he began working as mentor to Mary G. Miller on the Louisiana Freshwater Sponge Project, at Baton Rouge Community College. At the time of his passing in November 2023, his family entrusted Dr. Miller to oversee the sponge collection. The collection of 408 samples was obtained from his research lab at the University of New Orleans in July 2024. It consists of 21 species from 27 states and 15 countries, spanning over 100 years, from 1888 to 1998. When the samples were obtained, they consisted of dried and wet (preserved in ethanol) sponges that included extensive to limited classification information. Project participants confirmed and/or identified the sponge samples using phenotypic spicule observations and were organized based on the dates and origin of sample collection. Dr. Miller has worked with the Louisiana Universities Marine Consortium to house the samples at their Blue Works site museum. This poster will share the findings of his collection and how they can be obtained by other scientists.

115 - Relationship between benthic macroinvertebrate communities and environmental conditions in freshwater ponds on Bald Head Island, NC

Natalie Novak, Riley Westman, Allison Polinski, Elizabeth Darrow

Bald Head Island Conservancy, Bald Head Island, NC

Benthic macroinvertebrates are essential components of freshwater ecosystems. They provide numerous ecosystem services, and are effective bioindicators of ecosystem health, since they respond to changes in water quality in predictable ways. On Bald Head Island, North Carolina, there are over a dozen created freshwater ponds. We wanted to determine which environmental/habitat variables are responsible for differences in macroinvertebrate community compositions between these ponds. To do this, we conducted a survey of macroinvertebrates at six freshwater ponds on Bald Head Island in October 2024 by sweeping a dip net through the water column and emergent vegetation. We also collected water quality data using a YSI probe and bottle samples, substrate composition using a soil corer, and identified vegetation species using field guides. To characterize the differences in macroinvertebrate community composition between ponds, we calculated richness, abundance, and Shannon-Wiener diversity for each pond. We used ANOVA to determine how substrate composition differed between ponds. To relate environmental variables to macroinvertebrate communities, we used principal components analysis (PCA). We collected 21 unique genera of macroinvertebrates, of which none were present across all sites. In sites with a greater number of plant species, there was an increase in macroinvertebrate community diversity. Ponds with higher richness and diversity of macroinvertebrates were also characterized by lower chlorophyll-a and total nitrogen concentrations, higher dissolved oxygen, higher pH, and higher soil bulk density. One pond had higher salinity than the others, which led to significant differences in community composition in PCA. Although our small sample size limits the statistical significance of our findings, there are clear trends that emerge in these results. In future work we will sample additional ponds on the island, at different times of the year, which should allow us to better explain the differences in community structure we observe between ponds.

116 - Comparing host niche overlap of two biological control agents using ecological niche models (ENMs)

Samuel Schmid[1], Andrés Sánchez-Restrepo[2], Alejandro Sosa[2], Gray Turnage[1], Gary Ervin[1]

[1]Mississippi State University, Miss State, MS, [2]Fundación para el Estudio de Especies Invasivas, Buenos Aires, Buenos Aires, Argentina

Alligatorweed (*Alternanthera philoxeroides*) is an aquatic plant native to South America and invasive in the Southeast. This species has a long history of biological control, namely with the alligatorweed flea beetle (*Agasicles hygrophila*) which effectively defoliates alligatorweed. However, the cold intolerance of the flea beetle limits its biological control utility, as large portions of the alligatorweed invaded range cannot support overwintering populations of this agent. Another natural enemy, the alligatorweed thrips (*Amynothrips andersoni*) has shown better cold tolerance in laboratory experiments, but there have been no efforts to model the ecological niche of

this agent. This study seeks to construct ecological niche models (ENMs) for alligatorweed and these two biological control agents and compare their niche overlaps. These ENMs were developed using Maxent and predictions were made for present climate and two future climate scenarios. Under future climate scenarios, the total niche area of alligatorweed is predicted to decrease by up to 10% whereas the predicted niche areas of the two agents is expected to increase by up to 10%. Despite the expanding niche of both agents, the predicted niches of the thrips showed much greater overlap with alligatorweed than the niches of the flea beetle in all three scenarios. These findings suggest the thrips is much better suited as an alligatorweed control agent, particularly in regions where the flea beetle cannot overwinter.

117 - Seeing Scars: Dive into the scars and skin conditions of Pacific Coast Feeding Group gray whales

Serina Lane[1], Natalie Chazal[2], Leigh Torres[2]

[1]Georgia Gwinnett College, Lawrenceville, GA, [2]GEMM Lab - Oregon State University Marine Mammal Institute, Newport, OR

A small subset of Eastern North Pacific gray whales (Eschrichtius robustus), called the Pacific Coast Feeding Group, utilize the foraging grounds off the coast of Oregon. Anthropogenic stressors such as vessel traffic and fishing are increasing in and around important gray whale ecological locations in this area. Adobe Bridge was used to photo-analyze 8,667 gray whale sighting photos from the years 2015 and 2023. Photos were scored for photo quality, type of scarring, skin condition presence or absence, and confidence in each entry. Results show there is a statistical difference in male and female mean cumulative scar counts. With the framework created, the GEMM Lab can continue this type of analysis which can be used to generate and maintain long-term monitoring programs. This method of fine-scale photo analysis and extensive documentation can also contribute to research relating to gray whale skin healing.

118 - The Effects of Overhead Shades on Coral Bleaching of *Agaricia tenuifolia, Porites astreiodes,* and, *Porites divaricata*

Harrison Smith[1], Soraya Bartol[2]

[1]Shumadine Scholar at Virginia Wesleyan University, Alexandria, VA, [2]Virginia Wesleyan University, Virginia Beach, VA

Coral reefs are vital ecosystems that support marine biodiversity, protect coastal communities, and contribute significantly to the global economy. However, rising sea surface temperatures (SSTs) due to climate change are accelerating coral bleaching. This research explores the use of underwater shades with varying densities (50%, 70%, and 90%) to mitigate thermal and light stress on coral colonies. Conducted in Cozumel, Mexico, the study monitored three coral species—Porites divaricata, Porites astreoides, and Agaricia tenuifolia—over a gradual increase in SST. Results conclude that 90% light-blocking shades provided optimal cooling, in turn producing the healthiest individuals. While the healthiest individuals were found under the 90% shade, photosynthetically active radiation (PAR) measures were inappropriate for long term coral growth. Therefore, the 70% light blocking shade was concluded to be a compromise between optimal cooling and suitable PAR as individuals were seen to have a 23.16% health increase compared to unshaded colonies. Findings highlight the potential of shading as a cost-effective strategy for coral restoration, offering practical solutions to strengthen resilience against global warming's impacts. Further research is encouraged to refine applications across diverse coral species and habitats.

119 - The Effect of Salinity and Depth on Zooplankton Abundance and Diversity off the Georgia Coast

Dreanna Wildman, Mary Haney, Mark Schlueter

Georgia Gwinnett College, Lawrenceville, GA

Zooplankton are small floating animals that live in aquatic habitats. They play a critical role in the ecosystem by transferring energy from phytoplankton to larger animal predators (e.g. fish). The role of salinity on zooplankton abundance and diversity was investigated in marine, estuary, and freshwater ecosystems. Researchers aboard the R/V Savannah sampled zooplankton at 2 marine sites, 2 estuary sites (brackish water), and 2 freshwater sites near Savannah, Georgia on October 19 -20, 2024. Zooplankton were sampled using a weighted plankton net that was dragged at a depth of 1 meter below the water surface for 2 minutes. The zooplankton samples collected via the plankton net were examined within 5 minutes of their collection using a portable In-Situ Shadowgraph Imaging System that allowed the zooplankton to be visualized via a computer monitor. Portions of the samples were preliminarily examined in the wet lab aboard the ship, while the entire sample was videotaped and recorded for later analysis. Salinity, temperature, depth, and conductivity were measured using a CTD device (package of electronic sensors) directly lowered from the ship. Preliminary results indicated a larger diversity of zooplankton (jellyfish, comb jellies, arrow worms, and copepods) in the marine environments. Copepods were the most numerous zooplankton in all samples. As salinity decreased, however, fewer zooplankton species were observed. Freshwater samples often were limited to only copepods and an occasional crab larva.

120 - Murder Mystery: Extinction of *Galeocerdo aduncus* and *Isurus xiphodon*

Alessio Giammarinaro

Erskine College, Due West, SC

Competition amongst predators is a common, natural occurrence that keeps ecosystems balanced. However, competitive relationships change overtime when environmental pressures change. This is true of the Atlantic Plio-Pleistocene *Isurus* and *Galeocerdo* shark species *Galeocerdo aduncus*, *Galeocerdo cuvier, Isurus xiphodon*, *Isurus paucus*, and *Isurus oxyrinchus*. Of these shark species, *G. aduncus* and *I. xiphodon* become extinct by the mid Pleistocene, while the other three species survive to modern. The causes for the extinction of *G. aduncus* and *I. xiphodon* and the comparative fitness to the extant sharks; *I. oxyrinchus*, *I. paucus*, and *G. cuvier;* can be deduced by comparing tooth morphology, analyzing climate change during the Plio-Pleistocene, and analyzing modern shark responses to temperature change. During the Plio-Pleistocene, a drop in ocean temperature, the formation of the Central American Isthmus, and lower sea levels cause a change in temperature, low nutrient availability, and physically reduce habitats on the continental shelf. This initiates the start of a major extinction as the carrying capacity of habitats decreases and competition increases. Major differences are found in tooth morphology between *I. xiphodon* and the extant makos indicating a difference in diet, while *G. aduncus* teeth are only slightly different from *G. cuvier* conversely indicating similar diets. Fossil distributions of *G. aduncus* and *I. xiphodon* seem to indicate a preference for habitats on the continental but are not found in deeper water, while *I. oxyrinchus*, *I. paucus*, and *G. cuvier* are found in both habitats on the continental shelf and deep water in modern day. This difference in distribution seems to be the factor in making *I. oxyrinchus*, *I. paucus*, and *G. cuvier* more fit than *G. aduncus* and *I. xiphodon* because this allows the extant species to set up territories in deep water circumnavigating the areas of high competition on the continental shelfs.

121 - Consistency of Nutrient Fluxes from Three Caribbean Sponges Species

Kandrea Hamilton, Bee Karanik, Ellie Nedrich, Cole Easson, Amy Apprill, Cara Fiore

Appalachian State University, Boone, NC

Sponges are filter feeding animals that process vast amounts of water, thereby impacting the profile of particulate and dissolved nutrients. Many coral reef sponges are known to be a sink for particulate matter and dissolved organic carbon (DOC) and they may be a sink or a source of inorganic nitrogen. Often multiple individuals are sampled one time each, and an average net flux of nutrients is determined from those individuals. However, it is not known how consistent one sponge individual is in how it alters dissolved nutrients over time, and therefore, how representative a one-time sampling point may be for estimating nutrient fluxes. Here, we analyzed total organic carbon (TOC), total nitrogen (TN), silicate, nitrate, and ammonium concentrations for three sponge individuals of three common Caribbean sponge species over two or three days. The giant barrel sponge, *Xestospongia muta*, was largely consistent over three days for processing TOC and TN, silicate, and ammonium, all of which were generally a net sink, while the net flux of nitrate was more variable. The common yellow sponge, *Verongula rigida*, was also largely consistent with some variation in nutrient fluxes over two days of sampling but these were not significantly different over the two days. In contrast, the tube sponge, *Niphates digitalis,* was variable in the net flux of most nutrients across individuals and for one individual across three sampling days. This work has implications for better understanding the impact of sponge pumping and metabolism on coral reef seawater nutrient profile and for better constraining the net flux of nutrients on coral reefs.

122 - The Influence of Forest Diversity on Carbon Sequestration in Southeastern Oak-Pine Ecosystems

Olufemi E. Fatunsin, Kozma Naka

Alabama A&M University, Hunstville, AL

The forests of the Southeastern United States (SEUS) play a vital role in carbon sequestration, contributing to climate change mitigation. Understanding the factors that influence carbon storage in these forests is crucial for effective management. Previous studies suggest that structural diversity, defined by variability in tree sizes, may have a stronger link to forest productivity than species diversity. However, the direct and indirect effects of forest diversity metrics, including structural and species diversity on aboveground carbon (AGC) storage in Southeastern oak-pine ecosystems remain unclear. This study aimed to test the complementarity effects hypothesis, which posits that increased diversity leads to more efficient resource use, enhancing ecosystem functions like carbon storage. Using structural equation modeling and data from 4,316 Forest Inventory and Analysis (FIA) plots, we explored how structural diversity, species diversity, elevation, and climate impact AGC storage in mixed oak-pine forests. In line with the complementarity effects hypothesis, we hypothesized that: 1) climate and elevation would have stronger indirect effects on AGC via species and structural diversity; 2) structural diversity would be a more significant mediator than species diversity in AGC responses to climate and elevation; and 3) species and structural diversity would be positively correlated, with structural diversity exerting a stronger influence on AGC. The results showed that mean annual temperature had a direct negative effect on AGC, while precipitation indirectly increased AGC. Elevation indirectly promoted AGC by increasing species diversity. Both structural and species diversity had direct positive effects on AGC, with structural diversity being a stronger predictor. Thus, maintaining high structural diversity in mixed oak-

pine forests is crucial to enhancing carbon storage under changing climate conditions.

123 - Urban vs. Rural Preference for Overpopulating Mississippi Whitetail Deer

Simon Tipton

The University of Southern Mississippi, Hattiesburg, MS

Whitetail Deer and Mississippi are as synonymous as bread and butter. Conservation of this species (Odocoileus virginianus) contributes to the greater social landscape of the entire Southeast. The craft of hunting is becoming less popular to a younger population and cannot be fully supported by the aging Boomers and overworked Gen X. The underlying question is what does less predation (hunting) from lost interest or tighter regulation mean for our locality of whitetail deer?

The needed considerations are the grouping of large herds based in the suburbs, proximity to known CWD (chronic wasting disease) populations, and refusal of deer to populate ideal habitats created in rural settings. Whitetail deer are not alone in this move as wild turkey, rabbits, possum and vultures are all starting their way towards suburban life. Aside from the brilliant turkeys, it is not comprehendible that the wildlife understands the complexity of city zoning. However, this city entrance may shake a variety of natural predators as they are less likely to fare city life. A large concern is the populations of CWD or “Zombie Deer” encroaching closer to the suburbs giving the epidemic another chance to catch flame.

Field surveys across the state are called for with a focus on suburbs, rural trails and managed plots. This will be conducted with 50 game cameras tied to GPS coordinates and then checked for timestamped activity. Number of sightings and location can be compared with layers of human population and state published areas of CWD. Evidence will continue to cement early findings from living this story as an avid outdoorsman and being observant to one’s surroundings.

124 - Fringed Campion: Conserving an Endangered Species

Bryce Williams, Heather Bowman Cutway

Mercer University, Macon, GA

Silene catesbyi (fringed campion) is a federally endangered plant found in 26 locations throughout middle Georgia and northern Florida. This species has multiple threats – habitat destruction, invasive species, herbivory, and low seed production. Herbivory is especially of concern during flowering periods, in which S. catesbyi attracts the attention of herbivores, including deer. Rare plant populations are often fenced to deter herbivory, however, this might prevent pollinator visits resulting in even lower seed production. In this study, the production of rosettes, flowers, and seeds were compared between the fenced and unfenced patches. Our results indicate that seed production is inconsistent from flower to flower, but not impacted by the presence of fencing. Inconsistent seed production was also found in ex-situ populations where flowers were hand-pollinated. Further investigation is required to understand why seed production is significantly different from flower to flower.

125 - Evaluation of fish biodiversity and abundance on a restored vs. unrestored shoreline in Mosquito Lagoon, Florida

Zoe Stuckwisch, Corie Charpentier

Stetson University, DeLand, FL

Restoration of coastal habitats aims to enhance biodiversity and support ecological resilience. This study evaluated fish abundance and biodiversity at a restored and unrestored shoreline in Mosquito Lagoon, Florida. The restored site features oyster reef substrate and native vegetation, which replaced a seawall 1.5 years prior to this survey, while the unrestored site consists of concrete rubble. We hypothesized that the restored shoreline would support greater fish abundance and biodiversity due to improved habitat complexity. Fish were sampled using a seine net from late August to October 2024, with five collections per site during low tide. We compared species abundance and biodiversity between the restored and unrestored sites; biodiversity metrics included species richness, Shannon-Weiner index, Simpson’s index, and evenness. Overall, we collected > 20 fish species. However, results indicated no significant differences in fish abundance or biodiversity indices between the restored and unrestored shorelines. Spotfin mojarra, *Eucinostomus argenteus,* was the most abundant species at both sites. Juvenile lane snapper, *Lutjanus synagris*, was more prevalent at the unrestored site, while bay anchovies, *Anchoa mitchilli,* were more frequently captured at the restored site later in the season. Species-specific differences may be due to spawning-associated migrations or the geographic location of sites, as the unrestored site is closer to Mosquito Lagoon’s only inlet. We also recognize that long-term monitoring at the restored site may be needed to capture potential restoration impacts to fish biodiversity.

126 - Exploring how canopy cover and land use affects flying insects in the city

Isaac Jackson[1], Harlan Chapman[1], Elsa Youngsteadt[2], Peter Willadsen[2], Sarah Parsons[1]

[1]Western Carolina University, Cullowhee, NC, [2]North Carolina State University, Raleigh, NC

Recent reports of insect biomass decline have raised concern about the future of insect dependent food webs and ecosystem services, such as pollination and nutrient cycling. The causes of insect decline are difficult to pinpoint, but urbanization is a clear threat. Cities, however, are mosaics of land uses, which likely have different effects on different insect groups. Moreover, patterns in non-urban systems predict that urban forests will support the greatest net primary productivity (NPP) and insect biomass. Because of this, we hypothesized that sites with greater canopy cover would have more insect biomass and abundance city-wide. Here we examine links between canopy cover and insect biomass and abundance in various sites across Raleigh, NC. First, we developed urban canopy cover–insect biomass relationships by sampling insects with malaise traps at 30 sites in Raleigh, NC. Second, we measured within-city canopy cover and temperature within 200m and 1km of sites using geospatial data and correlated this data with insect biomass data. Contrary to our prediction, results show that sites with less canopy cover had more insect biomass in late summer. This would suggest that canopy cover/insect biomass relationships in cities may not exist in the way they do in non-urban systems. Our findings are important for understanding how city planners may be able to play a role in helping conserve insect biomass and wildlife both within cities and beyond.

127 - Using machine learning to streamline detection in camera trap research

Reegan Magee, Lisa McDonald

Lander University, Greenwood, SC

Camera trap research generates massive datasets that require extensive time collecting data from largely empty photos. Artificial intelligence (AI) models can be used effectively to streamline this analysis. Although most machine learning models show significant weakness in identifying species in photos, they can successfully filter out empty images and classify broader categories of observations. We used MegaDetector (version 5B) to batch filter images into folders identifying humans, animals, vehicles, and all possible combinations of these categories. We evaluated the general accuracy of this model compared to data collected manually from the same photos by members of our lab over the last 7 years. Human presence scores (number of disturbances per camera trap day) were calculated for each of our 30 camera trap stations (assessing 3,661,447 photos across our 7 study sites) from manually-collected data and using the MegaDetector model. By removing the empty pictures and including only those with a detection confidence of at least 0.2, the total number of photos to review was reduced by 83.9%. To determine how closely the results from the MegaDetector model resembled our manual calculations of human presence, we calculated the correlation between the two sets of human presence scores. We found a high correlation between these scores ($r = .9577$, $p < .0001$), which emphasizes the potential power in using AI models such as this one in place of fully manual evaluation. These results highlight the benefits of AI in aiding data organization and analysis by automating some of the most time-consuming tasks. This frees up large amounts of time that can be more efficiently spent on identifying the target animal taxa in collected photos and analyzing those data to answer important ecological and conservation questions.

128 - Baseline Assessment of Fish Communities and Habitat Structure Surrounding Peery's Mill Dam in Walland, TN

Gabriel New

Maryville College, Maryville, TN

Dams have been constructed for thousands of years to serve various human needs, yet they have been shown to impact the ecological health of lotic freshwater systems negatively. In the United States, thousands of low-head dams persist in waterways, often no longer serving their original function but continuing to alter aquatic communities and stream dynamics. This study assessed the ecological and geomorphic impacts of Peery's Mill Dam, a low-head dam on the Little River in Walland, Tennessee. Specifically, fish communities and stream geomorphology were assessed upstream and downstream of the dam. Fish communities were evaluated using snorkeling and seining surveys, while the geomorphology was characterized through stream elevation surveys and Wolman pebble counts. Results indicated no significant differences in fish community composition between sites, although species richness and diversity were high across all surveyed reaches. Substrate composition varied significantly between upstream and downstream sites, but the elevation survey revealed no significant differences. These findings suggest that while Peery's Mill Dam minimally influences fish community structure, it alters sediment distribution. This study establishes a critical baseline for future comparisons and highlights the need for post-dam removal monitoring, particularly within the reservoir zone, to evaluate ecological recovery and habitat restoration.

129 - Monitoring invasive bark and wood-boring beetles in an urban forest using eDNA

Erica Edinger[1], Craig Larcenaire[2], Kristen Wickert[2], Pamela Puppo[1]

[1]Marshall University, Huntington, WV, [2]USDA Forest Service, Morgantown, WV

Urban forests play invaluable roles in maintaining air quality, reducing heat, supporting local biodiversity, and improving the quality of life of city residents and visitors. Across North America, invasive bark and wood-boring beetles contribute to the destruction of native trees and threaten the sustainability of forests, including urban forests. To monitor the populations of these invasive insects, traps with chemical lures are set up next to trees. The insects caught in these traps are then sent for morphological identification, which is costly and has a wait period that can be up to 6 months. In recent years, environmental DNA (eDNA) has emerged as a promising method for the identification of organisms without the need for destructive sampling or morphological identification. eDNA amplifies traces of organisms' DNA from materials other than the organism itself. For this project, we aim to extract eDNA from liquid in the traps' collection cups and use it to identify the insects present in the traps. Our project takes place in Washington D.C., which is home to a unique urban forest ecosystem that also includes culturally significant trees, relevant to the history of the United States. By using eDNA to monitor invasive beetles, our project aims to detect their presence early in their introduction, thus limiting their impact and spread before they can cause irreparable harm in this important urban forest. The information produced by this project may also help to inform forest and conservation scientists and those who work in commercial timber in monitoring methods for wood-boring beetles.

130 - Restoring spring ephemerals in an urban forest

Zoe Robles, Kristy Hopfensperger, Denice Robertson

Northern Kentucky University, Highland Heights, KY

Establishing a diverse plant community is a key component of successful urban forest restoration. Spring ephemerals provide important resources for pollinators before most plants flower in summer. Understanding the optimal growth conditions of these species is essential for effective restoration. This study examined the growth and survival of five spring ephemeral species using three life forms—seed, plug, and bare root—at sites where invasive honeysuckle had been recently removed. We studied 30 restoration patches, each with three replicate plots, to evaluate how biological and environmental factors influence the re-establishment of different life forms. We analyzed differences in plant height across different life forms using ANOVAs. We also examined how life form success changed among patch locations due to environmental variables including soil and light metrics. As we learn that different species can re-establish faster than others, this study will provide insights into best practices for restoring spring ephemeral communities in urban forest landscapes.

131 - Understanding the soil microbiome of a montane longleaf pine ecosystem: does choice of soil DNA extraction method matter?

Olivia Walker, Isabella Vahle, Paula Jackson

Kennesaw State University, Kennesaw, GA

The longleaf pine (*Pinus palustris* Mill) is an ecologically diverse and resilient ecosystem. However, its vast historic range in the southeastern United States has significantly declined due to anthropogenic changes. Soil microbes such as bacteria are crucial to plant and ecosystem functions. Our long-term ecological study of the soil microbiome of a longleaf pine restoration site aims to understand factors that may influence the soil microbial community, such as seasonal changes, dominant herbaceous plant removal, soil chemistry, restoration practices, and forest age. For this, in our analysis, it is necessary to consider the methodology and its potential role in influencing the characterization of the microbiome. Hence, the soil DNA extraction kits used are critical. Between 2021 and 2023, we used the DNeasy PowerSoil kit (*original*) for our soil DNA extractions. Then, after its discontinuation, starting in March 2023 we used the DNeasy PowerSoil Pro kit (*new*). Given that we still had some *original* kits available, we aimed to answer the question: how do the two kits compare in terms of purity of DNA extracted and bacterial community representation? For this, DNA was re-extracted from frozen soil samples collected at Sheffield Wildlife Management Area (WMA) from March, July, and November 2023 using the *original* kit. Extracted DNA concentrations and purity ratios from both kits were measured using a NanoDrop spectrophotometer, and DNA was sent to LC Sciences for 16S rRNA sequencing to identify bacterial composition. Results obtained from both kits will be compared. Investigating differences in DNA extraction kits used for our study is crucial for scientific rigor and replicability. Ultimately, our efforts will contribute to the understanding of soil DNA extraction methodology and the scarce knowledge base of the soil microbiome of the longleaf pine ecosystem.

132 - Determining the Ideal Frequency and Duration of Conservation Grazing in Coastal Uplands

Maya Stratman[1], Madeline Schmuck[1], Eric Sparks[1], Jonathan Pitchford[2], Stephen Brewer[3]

[1]Mississippi State University, Biloxi, MS, [2]Grand Bay National Estuarine Research Reserve, Moss Point, MS, [3]The University of Mississippi, Oxford, MS

Currently, prescribed fire, mechanical removal and chemical treatments are the most common habitat management techniques. Conservation grazing has the potential to be an alternative, complementary, cost-effective and less intrusive technique for habitat management. Recently there was a study conducted by NOAA RESTORE Science Program Planning Grant (Gill, 2022) which found that over 96% of natural resource managers were interested in conservation grazing; however, no survey respondents were aware of any research-based information to inform grazing. This survey demonstrated that there is limited understanding of factors that could influence grazing success such as, duration, frequency, livestock type and seasonal timing. To determine the ideal frequency and duration of using goats for conservation grazing in coastal uplands of Mississippi, 25, 5x5 meter plots were constructed with field fencing in an area of coastal Mississippi with dense understory predominantly consisting of gallberry, wax myrtle, and yaupon holly intermixed with pine and hardwood trees. Each plot will then be grazed with goats using a combination of either high, medium or low duration and frequency of grazing. (i.e., combination of 4 treatments of 5 replicates each). Similarly, 5 of the plots will remain un-grazed to serve as controls. Within each plot, 1m2 quadrats will be used to assess vegetation species abundance and diversity, before grazing and at several time points after grazing. Additional data collected at each sampling event will include Normalized Difference Vegetation Index Camera (NDVI) photos, light sensor data, and soil cores. This study is one of the first in the region to assess how structured livestock grazing could potentially be used as a management tool for coastal uplands. Results from this study will be used to identify future research questions while also informing the development of a complementary management tool.

133 - Kudzu Management Strategies Had Minimal Effect on Soil and Microbial Communities

Maryann Cagle[1], Shawn Brown[2]

[1]Biology Department, College of Charleston, Charleston, SC, [2]Department of Biological Sciences, University of Memphis, Memphis, TN

Invasive plant species threaten biodiversity and ecosystem stability. Kudzu (*Pueraria montana* var. *lobata*) is a highly aggressive invasive species in the southeastern U.S. To evaluate the impact of kudzu management on soil chemistry and microbial communities, we conducted a randomized complete block design with treatments including herbicides (glyphosate, aminopyralid), a fungal bioherbicide (*Albifimbria verrucaria*), mowing, and combination treatments. Controls included untreated soil and a surfactant-only treatment. Treatment implementation and sample collection were conducted at the Edward J. Meeman Biological Station (University of Memphis; Millington, TN, USA) between May and September 2019. We evaluated soil enzymatic activity, edaphic chemistry, microbial community structure, and kudzu coverage. Our results indicated that soil chemistry and microbial communities remained stable across treatments, with minimal treatment-time interactions affecting bacterial and fungal populations. These findings suggest that land managers can effectively use herbicides at recommended rates to control kudzu without posing a significant threat to soil health.

134 - Attitudes towards Mexican Gray Wolves (*Canis lupus baileyi*) and Mountain Lions (*Puma concolor*) in Southwest New Mexico

Gage Bell[1], Travis Perry[1,2]

[1]Furman University, Greenville, SC, [2]Natural Curiosity, Hillsboro, NM

Human interaction with predators in the West has historically led to the extirpation of predators. As the ecological and economic importance of predators has become better understood, we have protected, managed, and reintroduced them. Negative attitudes towards predators tend to come from rural livestock owning communities that are more likely to suffer direct negative interactions with these species. Understanding and addressing the attitudes held by a local community towards a predatory species is critical to the responsible conservation and management of that species. In Southwest New Mexico, the mountain lion (*Puma concolor)* and the reintroduced Mexican gray wolf (*Canis lupus baileyi*) provide an important comparison of predators, because while they both kill livestock and pets, only wolves have been reintroduced by the federal government. We created and distributed a survey to record attitudes towards these top predators in southwest New Mexico. Surveys were distributed in four different communities surrounding the Gila National Forest. Attitudes were predicted to be more negative towards wolves than mountain lions. Using a one-tailed analysis we found more strongly positive attitudes towards Mexican gray wolves than mountain lions, although our results were not statistically significant ($p=.15$). There was also greater variation among Mexican wolf attitudes than mountain lion attitudes. We found that two participant rated statements were the most predictive of a participant's attitude towards these predators. These statements were 'New Mexico would be a better place without mountain lions/Mexican wolves' and 'You could tolerate wolves/mountain lions being introduced onto neighboring land if they weren't already there.' A lack of representation among the ranching community due to

unreturned surveys has affected our results, although the lack of response from this demographic is informative.

135 - Accelerating Texas state conservation assessment using Deep Learning

Emilia Gonzalez[1], Anna Maloney[1], Christopher Randle[1], Brooke Byerley Best[2], Kayla Hankins[2]

[1]Sam Houston State University, Huntsville, TX, [2]Fort Worth Botanic Garden, Fort Worth, TX

Coordinated conservation of species requires assessment of degree to which species are threatened. International and domestic agencies, such as the International Union for the Conservation of Nature and NatureServe, have established practices for assigning conservation rankings for species believed to be threatened, allowing prioritization of conservation effort. However, these practices include intensive field study to measure demographic parameters of these species. These standards can provide meaningful assessments at the national and state level. However, given the number of species that may be threatened at any given time, efficiently performing standardized demographic assessments may not be feasible given personnel and budgetary constraints. Artificial Intelligence tools using Deep Learning have been developed to assist with conservation assessment and have proven useful at the international level. In this study, established conservation rankings for Texas flowering plant species will be used to train Deep Neural Networks to make predictions about conservation rankings of other species that have not previously been assessed. A range of predictors including both natural (soils, climate, land cover) and anthropogenic (agriculture, industry, habitation) aspects of the environment will be used to train these networks, allowing additional assessment of factors most responsible for species rarity. This work will serve as a tool for first-pass prioritization of species threat rankings to guide more intensive demographic study.

136 - Historical Fire Regimes in an Urban-Adjacent State Forest and Recreation Area

Madison Cornett, Thomas Saladyga

Concord University, Athens, WV

Historically, frequent fires have promoted diversity in mixed pine-oak forests within the Appalachian region, but the suppression of fires since the early twentieth century has contributed to significant changes in forest structure and composition. In this study, we analyzed the fire histories of two sites within Kanawha State Forest, located just 11 km (or a 15-minute drive) from Charleston, the capital of West Virginia. Samples were collected from 33 fire-scarred pine trees at Shrewsbury Hollow (SHO) in February 2023, while 32 samples were collected at Wall Fork (WFK) in 2021 for a previous study. More than 100 fire scars were dated in the SHO samples, while 77 scars were recorded by trees at WFK. Fire years ranged from the 1840s to the early 2000s at SHO and from the 1790s to the 2010s at WFK. Before Kanawha State Forest was established in 1938, fires occurred every 5-7 years on average at both sites compared to 10-14 years during the suppression era. Across the landscape, fire activity peaked at the turn of the 20th century, but 'major fires' scarring at least two trees and 25% of samples have occurred as late as the 1990s and early 2000s. An analysis of fire-climate relationships revealed that fire events at both sites were associated with drier than average September-May ('dormant season') climate conditions. Land managers at Kanawha State Forest and in the immediate capital region should consider this long history of fire occurrence in restoration efforts, recreation planning, and wildfire education programming.

137 - Micropropagation Techniques of the Eastern Hemlock Tree and its Potential Reintroduction to Southern Appalachian Forests

Sloan Bradley

Erskine College, Due West, SC

Throughout the east coast of the United States, the eastern hemlock tree (Tsuga canadensis) can be found in large populations north into Canada and deep into the southern US states. Throughout this range, the invasive the hemlock woolly adelgid (HWA) can also be found living off many of these trees. After its accidental introduction to the eastern United States in the early 1950s, HWA spread throughout the east coast in every direction for the next seventy years. As HWA populations thrive and hemlocks die back to a near threatened status, many institutions and researchers have been conducting research into ways to preserve the eastern hemlock species and fight against the woolly adelgid. Of these attempts, the micropropagation and plant tissue culture of eastern and Carolina hemlock species through this experiment serves as a prospective solution to restore the native hemlock population and help it in bouncing back from the onslaught of HWA. Successfully tissue culturing would provide many genetically identical copies of a hemlock sample, and if an HWA-resistant hemlock is found or created, it can be cultured and spread. Though research and trials continue in this field, contamination and the reactivity and sensitivity of culture samples throughout the 5-stage micropropagation yield mixed results. Micropropagation and in vitro plant tissue culture serve as a potentially beneficial way to restore the embattled eastern and Carolina hemlock species along the Appalachian Mountain range on the east coast of the US as these trees continue to decline. I study the technique of using in vitro eastern hemlock seedlings in the micropropagation efforts of eastern hemlocks. To properly understand the ecosystems and environments that these hemlocks will be transplanted, researchers will need to better assess these specific ecosystems along the Appalachian Mountains to figure out if hemlocks can be realistically reintroduced into these

environments.

138 - How Fire Shapes the Colonization of Conifer Dwelling Lichens and Bryophytes in the Georgia Piedmont.

Isaac Robitaille[1], Melissa Caspary[2]

[1]Georgia Gwinnett College, Lawrenceville, GA, [2]Georgia Gwinnett College, Athens, GA

Because of ever-increasing urbanization and wilderness fragmentation, it is difficult to maintain the low intensity/ high frequency historic fire regime that the Georgia Piedmont's Oak-Pine-Hickory forests and woodlands rely on. This has led to the filling of canopies and underbrush as fire-intolerant trees such as the American Beech and Red Maple colonize, often taking the place of the fire-tolerant conifers (Edwards et al. 2013). These conifers can act as shelter and a means to access sunlight for several native lichens and bryophytes, that in turn provide crucial ecosystem services to the surrounding forest such as carbon sequestration and erosion prevention (Glime 2024, Walker 2024). Since many of these organisms can survive almost complete desiccation, we wanted to explore in this research project how their diversity is affected by the fire. We hypothesize that maintaining the historic fire regime promotes the biodiversity and abundance of lichens and bryophytes that live among conifer trees, especially those close to the ground. Percent cover data was taken on the cardinal direction faces of conifer trees at 3 feet off the ground, and 15x15m sites were chosen for burned and unburned locations at Hard Labor Creek and Fort Yargo State Parks. 22 trees were sampled across the parks with almost all having a dominant colonization of *Lepraria caesiella*. Contrary to expectations, there was minimal difference in species richness between the Unburned and Burned sites. Burned sites also had significantly less abundance and evenness than unburned sites. The implications of these findings indicate that an altered fire regime has allowed for the colonization of the lower body of conifers by bryophytes and lichens that a more stable one would have prevented in the past.

139 - Blue coloration in kingdom fungi: a review

Laird Bickford, Nicole Hughes

High Point University, High Point, NC

The subject of adaptive coloration in plants represents an area of research that has widely expanded over the last century; yet, adaptive coloration of fungi remains largely unexplored. The objective of the current study was to review the literature for information on the biochemical, evolutionary, and ecological basis for blue coloration in fungi. So far we have so documented blue coloration in 24 fungal genera, belonging to 18 families and 2 phyla. In some lineages, molecules responsible for imparting a blue hue are evolutionarily ancient (e.g. melanins and laccases), while in other lineages, blue molecules are unique to their family (e.g. xylindein- a quinone pigment produced solely by fungi in the genus *Chlorociboria*). In the vast majority of cases, however, the compound(s) directly responsible for blue coloration have yet to be isolated or described in the literature. In many taxa, differently-colored but structurally-related isomers and isozymes of the blue molecule occur within a species (most commonly white, yellow, or brown in color). These include melanins and laccases. In some cases, color change may be induced by changing media or growth conditions, but overall, it remains largely unknown why fungi would produce one colored molecule over another. Among the proposed functions of blue fungal pigments described in the literature include: protection from UV light, warming of sporocarps to create convection and disperse spores, and protection from host defenses.

140 - Characterization of Unique Basidiomycete Fungal Strains Isolated from the L. Frederick Collection

Keionna Beatty, Chinyere Knight

Tuskegee University, Tuskegee, AL

Fungi serve as essential decomposers in nature, playing a critical role in maintaining healthy and functional ecosystems. Their presence indicates effective nutrient cycling, while their absence may signal ecological issues such as nutrient deficiencies or pollution. Dr. Lafayette Frederick created a fungal collection of endophytes and other fungi that have been preserved for decades. This natural history collection is a valuable resources for ecological investigations. This study investigated the phenotypic screening and presence of bioactivity of unique basidiomycete fungal strains isolated from the L. Frederick Collection. Six fungal strains *Aleurodiscus thailandicus*, *Diatrype lijingenis*, *Efibula americana*, *Peniophore crassitunicata*, *Hypnoporia laricola*, and *Heterobasidion araucariae* were identified using ITS1/ITS4 molecular markers. Fungal growth was characterized by using media (Corn Meal Agar, CMA and Potato Dextrose Agar, PDA) and incubation temperatures (25° and 30°). Exposure and response to heavy metals (Zn and Pb) were determined. Additionally, the screening and quantification of bioactive components were interpreted by 6530 Accurate-Mass Q-TOF MS after inhibition assays conducted against the ESKAPE relatives (*Bacillus subtilis Acinetobacter baylyi*, *Enterobacter aerogenes*, *Erwina carotovora*, *Escherichia coli*, *Enterococcus raffinosus* and *Pseudomonas putina*). Future studies will use the six unique whole genome sequences from the L. Frederick collection to study the chemical diversity of their secondary metabolites. This research will transform a historical collection into a living legacy model for scientific investigation.

141 - Digitization and Collection Trends of the Frostburg State University Herbarium

Lily Ridgell, Mrs. Clara Thiel, M.S.

Frostburg State University, Frostburg, MD

The Frostburg State University Herbarium (FSUH) houses over 15,000 dried plant specimens that span many taxa and features various important regional collectors. Due to FSUH's location in Western MD, the collection includes several specimens that are unique to the Allegheny Plateau and Ridge and Valley provinces. Although curation of specimens began in the 1950s, the FSUH has yet to be cataloged, and the entirety of its inventory is currently unknown. To better understand the contents of the FSUH collection, recent digitization efforts in partnership with the Mid-Atlantic Herbarium Consortium (MAHC) aim to create a database that will assist in its accessibility and organization. Using this database, the collection will be analyzed to detect trends in taxonomy, location, and distribution. Analyses such as this will assist future collectors by identifying species or regional gaps in the FSUH inventory. As plant distribution patterns are altered by climate change, researchers can utilize FSUH's database to predict future trends of Western Maryland's flora. Digitization of FSUH and other small herbaria will improve the accessibility of its collection for future research and data sharing throughout central Appalachia and the greater Southeastern U.S.

142 - The Ethnobotanical Collection at the Marshall University Herbarium

Clara Minnich, Pamela Puppo

Marshall University, Huntington, WV

The Marshall University Herbarium (MUHW) primarily houses a vascular plant collection, but also includes several other collections, such as bryophytes, algae, fungi, and an ethnobotany collection. The latter was primarily collected by former MUHW curator, Dr. Dan K. Evans who conducted fieldwork in South America, where he received these artifacts from the Shuar and Achuar indigenous tribes in Ecuador. These tribes are among the eight ethnic groups that still exist within Ecuador today. In this presentation, we provide an in-depth analysis of the collection, including information on what the objects are, what material or plant they are made of, and the cultural context and relevance of these artifacts for the indigenous people of these tribes. To make this determination of the artifacts, several resources were utilized, including herbarium specimens, botanical literature, and databases like TROPICOS and SERNEC. Using these, the plants present in the collection were identified and classified, as well as the phytochemistry of certain objects. Our collection is composed of 40 items made from nine different plant families and spans fibers, ornamental items, cosmetics, hygiene products, medicine, and weapons. This research highlights the need for preserving scientific data and resources, as well as bridging the gap between science and indigenous plant use.

143 - Analyzing Microbial and Chemical Contributions to Seed Development and Germination in *Spartina alterniflora*

Tara Murano-Castrejon, Barbara Comer, Emma Riley

Georgia Southern University, Savannah, GA

Spartina alterniflora, commonly known as smooth cordgrass, is a vital salt marsh species predominantly found along the Atlantic and Gulf coasts of North America. This perennial grass thrives in intertidal zones, where it plays a crucial ecological role by stabilizing sediment, reducing coastal erosion, and providing essential habitats and energy for diverse wildlife. While the ecology, productivity, and growth of *S. alterniflora* have been extensively studied, little is known about the reproductive ecology of this species, including abiotic and/or biotic influences on seed germination and seedling development. The objective of this experiment was to determine if microbes and/or chemical compounds found in estuarine water play a role in seed development. *S. alterniflora* seeds and estuarine water were collected from two salt marsh locations in Savannah, Georgia. Collected estuarine water was filtered through a vacuum filtration system to remove debris and eukaryotic cells, and half of this filtrate was autoclaved for complete sterilization. To determine if microbes and/or chemical compounds in estuarine water aid in seed development, seeds from each plant were separated into three treatments: (1) control with seeds stored in deionized water, (2) seeds stored in filtered and autoclaved estuarine water (chemical compounds only), and (3) seeds stored in filtered estuarine water (chemical compounds and microbes). Seeds are currently in winter storage to break dormancy at 10°C. In Spring 2025, viability of a subset of seeds will be tested using the tetrazolium-chloride test, after which germination trials will begin. No results are available at this time but if seed viability and germination are greater in seeds stored in filtered estuarine water, then this would suggest that microbes and/or chemical compounds are present that facilitate seed development and germination.

144 - Fifty years of flowering, unripe fruit and ripe fruit phenologies of mountain holly (*Ilex montana*) throughout its range

Claire Epling[1], Nicholas Smith[1], Charles Kwit[2]

[1]University of Tennessee, Knoxville, Knoxville, TN, [2]University of Tennessee Knoxville, Knoxville, TN

Plant phenology (e.g. leaf-out, flowering) has been a topic of increasing interest, particularly during the past century-plus of globally warming temperatures. The timing of successive plant phenophases, however, has rarely been investigated across space and time. Understanding these patterns carries the potential to reveal challenges faced by interacting organisms. We describe the spatiotemporal appearance of flowers, unripe fruits, and ripe fruits of mountain holly (*Ilex montana*) throughout its range in eastern North America via online images of over 1500 herbarium specimens collected primarily between 1972 and 2018 that we categorized into three mutually exclusive phenophases: those exhibiting (1) flowers, (2) unripe fruit, or (3) ripe fruit. Using simple linear models, for each separate phenophase , we examined the effect of year, latitude and their interaction on the Julian date of year of specimen collection (DOY) with analyses of variance. For the presence of flowers and unripe fruits, DOY significantly declined through time, indicating a general advancement of these phenophases through time. For all three phenophases, DOY was significantly affected by latitude; lower latitude specimens flowered and had unripe fruits earlier than higher latitude specimens, while for ripe fruits, higher latitude specimens ripened before lower latitude specimens. This apparent quicker ripening at higher latitudes may be due to elevation and aspect of mountain holly sites at its high-elevation locations in the southern portion of its range, or perhaps genetically-based local adaptation. The latitude-dependent fruit ripening in mountain holly from north to south suggests that ripe mountain holly fruits are available to frugivorous migratory songbirds during their north-to-south transit throughout its range.

145 - Silicon Fertilization: A sustainable Strategy For Managing Crop Disease

Maryann Cagle

Biology Department, College of Charleston, Charleston, SC

Silicon (Si), the second most abundant element in the lithosphere, is an important inorganic nutrient for many plants. While not classified as an essential nutrient, Si is widely recognized for its beneficial effects on the growth and development of numerous plant species. Si has proven particularly effective in reducing disease severity across various plant pathosystems. Key mechanisms of Si-mediated resistance include strengthening cell wall mechanical properties, priming plant defenses by activating signaling pathways that induce defense-related gene expression, and stimulating antimicrobial compound production. This article underscores the significance and practical application of Si fertilizers in integrated disease management for crops.

146 - Identifying Potential Targets of AGL62 in *Arabidopsis thaliana*

Jordyn Smalls, Dongfang Wang

Spelman College, Atlanta, GA

Arabidopsis thaliana is a widely used model organism in plant biology. Similar to other angiosperms, Arabidopsis seed is made of the seed coat, the embryo, and the endosperm. After seed germination, the embryo will grow into a new plant, while the endosperm nourishes the embryo by storing essential nutrients. Proper endosperm development requires Agamous-like 62 (AGL62), which is a MADS-box family transcription factor that promotes syncytial endosperm development in Arabidopsis. However, the specific targets and regulatory pathways downstream of AGL62 are not fully understood. This study aims to answer: "What are potential targets of AGL62 in *Arabidopsis thaliana*?" Our lab has identified over 1,000 down-regulated genes in *agl62* mutant seeds via RNA-seq, 66 of which are known transcription factors. By performing hierarchical clustering on a set of seed-specific microarray dataset that are publicly available, we identified 17 of these transcription factors to be expressed in the endosperm. Among these, AGL33, another member of the MADS-box family, and C2H2 were chosen for further investigation. Given their co-expression pattern with AGL62 and their downregulation in *agl62/-* mutant, we hypothesize that AGL33 and C2H2 are direct targets of AGL62. To test this, we designed and made constructs that contain the promoter regions of these target genes in front of a GUS reporter. The next step is to use these constructs in a protoplast transient assay to test the direct interaction between AGL62 and the promoters of the candidate target genes in plant cells. This research expands the knowledge of transcriptional networks of *Arabidopsis thaliana* and provides a foundation for further investigation into the role of AGL62 in endosperm development.

147 - Breeding System of a Native Southern Appalachian Woodland Perennial (*Clintonia umbellulata*)

Cecilia Spann

Warren Wilson College, Swannanoa, NC

Clintonia umbellulata is a woodland perennial native to the southern Appalachian mountains. It is known to reproduce through rhizomes, but lacks published data on its sexual breeding system. In this study hand-pollination trials were used to test whether *C. umbellulata* is self-compatible or relies on outcrossing, by comparing seed set of self-pollinated plants with that of outcrossed plants. Pollinator limitation was also tested by comparing hand-pollination to an open-control group. The study population was found to be self-incompatible as well as pollinator limited. Within a forest community faced with habitat loss through logging and other human activity, these characteristics of self-incompatibility and pollinator limitation leave *C. umbellulata* vulnerable to future reproductive decline.

148 - Heavy Metal Impacts on *Alternanthera philoxeroides*

Christopher Beals, Katie Pattillo, Brianna Zupko

Abraham Baldwin Agricultural College, Tifton, GA

Investigations were conducted to study the tolerance of *Alternanthera philoxeroides*, or Alligator Weed, to various concentrations (1, 5, 10 ppm) of heavy metals including lead, copper, chromium, and nickel. Alligator Weed is a nonnative invasive plant that has been reported to be an effective heavy metal hyperaccumulator that originated from Brazil and Argentina but has been found infesting freshwater ecosystems throughout the southeastern United States. This study focuses on the ability of Alligator Weed to remove heavy metals from aquatic ecosystems, also known as phytoremediation, and determine metal translocation throughout the plant, such as the stems and leaves. Plants exhibited no increased stress due to heavy metal absorption making this plant an ideal candidate for such things as treatment of wastewater effluent, industrial pollution, or mining contamination of aquatic systems.

149 - Pigment composition and photosynthetic gas exchange in different colored autumn leaves of sweetgum, *Liquidambar styraciflua*

Alex Contreras, Kara Bensel, Nicole Hughes

High Point University, High Point, NC

The breakdown of chlorophyll during autumn corresponds with dramatic changes in leaf colors in temperate deciduous trees. However, several misconceptions remain among the general public and some scientists, related to pigment combinations responsible for certain autumn hues. We utilized the diversity of autumn leaf colors exhibited by sweetgum, Liquidambar styraciflua L., to characterize pigment combinations corresponding with yellow, orange, red, and purple/black autumn leaf colors. Reflectance spectra (400-700 nm) were obtained for three leaves per color using a SpectraSnap leaf spectrometer. Concentrations of total chlorophyll, total carotenoids, and anthocyanins were quantified spectrophotometrically using leaves from 11 different trees, over two field seasons. Histological locations of pigments were visualized under a compound microscope using thin, fresh leaf sections. Photosynthetic gas exchange under saturating irradiance and optimal watering conditions was also measured for different colored leaves of seven individuals. Trends were consistent with some aspects of common knowledge, e.g., yellow leaves result from the "unmasking" of carotenoids (yellow xanthophylls and orange β-carotene) following chlorophyll break-down. However, we demonstrate that orange colors are associated with the presence of low levels of anthocyanin (rather than merely the unmasking of carotenoids). We also demonstrate that red autumn leaves do not result from the unmasking of anthocyanins during chlorophyll breakdown, but rather, their de novo synthesis during leaf senescence. Indeed, not only are anthocyanins absent from green leaves, but their presence in combination with high amounts of chlorophyll results in purple/black coloration. Purple leaves exhibit photosynthesis and stomatal conductance rates in between those of green (highest) and other senescing leaves (lowest), suggesting purple coloration marks an earlier stage in leaf senescence than red, yellow, or orange. The trends we report here are consistent with those in the autumn leaf literature, and can be considered "typical" for other deciduous species that exhibit fall leaf color change.

150 - Functional Traits Influence Canopy Interception of Urban Trees

Noah Manuszak[1], Jorge Vera[1,2], Shane Welch[1], Elizabeth Moss[2], Kyle Palmquist[1]

[1]Marshall University, Huntington, WV, [2]WVSU Extension Service, Charleston, WV

As urbanization and impervious surfaces increase, flooding and pollution from surface runoff will further impact human and ecosystem health. Urban trees can reduce stormwater runoff during precipitation events and help prevent flooding by intercepting water. Previous studies suggest that evergreen trees intercept more water than deciduous trees, especially during the dormant season; however, this

evidence is from a limited number of species and geographic areas. Our work aims to identify which urban tree functional traits are most effective at intercepting and diverting water during precipitation events. Specifically, we asked: (1) which traits of urban trees determine their interception ability? and (2) how does the importance of these traits differ across seasons? We used numerous HOBO tip rain buckets to measure precipitation events and partition canopy interception into throughfall (water that comes through the canopy) and stemflow (water that comes down the trunk). Multiple individuals of five deciduous tree species, one broadleaf evergreen species (Ilex opaca), and one needleleaf evergreen species (Pinus strobus) were instrumented in urban areas of Charleston and Huntington, WV. Trait data were collected for each tree including height, DBH, biomass, leaf area index (LAI), canopy width and volume, canopy cover, wood cover, branch angle, and bark thickness. We used generalized mixed effects models to explore the relative importance of each trait. Our preliminary results suggest that leaf type, tree height, leaf area index (LAI), canopy cover, and canopy volume are important traits that determine how much water trees intercept. During one particularly heavy rainfall event on November 14, 2024, the canopy of an Ilex opaca intercepted 78% of precipitation while a nearby Acer rubrum intercepted 21% of precipitation. As climate change increases the intensity of storms during the dormant season, strategically planting evergreen trees may be one effective approach to mitigate flooding.

151 - Presence of Rutin in Viola species

Noel Cawley

Lincoln Memorial University, Harrogate, TN

Rutin is a flavonoid glycoside that has been reported to have antinociceptive and anti-inflammatory effects. Rutin is known to occur in the viola species, specifically Viola tricolor. The purpose of this study was to determine 1) if rutin is found in other species of Viola, 2) do all plants within a species contain rutin, and 3) are rutin concentrations equal among and between species. Six Viola species were collected from three different locations, not all species were collected from all locations. The presence and relative concentration of rutin was determined by High Performance Thin-Layer Chromatography (HPTLC). Results were highly variable. Viola blanda was collected from three locations but only one specimen at one location contained rutin. There were three samples of Viola rostrata, all of them contained rutin but at different concentration levels. Rutin presence and concentration varied by species and location.

153 - Effects of leaf developmental stage and roasting on the metabolic profile of yaupon holly, a native American tea

Ben Long, Jeffrey Bennetzen

University of Georgia, Athens, GA

Yaupon holly (*Ilex vomitoria*) is an evergreen shrub native to the southeastern US whose leaves can be roasted and brewed into a caffeinated infusion. While production and consumption of yaupon holly tea is growing rapidly, not much is known about what factors influence downstream levels of caffeine and other important metabolites contained within the leaf. To begin addressing these questions, we used targeted and untargeted ultra-performance liquid chromatography-mass spectrometry to measure the effect of leaf developmental stage and roasting — two factors known to be important in other caffeine-containing beverage plants — on the metabolome of yaupon holly leaves. We found that, for plants of the same genotype, caffeine levels were strongly negatively correlated with leaf developmental stage but were not significantly affected by the roasting process. We also were able to identify a key set of chemicals that were highly elevated in the roasted samples, which we hypothesize are products of the browning process that may contribute to the distinctive flavor and aroma of yaupon tea. These findings will help the budding yaupon industry in the southeastern US produce a more consistent, tailored product, as well as lend insight into how leaf biochemistry changes over developmental time.

154 - The impact of exogenous application of plant hormones and silicon on physiological responses of drought-stressed pepper (*Capsicum annum*) Seedlings.

Maryann Cagle, Maiya Buscaglia, Ben Eckert

Biology Department, College of Charleston, Charleston, SC

The exogenous application of plant hormones and a non-essential nutrient element, Silicon, is vital in regulating plant responses to drought stress. Yet, their effects on the growth of pepper (Capsicum annuum L.) seedlings in drought remain underexplored. This study aimed to evaluate the effectiveness of exogenously applied hormones by measuring physiological and biochemical parameters—including chlorophyll content, leaf nitrate and potassium levels, fresh and dry weights, shoot height, and leaf size—in hormone-treated plants subjected to drought stress. The experiment comprised six treatments: (1) control, (2) drought stress, (3) hormones mix (4) combined hormone mix and drought stress, (5) silicon, and (6) combined silicon and drought stress. Hormones and silicon were administered to 14-day-old seedlings, while drought stress was imposed on 21-day-old seedlings. All seedlings were harvested after 30 days for parameter assessment. The results indicated that hormones and Silicon treatments significantly mitigated

the adverse effects of drought on several physiological and biochemical parameters.

155 - Engaging Biology Students in Class Debates

Sahar Hasim[1], Archana Lal[2], Bhaswati Manish[3], Thiru Vanniasinkam[4]

[1]Alabama State University, Montgomery, AL, [2]Labette community College, Parsons, KS, [3]Metropolitan Community College, Omaha, NE, [4]Charles Sturt University, Wagga Wagga,, NSW, Australia

Active learning strategies significantly enhance student outcomes in various STEM disciplines. This poster presentation outlines the implementation of an active learning approach—Class Debate—within undergraduate biology, microbiology, and immunology courses across face-to-face, hybrid, and online formats. This activity enables students to explain the functions of immune cells and understand the interactions that contribute to the immune system's overall function. The objectives include increasing student engagement, improving comprehension and retention of immune cell information, fostering inclusivity and collaborative learning, and developing science communication skills. Assessment methods comprise a pre- and post-quiz featuring six questions at lower and higher levels of Bloom's taxonomy, along with a perception survey to capture student feedback. The results demonstrate the efficacy of Class Debate as an engaging and effective pedagogical tool in STEM education.

156 - Design and Implementation of a Needs Assessment for the Artemis Program for Women in STEM

Mary Jane Carmichael, Kaila Thorn, Michael Gettings, Dan Derringer, Molly Lynch, Darla Schumm

Hollins University, Roanoke, VA

In response to prior proposal feedback that programming interventions were not closely targeted to the needs of our specific population of students, a needs assessment was designed to inform evidence-based student support services and programs for Hollins University's Artemis Program for Women in STEM. Broadly, a questionnaire and focus group were conducted, asking students what was working well for them in STEM and what was not working well for them- academically, socially, and from a wellbeing perspective. The questionnaire was distributed to all STEM majors at Hollins (n=195), with 65 responses, a ca. 33% response rate. A focus group, consisting of students who would have been eligible to receive financial support through the S-STEM program, was also interviewed to determine if the needs of these students were similar to or different from the larger STEM student population. A total of 26 students were invited to participate in the focus group, with 5 attending, a ca. 20% acceptance rate. Results from the questionnaire and focus group were strongly aligned. These data were used to design a tailored, comprehensive suite of student support services and programs which supported the justification of funding for the new Artemis Program for Women in STEM that welcomed its' first cohort of Scholars in the 2024-2025 academic year. Within the institution, these data have also been used to successfully argue for additional funds to be allocated to support tutors in introductory STEM courses and to initiate departmental and institutional conversations about how to better support all STEM majors at Hollins University, a historically women's college.

157 - Innovative Teaching Strategies for Mastering Laboratory Mice Skills: Flipped Classrooms in Biology Education

Feng-Zhi Chen[1], Li-An Chen[1], Cai-Chieh Tseng[1], Ching Hua Pai[1], Kai-En Tsai[1], En-Ci Liang[1], Chi-Wei Chen[1,2]

[1]National Dong Hwa University, Hualien, Taiwan, Taiwan, [2]Appalachian State University, Boone, NC

This study investigates the impact of a flipped classroom model combined with interactive learning tools on student engagement and learning outcomes in a life sciences laboratory course. Despite extensive evidence supporting active learning, the application of flipped classrooms to laboratory-based education remains underexplored. To address this gap, we designed a curriculum for the "Introduction to Laboratory Mice" course that integrates the MITAKA SUPPLY Mimicky® Mouse model with digital tools such as Google Classroom, Kahoot, Mentimeter, Quizizz, and Zuvio. The approach involved pre-class delivery of foundational knowledge, hands-on laboratory training, and interactive peer-learning activities. We conducted pre- and post-tests alongside performance assessments to evaluate students' conceptual understanding and practical skills. Additionally, student outcomes were examined through graded evaluations and direct observation of task competency. Attitudinal surveys provided supplementary data on student perceptions of learning effectiveness, confidence, and engagement. Results showed a significant improvement in knowledge retention, skill acquisition, and student engagement when combining flipped classroom strategies with hands-on practice. Importantly, direct measures of learning outcomes corroborated student-reported benefits, underscoring the efficacy of this approach. This study highlights the potential of flipped classroom methodologies to enhance practical skill development and critical thinking in laboratory courses. Future research will explore optimizing resource use and the long-term impact on student performance. These findings address gaps in applying flipped classroom models to laboratory education, providing actionable insights for instructors in life sciences curricula.

158 - Immersive Learning in Molecular Biology: Exploring Cellular Processes with 3D-Printed Manipulatives and Holographic Technologies

Vonny Salim

Louisiana State University Shreveport, Shreveport, LA

Cellular signaling on the cell membrane is complex and often difficult for undergraduate biology students to grasp, particularly the actions of receptors, molecular switches, and their conformational changes that lead to intracellular events. This challenge hinders their understanding of how multiple proteins on the cell membrane interact with extracellular signals and cause more complex consequences. To address this, we developed 3D-printed manipulatives representing the lipid bilayer membrane structure, integral proteins, and ligands that interact with relevant proteins to demonstrate cellular signaling activation. In the classroom, cell and molecular biology students interact with these models, and observe how components fit together. This hands-on experience helps students visualize the step-by-step process leading to the activation of downstream intracellular pathways. Students then use these models to work on problem sets that explore the consequences of activation in scenarios such as hormone signaling pathways. The detailed models of proteins are also visualized in a holographic environment. This exercise further enhances learning by linking protein structures to their specific functions. Both 3D-printed and holographic models were created through teamwork between science and digital art students, another form of collaborative learning experience in which they integrated artistic and scientific components. The introduction of these personalized manipulatives and holographic tools has significantly improved students' comprehension of the molecular mechanisms of cellular signaling. Here, we present evidence supporting the continued incorporation of these technologies to further enhance the learning of complex biological concepts.

159 - Breadth of knowledge versus curriculum flexibility: Assessing trade-offs in a biology program

Emily Prince, Lisa McDonald

Lander University, Greenwood, SC

The Lander University Department of Biology assesses how much graduates have learned using the ETS Major Field Test (MFT). We can also use the MFT to see how curricular changes affect student knowledge and identify our program's strengths and weaknesses. To understand what predicts student performance on the MFT, we used multiple linear regression to create a model for student MFT scores. We found that some aspects of student MFT performance were determined by student characteristics before they matriculated at Lander, namely standardized test scores and whether they were first-generation college students. However, student MFT performance was positively associated with a high Lander biology GPA. MFT performance was also negatively associated with a 2017 curricular change that increased program flexibility. The revised curriculum allows students to choose courses in areas of interest and resulted in significant increases in graduation rates. To understand the effects of the curricular change on MFT scores more completely, we compared student performance on 9 MFT subscores between the new and old curriculum. In the new curriculum, MFT scores were unchanged for both biochemistry/cell energetics and for diversity of organisms, likely because these areas are covered primarily in the expanded introductory biology courses taken by all students. MFT scores were also unchanged for evolution, likely because the new curriculum now includes a required evolution course. MFT subscores were significantly lower in all other areas. However, students who took more courses on a particular topic (for example, courses focused on plant biology) performed significantly better on that subscore than students with fewer courses on that topic. Overall, our results indicate that students continue to perform well on the MFT in their areas of focus. However, results also suggest a trade-off between curriculum flexibility and breadth of knowledge, which should be considered in curriculum design.

160 - Empowering Undergraduate Success Through a Biology Mentorship Initiative

Maegan Ennis, Sarah Boyer, Shonteria Johnson

Mercer University, Macon, GA

The biology mentorship program was established to support undergraduate students, in Introductory Biology, who may require additional assistance. The mentorship program has also expanded to support students in upper-level courses (Genetics, Animal & Plant Physiology, etc.). The program focuses on offering first-generation and Pell Grant-eligible biology students guidance and support to overcome academic, cultural, and social challenges. For mentors, the program offers personal growth and encourages problem-solving skills, critical thinking, and creativity to address students' questions and challenges. Weekly office hours and regular communication of mentors with mentees ensure a consistent and supportive learning environment, with mentors documenting interactions to track progress and student success. Students benefit from one-on-one tutoring, personalized advice on topics such as study skills, opportunities to foster connections on campus, and access to resources for pursuing on- campus research and pre-professional tracks. The program provides a rewarding experience for both mentors and mentees by fostering academic success and personal development.

161 - Can Corvids Adapt? The Effects of Anthropogenic Noise Pollution on Referential Calls

Miguel Hernandez, Soraya Bartol

Virginia Wesleyan University, Virginia Beach, VA

Corvids are adaptive birds and can be found inhabiting both rural and urban areas. Corvids utilize vocalizations for a variety of signals, including to induce organizational behavior of conspecifics, for social learning and to alert others of food or predators (i.e. referential calls) and thus calls have various meanings depending on the tone and context. Previous studies have shown birds adjust their vocalizations in the presence of anthropogenic noise pollution and adjust antipredator response depending on a number of environmental factors. I investigated whether referential calls are affected by noise pollution in urban areas. Two species belonging to the Corvus genus (American Crow, *Corvus brachyrhynchos*, and Fish Crow, *Corvus ossifragus*) were observed in Virginia Beach, VA., Northeast Texas, and Southeastern Florida between February-December 2024. I recorded 3 types of calls for each species. Subtypes of these calls were identified based on the number of times each call is emitted in a call sequence resulting in a total of 12 *C. brachyrhynchos* and 6 *C. ossifragus* recordings. I then conducted playback experiments, in 10 minute increments, in the morning, midday, and the evening and resulting behaviors were recorded. Results indicate that urban noise pollution did not affect these referential calls and that *C. ossifragus* could respond to heterospecific referential calls. These results could help guide future studies to determine the exact meaning of these calls and communication between heterospecifics and on the effects of noise pollution on other avian species communication.

162 - Eager Empty Nesters: Does Parental Personality Influence Age of Fledging?

Elise Gray, Lynn Siefferman

Appalachian State University, Boone, NC

The timing behind fledging in altricial birds is elusive and rarely studied. But this stage, where offspring transition from dependent nestlings to semi-independent fledglings, is the most important time for developing songbirds. Predation is one of the more studied aspects for the timing of when fledging occurs. This stage is risky as predation is high, and the maturation level of the nestling is what was thought to be the driving process. Maturity level is closely tied to predation, nest predators (e.g., snakes) generally trigger earlier fledging (e.g., less mature feathers), while the opposite occurs for predators targeting independent young (e.g., hawks). Current knowledge suggests that predation drives the timing of fledging, but the role of parent behavior has not been considered. Predation rates vary, but how parents react to predation also varies. Recent studies with different birds, including Tree Swallow (*Tachycineta bicolor*), display consistent personality types. Aggressive individuals may attack or mob a predator, while the opposite would occur for a meek individual. Parents with different personalities may differ in pressure on nestlings to fledge. My research will focus on how the personalities of parents affect the growth rate and timing of fledging in tree swallows. I hypothesize that parental personality influences the age of fledging and predict that the more aggressive parents will rear offspring that fledge at a younger age with less mature wings. During the breeding season of 2024, I followed 119 nests of breeding Tree swallows. I quantified the personality of 73 pairs of breeding Tree Swallows by observing their response to mock predators of nestlings (American crow). I also monitored the growth rate of offspring during the nestlings' stage and then observed the age of fledging.

163 - Relationship between Personality and Offspring Provisioning in Breeding Tree Swallows

Elizabeth Payne, Elise Gray, Lynn Siefferman

Appalachian State University, Boone, NC

Individual variation in behavior, often termed 'personality,' can have important ecological and evolutionary consequences. In many avian species, both personality traits and food provisioning behaviors are linked to reproductive outcomes, yet the connections between these two factors remain poorly understood. Here, we investigate the relationship between parental personality and nestling feeding rates in Tree Swallows (*Tachycineta bicolor*). We captured and individually marked breeding birds and then used standardized predator trials to quantify boldness of parents toward predators. Adults were categorized along a continuum of personality types based on specific defense behaviors, such as diving and circling in proximity to a simulated nest predator. Concurrently, we recorded provisioning efforts—including the frequency of feeding visits and time spent at the nest—to assess how boldness to predators might predict parental investment. Because it was not always possible to discriminate between males and females feeding the young, we focused on overall nest provisioning rates and predict that bolder parents may feed offspring less often. This study aims to identify potential trade-offs or pathways through which personality traits influence fitness-related behaviors. Our findings will contribute to a deeper understanding of how individual differences in behavior mediate parental care strategies and may have broader implications for life-history theory and the evolution of personality in avian systems.

164 - Field data collection using BEAM: preliminary results

Raiz Mohammed, Vien Trieu, Paul Zwiers

Francis Marion University, Florence, SC

Remote data recorders, e.g. camera traps and audio recorders, are an excellent way to collect data while limiting human interference, and at times or locations where continuous observation is difficult. Yet, several significant challenges arise when using deployed hardware, including the need for battery changes and data card collection, leading to added wear and tear, opportunities for dirt and humidity to damage sensitive components, and regular maintenance. In addition, downloading large datasets from data cards can take multiple hours. The BEAM (Biodiversity and Environmental Automated Monitoring) system is comprised of individually deployable, solar-powered nodes, each of which can collect a variety of data using camera modules, high quality sound cards, and terrestrial and aquatic environmental sensors. Nodes are connected wirelessly to a central data acquisition and storage system which acquires data from each node utilizing an automated call/response request. Based on the Raspberry Pi computational platform and running Python, these nodes are inexpensive to produce allowing researchers to blanket a study area, allowing for data to be collected at the micro-habitat level. Our objectives for this project were to create three deployable nodes capable of recording audio, and collecting temperature, humidity, barometric pressure, and luminosity data. Units are powered using "off-the-shelf" solar battery chargers, and data is saved to a removable usb-c flash drive to increase data transfer. Based on these results, our next objectives are to construct a solar-charged battery capable of providing status information including rate of solar generation, battery capacity from new, current battery charge, and power draw. In addition, we will test mesh network protocols allowing for automated data acquisition.

166 - Assessing Color Vision in Crayfish with Conditioning

Lydia DiBiagio, Katherine Torrance, Zackary A. Graham

Department of Biological Sciences, West Liberty University, West Liberty, WV

Despite being most associated with cryptic colors like brown and tan, crayfishes often exhibit conspicuous colors like orange, red, and blue. Surprisingly, the function of such bright colors are unknown. Many hypotheses suggest that crayfish colors serve a function in interspecific communication, but research on crayfish vision is lacking. Physiological evidence suggests crayfishes are either monochromatic or dichromatic, but no studies have behaviorally demonstrated color vision in crayfish. The current study explores whether the blue crayfish, *Cambarus monongalensis* can discern between colored and uncolored stimulus. We conducted classical conditioning trials in an arena with 11 shelters; 4 of which are blue and 7 of which are gray. Gray shelters varied in achromatic aspects (brightness), whereas blue shelters varied in achromatic aspects and chromatic aspects (hue). Five crayfish were obtained and routinely fed in randomly selected blue-colored shelters across a 14-day period. While the study has not yet produced data that can be analyzed, preliminary data suggest some of the crayfish began to associated food with blue shelters.

167 - Temporal and Geographic Genetic Dynamics of the Invasive Kudzu Bug (*Megacopta cribraria*) Across the Southeastern US

Evelyn Page[1], Scott Harrison[2]

[1]James Madison University, Harrisonburg, VA, [2]Georgia Southern University, Statesboro, GA

Megacopta cribraria, also known as the kudzu bug or bean plataspid, is a species of stink bug native to Asia. Since their introduction to northern Georgia in 2009, these legume-eaters quickly colonized the southeastern US, eventually spreading across 15 states. While useful for managing the invasive kudzu vine, kudzu bugs act as nuisance pests and damage soybean crops. A preliminary genetic analysis conducted in 2011 indicated a single introduction from Japan. Now, over 25 kudzu bug generations later, this research aims to characterize their genetic variation over space and time. We hypothesized that genetic variation would increase over time in introduced US populations and that populations at the edges of range expansion would differ in allele frequency from populations at the origin. Genetic variation was assessed in samples collected around the southeastern US in 2013 and 2024 and from two native populations in China using seven nuclear microsatellite loci and the mitochondrial COI gene. Genetic variation was consistently low within and among US populations with an average of 2.24 ± 0.24 (2013) and 2.48 ± 0.35 (2024) alleles per microsatellite locus ($p > 0.05$). Notably, a single mitochondrial haplotype was observed in all US specimens suggesting a single introduction event. Introduced US populations were homogenous over space and time ($Fst < 0.009$) but significantly distinct from Chinese samples ($Fst > 0.360$). COI sequences did not match any database sequences from native populations but phylogenetic analysis indicated a close relationship between kudzu bugs from the southeastern US and from the Kyushu, Japan region. The high level of genetic differentiation of samples from the Kunming region of China (> 6% COI sequence divergence) from all other samples raises questions of species designation.

168 - Total Phenolic content of tomato (*Solanum lycopersicum*) cultivars and the larval development of *Spodoptera frugiperda* and *Trichoplusia ni*.

Johannamarie Nwanagu, Ethan Hughey, Foster Campbell, Dr. Grace Freundlich

Furman University, Greenville, SC

In our study, we investigated whether total phenolic content differed significantly among tomato cultivars and if specific phenolic compounds influenced the growth rates of two generalist herbivores commonly found in Upstate South Carolina. Phenolic compounds were a subject of study for their role in the defense mechanism of many plants, like tomatoes, and in our experiment the total phenolic content was extracted from the leaves of thirteen different cultivars of organic tomatoes using 80% methanol as a solvent and quantified using UV spectroscopy. The effect of the phenolic compounds gallic acid, naringenin, rutin, and quercetin on S. frugiperda and T. ni were measured using a feeding assay in which the subjects were fed insect diet treated with different concentrations of the aforementioned compounds. We found that there was not a significant difference in the total phenolic content of tomato cultivars, with the exception of the heirloom variety Indigo Rose Plum Cherry which was significantly lower than other varieties. However, for S. frugiperda all phenolic compounds have a negative effect on head size and body length with quercetin having the most negative effect. However, T. ni treated with quercetin had a significantly positive effect on body length but other phenolic compounds did not have any significant effect on head size or body length. Our research concluded with many new questions for future avenues of research such as identifying what phenolic compounds would negatively affect T. ni and what was the composition of the total phenolic extract recovered from the different cultivars.

169 - The second invader: Characterization of the bacterial endosymbiont *Wolbachia* in the invasive kudzu bug (*Megacopta cribraria*)

Samantha Haley, Scott Harrison

Georgia Southern University, Statesboro, GA

Bacterial endosymbionts often significantly impact host physiology and ecology and can, therefore, influence ecological processes such as species introductions. *Wolbachia pipientis* is an intracellular endosymbiont common in arthropods that are vertically transmitted to offspring through the egg. *Wolbachia* can have diverse effects on the host, including cytoplasmic incompatibility, mate choice, parthenogenesis induction, nutritional enhancement, pathogen resistance, increased fertility and lifespan, and energy conservation, to name a few. The kudzu bug (*Megacopta cribraria*) is a legume-eating insect native to Asia introduced into northern Georgia in 2009. Since the introduction, kudzu bug distribution has expanded throughout the southeastern US and is now common in 15 states. Kudzu bugs harbor two bacterial symbionts: *Candidatus Ishikawaella capsulata* and *Wolbachia pipientis*. The relationship between kudzu bugs and *Candidatus* is well studied, but that with *Wolbachia* is less understood. This study uses multi-locus sequence typing to characterize *Wolbachia* in kudzu bug samples from early in the US introduction (2013) and current populations (2024). We specifically address the following questions: 1) Did the frequency of *Wolbachia* infection change over time introduced populations? and 2) Is there genetic variation in *Wolbachia* between native and introduced kudzu bug populations or between 2013 and 2024 introduced populations? Preliminary results indicate that all samples from introduced populations are infected with *Wolbachia* and that the level of sequence divergence between *Wolbachia* strains in introduced and native populations ranges from less than 1% to >5%.

170 - *Alloglossidium progeneticum* (Trematoda: Macroderoididae): A parasitic Trematode of Native and Invasive Crayfish in an Urban Watershed

Tyler Bulot, Riccardo Fiorillo

Georgia Gwinnett College, Lawrenceville, GA

Alloglossidium progeneticum is a trematode originally described from the antennary glands of the white tubercled crayfish (*Procambarus spiculifer*) and typically uses a 3-host life cycle (snail, crayfish, catfish). In Georgia, several populations of this trematode show a precocious truncated 2 host life cycle (snail, crayfish) and have been reported in white tubercled crayfish from the Oconee and Flint River watershed (Kasl et al. 2015) and in the Ocmulgee watershed (De La Hoz and Fiorillo, 2016). In 2016, De La Hoz and Fiorillo sampled 3 localities on the Yellow River (Gwinnett Co., GA) and reported an overall prevalence of 57%. In this study, we sampled the yellow river and some of its tributaries. We collected a total of 62 white tubercled crayfish and also 8 red swamp crayfish (*P. clarkii*), an invasive recently reported in Gwinnett Co. GA. In the white tubercled crayfish, we collected 836 worms most of which were heavily gravid, showing again that *A. progeneticum* in this watershed is truncating its lifecycle. The overall prevalence of infection was 89% and greater than in 2016. Comparatively, 50% percent of red swamp crayfish were infected with 62 *A. progeneticum*. Sample size of these crayfish was low, but it is a new host record for this trematode. Overall, host sex and size does not appear to influence infection patterns.

171 - Influence of Environmental Factors on Population Density and Growth of an Invasive Earthworm

Madeline Cecil, Ali Wyer, Jason Ake, Jeremiah Dann

Department of Organismal Biology, Ecology, and Zoo Science, West Liberty University, West Liberty, WV

The eastern United States has seen a great increase in the presence of the invasive pheretimoid earthworm, Amynthas aggrestis. They commonly disrupt the environment by consuming massive amounts of leaf litter and draining usable nutrients from the soil. These worms are greatly under-researched, including knowledge gaps in their population ecology. Understanding the population ecology of invasive species is often the first step is designing methods to slow growth and spread or even extirpate these animals. This study took place from May-July 2024 in the West Liberty University campus woods. During the 2024 field season, Amynthas worm density showed a steady weekly decline. Linear regression models were used to determine whether changes in environmental variables could predict the overall density of Amynthas worms in our study area. Initial analysis found that most of the environmental variables could significantly ($p < 0.05$) predict Amynthas densities for our sampling efforts. A single parameter, soil pH, showed a significant negative effect on Amynthas density during sample week 6 ($p < 0.01$). Although it was not statistically significant, results of linear modeling did indicate that soil moisture may be playing some role in predicting worm densities. Alternate methods of data analysis may increase this significance, or it is possible that the interaction of moisture with other environmental variables may help explain our results. In addition to counts, worm lengths were also measured in the field in an effort to determine the average rate of change for worm length over time. The average rate of change for Amynthas worms for this season was 0.232 cm/week which is lower than rates observed in previous years (0.35 cm/year in 2023). It should be noted that these results are likely impacted by the sharp decline in worm densities compared to previous years.

172 - Garbology: A Passive Survey Technique With Entomological Applications

Jules Stowe, Kimberly Cook, Joseph Burger

University of Kentucky, Lexington, KY

Bottle surveys provide a non-destructive passive survey method for collecting data on both vertebrates and invertebrates in protected areas, such as the North Carolina Highlands, where pitfall traps are either illegal or inefficient. While bottle trapping has previously been used to study small mammal populations (e.g., shrews), its application to insect population dynamics remains undocumented. This study explores the use of bottle surveys to observe insect populations, with a focus on decomposing species. Our survey in the North Carolina Highlands successfully collected mammal skeletal remains and beetle elytra, offering insights into insect decomposition processes and population dynamics in the region. The methodology involved driving along the Blue Ridge Mountain Parkway, stopping at overlooks, and collecting bottles from road-side valleys where litter tends to accumulate. We conducted field work between spring of 2023 and 2024. Bottles (n_T=1061) were labeled as "full" (n_F=76) or "empty" (n_E=985) based on initial observations of debris. Full bottles were processed by isolating and cleaning any potential remains before tagging them with a unique identification number and corresponding location. Beetle elytra, more durable than other insect body parts, can persist in water-filled bottles without decomposition, allowing for extensive data on detritivore species to be obtained through bottle surveys. From 34 pull-off locations, and approximately 100 bottles, we recovered 123 rodent and shrew skeletal remains representing 4 species, with an average of 20-25 beetle shells per bottle containing remains, representing approximately 5 different species.

173 - Sex Differences in Parasitism and Morphology in the Freshwater Snail *Elimia virginica*

Kate Green[1], Abbie M. Tomba[2]

[1]University of Mary Washington, Fredericksburg, VA, [2]University of Mary Washington, Department of Biology, Fredericksburg, VA

The differential impacts of parasitism on male and female freshwater snails by trematodes, a flatworm, is largely unstudied. While trematode diversity indicates the health of aquatic ecosystems, they have a negative impact on snails by sterilizing them. Snails are vital in aquatic ecosystems; they are an important food source, and their role as dominant grazers of detritus and algae improves water quality. To better understand interactions between snails and trematodes, it is necessary to examine how effects of parasitism differ between sexes, as well as the differences in shell morphology and habitat distribution in both parasitized and non-parasitized snails. In this study, snails of species Elimia virginica were collected from the Rappahannock and Potomac rivers; these distinct populations were sampled randomly within 10-15 square-foot quadrats per sampling location, where flow, depth, and substrate size were measured, as well as non-randomly. All were dissected, with the aperture width, length, shell thickness, and shell width measured with digital calipers and the program ImageJ. Sex and parasitism were determined. Parasitized snails were preserved, with the number and size of parasites quantified. Preliminary results indicate that the shells of female snails were overall larger than males ($p < 0.002$), and parasitized snails were generally larger than non-parasitized ($p < 0.0003$, $p = 0.1795$ for shell thickness). Parasitized males and females were the same size ($p > 0.45$); but males were more likely to be parasitized than females ($p = 0.007$), at 10.36% and 4%, respectively. Depth and substrate size were slightly positively correlated with percent parasitism ($p = 0.027$, $r = 0.31$; $p = 0.04$, $r = 0.28$), but further analysis is ongoing. Preliminary results suggest that parasitism is influenced by sex, and habitat usage and life

history differences may account for some of the observed bias.

174 - Pollination Energetics in a Changing Climate

Hannah Wright, Jennifer Geib

Appalachian State University, Boone, NC

Environmental shifts such as warming and drought can limit floral food resources and habitat availability, facilitate novel competition for resources as species ranges shift, and can also result in phenological mismatches between plants and their pollinating counterparts. These environmental conditions also manifest through smaller floral displays and lower quality floral rewards from host plants, in turn making foraging a longer and more energy intensive process for pollinators. This is concerning for bees and other insect pollinators due to their heterothermic nature, and the high costs of thermoregulation they already experience. My research aims to explore the impacts of climate change conditions on bumble bee thermoregulation and energetics during the foraging process by measuring their surface level body temperature using an infrared camera.

175 - Patterns of gregarine parasitism in flat-back millipedes exhibiting mass migration

Reagan Reese[1], Synclaire Motley[1], Tuyen Pham[2], Nhien Le[1], Jennifer Zettler[1]

[1]Georgia Southern University, Armstrong Campus, Savannah, GA, [2]Department of Biology, Georgia Southern University, Armstrong Campus, Savannah, GA

Eurymerodesmus varius is a common species of flat-back millipede that is widely distributed across the Southeastern United States. In the winter, wandering groups of millipedes will enter buildings which can make them a nuisance to homeowners during these short periods of mass migrations. The function of this synchronized group movement is unknown but can be triggered by changes in temperature, humidity or food availability. In our study, we dissected actively migrating millipedes and found gregarine parasites occupying the gut and hemolymph. Gregarines are unicellular apicomplexan parasites that are found in the body cavities and digestive systems of various invertebrates. Though there are many families of Eugregarines, most gregarine parasites in millipedes belong to the Stenophoridae family. While gregarines are often considered parasitic and capable of inducing behavioral changes in their hosts, they can also engage in commensal or mutualistic relationships, offering survival benefits. In this study, we compared the presence, abundance, and diversity of gregarines in both actively migrating and sedentary millipedes.

176 - Parasitism by the twisted-winged parasite *Xenos peckii* (Strepsiptera) and its effects on the reproductive health of their host paper wasp, *Polistes metricus* (Hymenoptera)

Alex Snyder, Jennifer Zettler

Georgia Southern University, Armstrong Campus, Savannah, GA

Strepsiptera are generally described as parasitic castrators as they cause the reproductive death of the hosts. In southeast Georgia, only a handful of paper wasps are hosts for twisted-winged parasites. One such species Polistes metricus is parasitized by a twisted-winged parasite, Xenos peckii. Previous studies document that host survivorship at most developmental stages was not largely influenced by the presence of X. peckii. As a means of determining if X. peckii can affect their host's ability to survive and reproduce, we dissected P. metricus to determine ovary development and presence of X. peckii parasites. Following these dissections, we analyzed abdominal fat levels. We aim to also perform genetic testing to determine both the presence of any undetected larval X. peckii as well as the level of interbreeding between Polistes metricus and Polistes fuscatus, a closely related species to determine if hybridization has any effect on parasite presence, ovary development, and abdominal fat levels.

177 - Go toward the light: Using glow sticks to increase salamander capture in both aquatic and terrestrial traps

Leslie Goebel, Christopher Brown

Georgia Gwinnett College, Lawrenceville, GA

Monitoring salamander populations can be difficult due to the cryptic lifestyle of many species. Surveying seasonal pond-breeding species during mating periods can be accomplished with drift fences surrounding proven breeding ponds. However, this is labor-intensive. Surveying stream-dwelling, fully terrestrial, or wetlands-breeding salamanders is challenging, particularly in urban environments with a range of habitat types and low species density. Recent research has shown that placing glow sticks in funnel traps increases salamander capture rates 2-8 times.

Our study tests the effectiveness of glow stick bait across various aquatic *and* terrestrial habitats in the fragmented suburban landscape of the Yellow River Basin. We set funnel traps (i.e., minnow traps) in a tributary of the Yellow River both upstream (where *Eurycea* brook salamanders have been captured) and downstream of a small impounded residential lake, the wetland floodplain of the tributary (where spotted salamander *Ambystoma maculatum* breeding has been observed), as well as a nearby landlocked retention pond. We expected fewer salamanders downstream of the lake where large predaceous fish are found. We also set pitfall traps upland from the wetland where eastern red-backed salamanders are often observed. To our knowledge, this is the first test of glowsticks on terrestrial salamander capture.

Demonstrating the effectiveness of glow sticks in increasing capture rates across multiple habitats and trap types could be applied to a range of future salamander population studies, increasing efficiency and data accuracy and decreasing cost. Efficiently and accurately estimating salamander populations has important conservation implications, particularly in developing urban areas, as these surveys inform land stakeholders of species' habitat use and movement patterns. Effective trap capture will also aide researchers surveying salamander populations for the appearance of the emerging Bsal pathogen.

178 - Quantifying the effects of restoration efforts on Eastern Hellbender *(Cryptobranchus alleganiensis)* habitat in Virginia's Upper Tennessee River Valley

Bryce Cheers[1], Savanna Busick[1], Zack Edwards[2], Walter Smith[1]

[1]The University of Virginia's College at Wise, Wise, VA, [2]Conservation Management Institute, Virginia Tech, Blacksburg, VA

The Eastern Hellbender (*Cryptobranchus alleganiensis*) is currently undergoing dramatic population declines, with ongoing work aiming to reconstruct appropriate habitat in river reaches that have experienced historic habitat degradation. However, little research has been done examining the effectiveness of habitat restoration efforts. This project aimed to study how a long-term restoration effort affected the viability of degraded riverbed habitat in the Middle Fork Holston River in Smyth County, Virginia. Habitat monitoring for the project began five years ago, with restoration occurring over the last two years. Throughout this period, we compared cover rock attributes, fine sediment intrusion levels, substrate distributions (pebble counts), and hellbender eDNA samples at six approximately 200 m reaches along the Middle Fork Holston River. Three of these reaches experienced restoration efforts that were completed in 2023, while the remaining reaches were unaffected by recent anthropogenic disturbance and served as reference sites. Our results indicate that restoration efforts successfully improved hellbender habitat conditions, placing restored reaches on a similar trajectory as nearby reference reaches. Specifically, fine sediment intrusion levels decreased and rock cover improved at restored reaches. Our results indicate that restoration methods can be used to improve hellbender habitat across the species' range, as well as give us insight into exactly which microhabitat features are impacted by anthropogenic riverbed alterations. Additionally, the data we collected gives us interesting insight into how Hurricane Helene, which impacted our target drainage at the end of our sampling period, affected riverbed structure, the habitat available to hellbenders, and the resiliency of restored river reaches.

179 - A preliminary investigation of temporal variation in the frequency of alternative reproductive tactics in an Appalachian salamander

Sofia Friedman[1], Casey Meisel[1], Cooper Kework[2], Todd W. Pierson[2]

[1]University of North Carolina at Chapel Hill, Chapel Hill, NC, [2]Department of Ecology, Evolution, and Organismal Biology, Kennesaw State University, Kennesaw, GA

Blue Ridge Two-lined Salamanders (Eurycea cf. wilderae) have developed two distinct male phenotypes with discrete reproductive tactics. "Searching" males leave the stream to court terrestrially, whereas "guarding" males guard mates with their powerful jaws in the stream. The proximate cause of these alternative reproductive tactics is a Y-chromosome polymorphism. However, we know little about the mechanisms responsible for maintaining the polymorphism in wild populations. Here, we present preliminary results from the beginning of a long-term study on temporal variation in the frequency of E. cf. wilderae alternative reproductive tactics at Highlands Biological Station. Using a genotyping assay, we characterized the frequency of searching and guarding males for three consecutive cohorts of larvae, and we evaluated the the effect of humidity and precipitation on variation in relative frequency. We also collected data on terrestrial activity to better understand how weather might influence reproductive opportunities in adults. This study system provides a unique opportunity to understand the mechanisms responsible for maintaining variation in a wild population of vertebrates.

180 - Preliminary Assessment of the Developmental Toxicity of Lionfish Venom on *Xenopus laevis* Embryos: Morphological and Growth Impacts

James Rayburn, Alex Barnes

Jacksonville State University, Jacksonville, AL

Lionfish, an invasive species introduced to the Atlantic Coast, have spread into the Gulf of Mexico, threatening its ecological balance. This preliminary study investigates the developmental toxicity of lionfish venom using *Xenopus laevis* embryos as a model through the Frog Embryo Teratogenesis Assay-Xenopus (FETAX). Venom samples were obtained from a deceased lionfish provided by the Dauphin Island Sea Lab's Alabama Aquarium. Dorsal, caudal, pectoral, and pelvic spines, along with venom gland-associated tissues, were dissected, homogenized in FETAX solution, centrifuged at 1,000 RPM for 10 minutes, and the supernatant was collected, aliquoted, and analyzed for protein content. Fertilized *Xenopus laevis* embryos were produced via hormonal induction with human chorionic gonadotropin. Embryos at the small-cell blastula stage were exposed to various concentrations of venom extract for 96 hours in 20x15 mm Petri dishes, with two or four replicates per concentration across two independent experiments. Solutions were refreshed daily. At the end of the exposure period, survival (heartbeat presence), malformations (based on a FETAX atlas of abnormalities), and embryo lengths were recorded using ImageJ. Means, standard deviations, and two-factor ANOVA with Bonferroni's T-test were conducted to determine statistical differences, pooling mortality and malformations by replicate. Results indicated minimal mortality but notable malformations, though not significantly different from controls. However, embryo lengths were significantly reduced, potentially influenced by protein concentration in the venom extract. These findings highlight the need for further research to validate these effects and explore the underlying mechanisms of toxicity.

181 - Sex-specific habitat use across seasons in eastern red-spotted newts *(Notophthalmus viridescens viridescens)*

Marquessa Rillamas[1], Bradley Lamphere[2]

[1]University of Mary Washington, VA, [2]University of Mary Washington, Fredericksburg, VA

The eastern red-spotted newt *(Notophthalmus viridescens viridescens)* is a semi-aquatic amphibian known for its complex, four stage lifestyle, divided into distinct terrestrial and aquatic phases. Previous research done on these newts are indicative of a significant amount of variability in their behavior once they reach adulthood. Since the newts are reliant on wetlands, which can be particularly vulnerable to human activity, knowing their seasonal distribution has the potential to reveal information about habitat preferences and help estimate their survival when environmental conditions change in their habitats. Despite the wide distribution of the eastern red-spotted newt, there are still gaps in the knowledge of their behavior as adults. The primary goal of this study is to explore this gap and assess if there are any significant preference patterns of eastern red-spotted newts across their foraging and breeding seasons, representing differing habitat valuation between seasons. The study was conducted using mark-recapture techniques and also examined if sex influenced habitat preference. This study was conducted in a large freshwater pond with an inlet stream and focuses on aquatic adult newts during the autumn foraging season, the early-winter dormancy season, and the late-winter breeding season. The data show how newts' habitat preferences appear to change throughout the foraging-breeding cycle.

182 - The Effect of In-stream Large Woody Debris Management on Riparian Salamander Population Dynamics

Sydney Hermann[1], Anne Axel[1], Jayme Waldron[1], Chad Landress[2]

[1]Marshall University, Huntington, WV, [2]Monongahela National Forest, Bartow, WV

The addition of large woody debris (LWD) into streams is an increasingly common habitat restoration method for supporting brook trout and other sensitive freshwater species. Instream wood jams interact with streamflow to create localized reductions of water velocity and energy, resulting in increased organic matter retention, overbank flows, and stream habitat heterogeneity. Due to the increased frequency of overbank flows, regions treated with LWD have more interaction between the floodplain and the stream. An increase in floodplain connectivity influences variation in forest habitat variables such as leaf litter, soil pH, woody debris, moisture, and invertebrate abundance. Salamander demographics reflect the stability of these forest habitat variables, making salamanders an ideal biological indicator species that can be indicative of environmental disturbance, stress, or change. We aim to quantify the effect that LWD management actions have on terrestrial and aquatic dwelling salamanders. To investigate the influence of LWD management on salamander abundance and species richness, we conducted terrestrial flip-and-search transect surveys and in-stream leaf litter bag sampling in 3 streams in the central Appalachian Mountains in the Monongahela National Forest, West Virginia. These streams have varying ages of LWD addition (5, 7, 10 years), which we used to define the study sites. We hypothesize that salamander abundance and species richness will increase as the age of LWD additions increase. Additionally, we hypothesize that salamander abundance and species richness will be higher in riparian regions of streams treated with LWD compared to stream

regions not treated with LWD. We aim to conduct N-mixture occupancy modeling with site covariates and an ecological community analysis. Preliminary analyses suggest that aquatic salamander abundance is higher at LWD treatment sites, terrestrial salamander counts at LWD sites have higher variation than counts of aquatic salamanders, and salamander diversity does not appear to be impacted by LWD treatments.

183 - Persistence and Recapture Durations of Marked Hylid Frogs in a Long-Term Pipe Trap Study in North Georgia

Christopher Brown, Olivia McMahon

Georgia Gwinnett College, Lawrenceville, GA

Marked hylid tree frogs have been observed for 3.5-years in the Piedmont ecozone of north Georgia. In 2019, five sets of five pipe traps were placed near buildings on a college campus, and three sets were placed in different habitats (upper edge, interior, and bottomlands) of a nearby wooded area. Traps were checked monthly, and frogs meeting a sufficient size were tagged with Biomark PIT tags. As of this abstract, 27 squirrel tree frogs (*Hyla squirella*), 57 gray tree frogs (*H. chrysoscelis*), and 125 green tree frogs (*H. cinerea*) have been marked. Approximately 50% of individuals were captured again after tagging. Median recapture durations (days between initial tagging date and the date of last capture) were 49 days for green tree frogs, 145 days for squirrel tree frogs, and 186 days for gray tree frogs. One green tree frog was recaptured 808 days (2.2 years) after initial marking. While there was a significant difference in mean recapture durations between species, no difference was found between locations. Grays tend to persist longer than greens on average. This ongoing study highlights the endurance of both frogs and PIT tags in this region. Alternative influences are discussed.

184 - Assessing the efficacy of pattern recognition software in population monitoring of Eastern Newts (*Notophthalmus viridescens*)

Lucas Reynolds

Warren Wilson College, Swannanoa, NC

Salamanders in North America are currently of high conservation concern due to the potential introduction of the pathogen *Batrachochytrium salamandrivorans* spreading in Europe. The Eastern Newt (*Notophthalmus viridescens*) is a widespread salamander species in eastern North America expected to be severely affected by *B. salamandrivorans* given its introduction. Population monitoring is a central component in protecting vulnerable species. Typical methods of population monitoring in salamanders include PIT tagging and toe clipping, which cause physiological stress or injury to the animal. Software-assisted pattern recognition is a newer and noninvasive method of population monitoring that has been successful in other amphibian species. This method allows researchers to perform capture-mark-recapture studies without marking each individual, but instead by comparing photographs of its pattern to those of previously captured individuals. In this study, I examine the effectiveness of the software I3S Pattern+ in correctly matching photographs of Eastern Newts to separate photographs of the same individual. I first compare I3S's matching accuracy between three different photographic databases of 30 individuals. I then examine the software's effectiveness when searching within a larger database of 90 individuals. In the three databases of 30 newts, 83-93% of individuals were matched correctly within the top two results. When testing the larger database, I found no significant difference in matching accuracy from the smaller databases. This supports the use of pattern recognition software in monitoring Eastern Newts, as the majority of individuals were correctly matched in each of three distinct trials. I3S also appears to remain equally effective in a database of 90 individuals. With further refinement of photography and image processing methods, pattern recognition software could be used as an effective and noninvasive method of population monitoring in Eastern Newts.

185 - How methodology impacts biodiversity surveys in salamanders; a comparison of natural cover versus plywood.

Haylie George, Dawson Cashier, Jennifer Borgo Raia

Coker University, Hartsville, SC

Salamanders serve as valuable indicators of ecosystem changes, making accurate sampling methods crucial for detecting environmental shifts. This study aimed to evaluate the effectiveness of coverboards, a widely used technique for sampling salamanders, compared to natural cover objects. While coverboards simulate natural habitats and allow for minimally invasive observation, their accuracy in providing a diverse sample remains uncertain. This study occurred within Kalmia Gardens (Hartsville, SC), a 14-hectare botanical garden bordered by Black Creek that is open to the public. There is a distinct elevation gradient within Kalmia Gardens that may support a larger diversity of salamander species. We placed 81 coverboards split evenly into 9 plots along

that elevation gradient. We also used natural cover which was noted within the 9 different sections. Additionally, microclimate characteristics were recorded for all objects, artificial or natural, under which salamanders were found. Between May and November 2024, we found 3 salamanders under coverboards and 10 under natural cover. The species found were *Desmognathus auriculatus* (4 specimens), *Eurycea cirrigera* (7 specimens), *Pseudotriton ruber* (1 specimen), and *Plethodon glutinosis* (1 specimen) The utilized coverboards were all located within the floodplain for Black Creek, while the salamanders found under natural cover were all within the same drainage area in that floodplain. Overall, there was a low use of coverboards within our area, particularly as we moved away from Black Creek. Most salamanders were found under rocks along a storm water drainage. The age of our coverboards may have impacted their use in this study. Future studies should expand the search of natural cover and evaluate any changes in coverboard use as they continue to age in the field.

186 - Exposure to Ultraviolet Radiation Increases Plasma 25-Hydroxyvitamin D_3 Concentrations in Pine Snakes (*Pituophis spp.*)

Ian Drerup[1], Lorelei Eagle[1], Kinsey T. Skalican Guthrie[2], Zachary Loughman[1]

[1]West Liberty University, West Liberty, WV, [2]Department of Organismal Biology, Ecology, and Zoo Science, West Liberty University, West Liberty, WV

Many species of reptiles require ultraviolet-B (UV-B) light to biosynthesize vitamin D_3, which is needed to maintain proper calcium levels. Despite the importance of UV-B, there is a deficit of knowledge on the effects of UV-B on snakes. UV-B light causes the biosynthesis of provitamin D_3 into pre-vitamin D_3 which is then converted into 25-hydroxyvitamin D_3. Vitamin D_3 is necessary for controlling calcium absorption. This study aimed to investigate the effects of exposure to natural UV-B on plasma 25-hydroxyvitamin D_3 concentrations in snakes of the genus *Pituophis*. Blood was drawn from 15 snakes before exposure to UV-B. 6 snakes (Group 1) were then kept outdoors with exposure to UV-B from the sun for 83 days and 8 snakes (Group 2) remained indoors without exposure to UV-B. After this period blood samples were taken again. After exposure to UV-B, snakes had higher mean 25-hydroxyvitamin D_3 concentrations than initial concentrations. Snakes with exposure to UV-B also had higher mean 25-hydroxyvitamin D_3 concentrations than the snakes kept indoors. The increase in 25-hydroxyvitamin D_3 concentrations seen in UV-B exposed snakes implies *Pituophis* snakes are able to biosynthesize 25-hydroxyvitamin D_3 from UV-B. Providing snakes with UV-B is important for replicating snakes' natural conditions and could have benefits for snake health, welfare, and reproductive success that future studies need to investigate.

187 - Regulation of abscission zone-associated lignification in *Arabidopsis* flowers by the AS1 and BP transcription factors

Dikshya Niraula[1], Sarah Liljegren[2]

[1]The University of Mississippi, Oxford, MS, [2]University of Mississippi, Oxford, MS

Plants have a natural ability to shed organs like leaves, flowers and fruit at specific points during their life cycle. Flowers of the model plant, Arabidopsis thaliana, release their sepals, petals, and stamens after fertilization. Cell separation within specialized abscission zones allows detachment of these floral organs. Within the sepal abscission zone, lignification of a set of cells forms a structural brace that prevents the diffusion of cell wall degrading enzymes. Previous studies have shown that the ASYMMETRIC LEAVES (AS1) transcription factor plays a critical role in flower and leaf formation by restricting expression of BREVIPEDICELLUS (BP). In as1 mutant flowers, ectopic BP activity shifts the position of the sepal abscission zone, which is restored in as1 bp flowers. In this study we examined whether placement of the lignin brace is regulated by AS1-mediated regulation of BP. Using confocal microscopy and basic fuchsin staining, we observed that deposition of lignin in as1 sepals occurs in an inverted V-shape corresponding to the altered position of the abscission zone. However, while the basal position of these lignified cells is rescued in as1 bp sepals, a distally expanded region of lignified cells was observed in as1, bp and as1 bp sepals compared to wild type. Taken together, these results suggest that additional interactions inhibit lignification of cells adjacent to the sepal abscission zone.

188 - Age Predicts Glioblastoma Patient Survivability

Anya Riggins, Jennifer Hurst-Kennedy

Agnes Scott College, Decatur, GA

Glioblastoma, although rare, is a relatively fast-acting cancer. The responsiveness of the cancer to therapies and the outcome of the patient is based on multiple factors. Some of these include environmental, genetic, and exposure to carcinogenic chemicals. In this study, age as a contributing factor for diagnosis was investigated. This was done by using cBioPortal to analyze glioblastoma patient tumor genomic sequencing data from the 2020 Pan-Cancer Atlas. Kaplan-Meier Survival graphs showed there was a clear correlation between age and survival, showing that patients diagnosed at an older age had a poorer chance of survival as compared to someone diagnosed when younger. Oncoprints generated from glioblastoma patient data show there was a higher frequency of alterations in the CDKN2A, CDKN2A-AS1, CDKN2B-AS1, and CDKN2B as patients aged. This suggests that these genes may be involved in the

poorer survival of older glioblastoma patients.

189 - Linking Pectin Modifications to Moss Spermatogenesis through functional characterization of *PpBURP4*

Michael Gilbert, Eric Johnson

Virginia Wesleyan University, Virginia Beach, VA

Spermatogenesis in seedless plants involves the development of chemically unique cell walls, culminating in the production of the only naked plant cells. Through transcriptomic analysis of the model moss *Physcomitrium patens*, we identified a group of BURP domain-containing proteins (BDPs) that are expressed during the late stages of sperm development. Other ultrastructural studies have revealed changes in pectin structure that align with our observed BDP expression patterns. Related studies in *Arabidopsis thaliana* suggest a role for BDPs in pectin modification of the model flowering plant, particularly under aluminum stress.

We hypothesize that BDPs have an evolutionarily conserved function in pectin modification. To test this, the most highly upregulated BDP during *P. patens* spermatogenesis, *PpBURP4*, was expressed in *Arabidopsis* and exposed to aluminum stress. This was to investigate pectin modifications previously linked to the closely related BDPs: Polygalacturonase 1 β-Like (PGL)-1, -2, and -3, whose mutants and overexpression lines exhibit altered root growth and changes in total pectin levels.

Our results show altered root growth in response to aluminum exposure in *PpBURP4* overexpression lines. Additionally, *PpBURP4* overexpression leads to increased aluminum accumulation in trichomes, identified through histochemical staining, mimicking the effects we observe in 35S::PGL3 lines. These findings support a role for *PpBURP4* in modifying pectin structure. Further discussion will include the effects on total pectin levels and quantification of pectin epitopes using a dot blot assay.

190 - Interplay Between Canonical NF-κB and Tumor-Associated Macrophages Regarding CXCL10 Expression

Dalton Ard

Augusta University, Augusta, GA

This study investigated the interplay between bone-marrow-derived macrophages (BMDM) and triple-negative breast cancer (TNBC) cells to determine the role of the tumor microenvironment on the progression of TNBC. BMDM undergo polarization to an M1 or M2 phenotype when activated, with M1 macrophages being tumoricidal and M2 macrophages being tumor-promoting. A number of inflammatory molecules are secreted from these macrophages, such as cytokines and chemokines. The nuclear factor-kappaB (NF-κB) signaling pathway promotes the transcription and release of many of these inflammatory molecules that play a role as either tumor-fighting or tumor-promoting. To effectively knock out the NF-κB pathway, novel p65 knockout mice were used along with LysMCre mice as controls. From qPCR data of BMDMs co-cultured with TNBC, it was observed that the chemokine CXCL10 had a statistically significant increase in expression when p65 was knocked out. To further confirm, a cytokine array showed similar results with CXCL10 protein expression increasing in samples from the p65 knockout mice. Lastly, an invasion assay and a polarization experiment were performed to determine if CXCL10 can induce invasion of TNBC cells and if the polarization of macrophages has a difference on this effect. Along with investigating the effects of CXCL10 on invasion, the contributions of the NF-κB pathway were also analyzed by utilizing p65 knockout BMDMs and control BMDMs to determine whether NF-κB activation or deletion has an effect on promoting TNBC metastasis when treated with CXCL10. Gene expression was determined via qPCR to determine whether treatment of BMDM with CXCL10 altered polarization to M1 or M2 phenotypes.

191 - The Impact of C507 Mutations on Fus1 Fusion Efficiency in *S. cerevisiae*

Kristine Lynn Rodriguez, Jean Smith

Stetson University, DeLand, FL

Cell fusion is a fundamental biological process required for cellular functions such as organ development, placenta development, and sexual reproduction. Understanding the mechanisms behind membrane fusion provides insight into cellular organization and communication, with implications for addressing diseases involving fusion defects, such as cancer. In the yeast Saccharomyces cerevisiae, mating requires fusion, where two different cells fuse to form a diploid. Once the fusing cells come into contact, their cell walls are degraded at the zone of cell fusion (ZCF) to allow for plasma membrane fusion. Fus1 is a transmembrane protein that localizes to the ZCF and is required for cell wall degradation. While gene deletions have confirmed Fus1's importance, this study targeted specific mutations to dissect conserved residue contributions. Along with its transmembrane domain, Fus1 contains a conserved C-terminal SH3 domain hypothesized to facilitate protein-protein interactions and is suggested to act as a scaffold, retaining

essential fusion components at the ZCF. Here, we mutated a conserved cysteine in the SH3 domain, C507, to either alanine (C507A) or serine (C507S). The C507S mutation preserves the general size and polarity of the original residue. While attempts were made, C507A was integrated successfully into E.coli but was unable to bind onto the HO locus in yeast. Mutations were introduced via site-directed mutagenesis and homologous recombination. Cell fusion efficiency was analyzed via growth-based and microscopic assays using a lipophilic membrane dye. We found that Fus1-C507S performed similarly to WT. These findings underscore the importance of the C507 residue in Fus1's localization and function, contributing to a deeper understanding of protein scaffolding and membrane fusion.

192 - Manipulation of Apoptosis and Autophagy During Onset of Symbiosis in the Model Anemone *Exaiptasia diaphana*

Amelia Ousley, Shelby Williams, Angela Poole

Berry College, Mount Berry, GA

Coral bleaching, a critical ecological issue, occurs when elevated ocean temperatures or other stressors cause the coral to expel the dinoflagellates that live symbiotically within them. Coral bleaching negatively impacts both the coral host and the other species living in the reef, leading to decline of the ecosystem. It is known that the cell death processes autophagy and apoptosis play key roles during bleaching, however, their role during the onset of symbiosis has not been thoroughly investigated. More specifically, while apoptosis has been shown to be involved in the removal of incompatible symbionts, autophagy's role during symbiosis onset remains unexplored. Therefore, the objective of this project was to determine if manipulating (promoting or inhibiting) apoptosis and autophagy during the establishment of symbiosis impacted the successful uptake of symbionts. To do so, the anemone *Exaiptasia diaphana*, a model for studying coral symbiosis, was exposed to chemicals capable of manipulating cell death processes. To target autophagy, 3BDO was used to inhibit the process, while rapamyacin was used to promote it. For apoptosis, venetoclax was used to inhibit the process and BAI1 was used to promote it. Anemones were pretreated with each chemical for 24 hours, before the addition of dinoflagellate symbionts at a final concentration of $1x10^4$ cells/mL. After 48 hours, anemones were sampled, and fluorescence microscopy was employed to quantify dinoflagellate uptake. The results indicate that higher concentrations of venetoclax significantly reduced uptake of symbionts, suggesting that activation of apoptosis negatively impacts symbiosis establishment. Conversely, preliminary findings indicate BAI1 and 3BDO have minimal impact on native symbiont uptake, suggesting that apoptosis and autophagy are not activated during symbiosis establishment with compatible symbiont types. Overall, this research advances our knowledge of cell death processes in cnidarians and their role in symbiosis.

193 - Identifying protein domains required for yeast cell fusion

Yireh Martinez, Jean Smith

Stetson University, DeLand, FL

Cell fusion is a highly regulated process that only occurs in certain conditions. It is essential during many stages of eukaryotic life, from fertilization to muscle development, and is an important biological mechanism. Cell fusion in the budding yeast, *Saccharomyces cerevisiae*, serves as an ideal model for examining the molecular interactions required for fusion. Yeast cell fusion occurs when two haploid cells of different mating types join to form a diploid zygote. This process involves cell cycle arrest, transcription of mating-specific genes, and cell polarization towards the mating partner. The fusing cells then connect to form a flat interface called the zone of cell fusion (ZCF). Before their plasma membranes can fuse to form a single cytoplasm, their cell walls must be degraded specifically at the ZCF. One protein known to regulate this process is Fus1, which is a mating-specific transmembrane protein that localizes at the ZCF. Fus1 contains a cytoplasmic C-terminal SH3 domain. Given that SH3 domains tend to mediate protein-protein interactions, Fus1 is thought to act as a scaffold for other fusion proteins at the ZCF. Although one study has found that creating a mutation in the SH3 domain affects the mating efficiency, its exact function is still unknown. Here, we created two truncations of the SH3 domain in the Fus1 protein, one full truncation and one where just the 17 amino acids containing the distal loop and last beta sheet of the SH3 domain are removed. Both truncations were created using molecular cloning methods and included a C-terminal GFP tag for protein localization studies. These mutations were incorporated into yeast using homologous recombination and their fusion efficiency was assayed using both growth-based and microscopy-based assays. We found that both mutations reduced yeast fusion efficiency, suggesting that the SH3 domain is critical for Fus1's function.

194 - Characterization of acetylcholinesterase in two protein fractions for a bioassay of the eastern oyster (*Crassostrea virginica*)

Angela Ayala, Taryn Tu, Ryan Shanks, Nancy Dalman

University of North Georgia, Dahlonega, GA

As filter feeders, eastern oysters (*Crassostrea virginica*) may accumulate contaminants and are commonly used both as a food source and to gauge the health and safety of an environment. Georgia is currently working to develop a sustainable oyster mariculture industry, which will require routine monitoring of the organisms' health. A commonly used bivalve biomarker, acetylcholinesterase (AChE), is used to assess organisms' exposure to pollutants. However, many studies fail to independently characterize the insoluble and soluble fractions of the AChE protein, thus neglecting a potentially unique pool of AChE that may be more sensitive to environmental changes. Failing to distinguish these two unique fractions may diminish the value of oyster AChE as a biomarker. For this study, insoluble and soluble protein fractions were isolated from the gill tissues of oysters collected on Sapelo Island, GA. Western blot analysis was used to measure relative AChE protein abundance, and corresponding enzyme activity was measured using the Ellman's method in the same samples. Our preliminary results suggest the presence of AChE in both soluble and insoluble fractions with the highest overall enzyme activity in the insoluble fraction. Conversely, protein abundance was highest in the soluble fraction. This highlights the importance of measuring enzyme protein amounts when considering measured changes in enzyme activity, which we now suggest should be the standard for future studies. Our data also suggest there may be unique structural differences between AChE in the two fractions with potentially different pollutant susceptibilities. Taken together, these data provide an invaluable resource for coastal managers and scientists for both economic and environmental decisions, as well as for informing future use of AChE as a biomarker.

195 - A second-site mutation partially rescues plasma membrane transport of mutant CFTR-N1303K protein in HEK293 cells.

Kerwin Yost, Mary Ann Garren, Andrea Holguin, Joseph Taylor, Robert Youker

Western Carolina University, Cullowhee, NC

Cystic Fibrosis (CF) is an autosomal recessive genetic disorder caused by mutations in the Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) membrane protein. CF patients can experience symptoms throughout their body, especially in areas such as the lungs, pancreas, or intestines, often presenting as a build-up of excess mucus caused by an imbalance of water and ions in these tissues. The CF causing mutation N1303K occurs in the second nucleotide binding domain (NBD2) of CFTR. This mutation causes the protein to become misfolded and degraded inside the cell instead of being transported to the surface where it functions as a chloride channel. Previous computational work from the Youker laboratory identified two potential second-site mutations (L1254A and L1346F) that could stabilize the NBD2 domain of CFTR. We have successfully expressed GFP-tagged versions of wildtype, N1303K, N1303K-L1254A, and N1303K-L1346F in HEK293 cells. Transport of these proteins to the cell surface was measured using confocal microscopy and WGA-Texas-Red to mark the plasma membrane. Wildtype CFTR had a median Mander's correlation coefficient (MCC) of ~40% compared to 0% for N1303K that is known to be retained and degraded inside the cell. In contrast, The N1303K-L1254A double mutant had a median MCC ~25% suggesting enhanced transport to the cell surface. Interestingly, the N1303K-L1346F mutant that was predicted to help protein stability and transport was not improved (median MCC=0%). Molecular dynamic simulations of the NBD2 domain reveal the N1303K-L1254A double mutant has RMSF, RMSD, and SASA values closer to wildtype values and in contrast to the single mutant N1303K. We are currently optimizing an CFTR activity assay to measure the chloride conductance through wildtype and mutant CFTR proteins to determine if N1303K-L1254A has restored channel activity.

196 - La Crosse Virus detection through optimization of a commercial Immunofluorescence Assay

Hunter Cabe, Brian Byrd, Robert Youker

Western Carolina University, Cullowhee, NC

La Crosse virus (LACV) is an arthropod-borne virus primarily transmitted to humans via infected mosquitoes. Aedes triseriatus is the primary mosquito responsible for spreading LACV and is commonly found in the eastern parts of the United States in hardwood trees. LACV is typically asymptomatic but can cause headaches, fever, vomiting, and more severe symptoms such as seizures and status epilepticus. There are a reported 30-90 neuro-invasive cases per year in the United States, but less severe and asymptomatic cases are heavily unreported, so the true number is not known. Diagnosis traditionally involves serological tests, such as Immunofluorescence Assay (IFA). This research aims to validate and optimize LACV testing methods using a Focus Diagnostic Arbovirus IFA IgG kit. Patient serum samples were tested alongside CDC samples confirmed by genetic methods to be positive for LACV. Two of the three CDC samples were positive based on the IFA. A positive score was returned up to dilutions of 1:128 and 1:512 for the two CDC samples. Only a few of the patient samples tested positive (5 out of 60) while 8 were inconclusive for LACV due to nonspecific staining.

197 - Investigating selective toxicity of targeted DNA damaging compounds on prostate cancer cells

Logan Boyet, Tiffany Bonn, Mackenzie Custer, Sarah Faragher, Kai Smith, Maura Schoppa, Sridhar Varadarajan, Arthur Frampton

University of North Carolina Wilmington, Wilmington, NC

Globally, prostate cancer (PCa) is the second leading cause of cancer-related death in men. Current chemotherapeutics lack the ability to selectively target PCa cells. One common form of treatment is androgen deprivation therapy (ADT), which reduces androgens such as testosterone that function as primary growth signals. A drawback is that mutations within the androgen receptor (AR) can lead to aberrant signaling and activation of AR in the absence of testosterone, a condition termed castration-resistant prostate cancer. Our current strategy is to develop compounds that specifically target the overexpressed AR in PCa cells. This study follows previous research conducted in our labs where we showed the efficacy of similar compounds developed to target the estrogen receptor in breast cancer cells. These targeted compounds will be more effective at specifically destroying PCa cells while minimizing toxicity to normal prostate epithelium. The compounds contain a targeting ligand, a DNA-binding domain, and a methylsulfonate that will form toxic DNA adducts in the targeted cells. There are various forms of these AR-targeted compounds that will be tested on PCa cells. The cell lines include AR-negative PC-3s and AR-positive LnCaps and C4-2Bs. LnCaps are early-stage androgen-dependent, while C4-2Bs are late-stage androgen-independent. Our preliminary data suggests the control testosterone methylsulfone compound displays minimal toxicity that is similar on the three PCa cell lines as expected due to the methylsulfone unit lacking the ability to damage DNA. We will next assess the toxic analog of the control compound, where the only difference is the presence of a DNA-damaging methylsulfonate group. We hypothesize that the methylsulfonate-containing compound will exhibit selective toxicity on the AR-expressing cells (LnCap and C4-2B).

198 - Investigating HuR as a target for the treatment of Metabolic Disease

Ally Goad, Maitri Chauhan, Layla Loftis, Christin Rickman, Jaycob Warfel

The University of Tennessee at Martin, Martin, TN

HuR is an RNA binding protein that regulates cellular levels of a wide variety of RNA. It has long been studied for its role in cancer proliferation, but in recent years its role in the control of cellular metabolism has become an important area of investigation. Various tissue specific knockout mouse models have been generated and have shown that HuR is an important regulator of fat metabolism in skeletal muscle, liver, and adipose tissue, and that knockout of HuR from any of these tissue results in pathology associated with increased fat deposition. Importantly, however, our results as well as others have shown that animal adiposity can be controlled with diet, and that leaner animals show increases in preference for glucose relative to control animals. These studies have highlighted the importance of HuR inhibition in the selection of carbohydrates as metabolic fuel, suggesting a potential avenue for the treatment of metabolic disease. The aim of the present study is to test the efficacy of pharmacological inhibition of HuR to recapitulate the preference of carbohydrates we see in skeletal muscle cells in which HuR has been silenced. Previous studies have shown that a natural, non-toxic biologic compound extracted from *Actinomyces* broths known as MS-444 has the capacity to inhibit HuR action in the cell. We have begun this investigation by performing control experiments in skeletal muscle cells to determine what level of siRNA exposure is necessary to knockdown HuR, and will continue our investigation in cell culture exposed to varying levels of MS-444, followed by analysis of expression of metabolic genes.

199 - Extracellular Vesicle Isolation from Various Sources and Applications

Jack Quintana[1,2], Elyse Zeffiro[1], Elijah Sage[1]

[1]High Point University, High Point, NC, [2]Grekin Labs, MI

Extracellular vesicles (EVs) are small, cell derived, membrane bound pockets of DNA, RNA, proteins, and other bioactive molecules utilized for intracellular signaling. Along with being easy to store, EVs also act as a natural delivery system without the risk of introducing whole cells into the body. Human stem cell EV research has demonstrated incredible immunomodulatory and regenerative effects in the treatment of dementia and ALS in rodents, as well as completely reversing venous skin ulcers in humans. Even so, the harvest of EVs from stem cells can be quite expensive and ethically ambiguous when sourcing from the umbilical cord or embryonic stem cells. Recent research has shown that EVs from other cell types can interact in the human cell ecosystem as a therapeutic treatment. Our research is therefore focused on defining EV isolation protocols from other sources such as bacteria, milk, carrots, watermelon, and invasive Kudzu to create methodologies to be applied at an industrial scale, increasing availability and lowering treatment cost. Furthermore, we intend to extend EV research towards identifying genetic differences using proteomics and transcriptomics, testing cargo modifications, and starting in vivo experiments in rats to study immune system response and wound healing properties with EVs from different sources.

200 - Understanding the Ability of *Bacillus thuringiensis* to Act as an Insecticide Using Mutations in GerE

Tyler Galley, Dinene Crater

High Point University, High Point, NC

Bacillus thuringiensis (*Bt*), a common bacteria used in agriculture, possesses insecticidal properties which are effective at terminating unwanted insects. Previous research suggests that *Bt's* ability to sporulate has contributed to its effects as an insecticide. Typically seen in *Bacillus* species, rather than utilizing typical cell division, they undergo sporulation and form an endospore to continue survival. As a DNA binding protein, GerE has been shown to be crucial in sigma K-associated transcription regulation of sporulation in *Bacillus subtilis*. This project will uncover GerE's role in the ability for *Bt* to sporulate and cause death in insects. As GerE has been found to be active during sporulation, our goal is to find if GerE is crucial in *Bt's* insecticidal properties. Using CRISPR, mutations will be created in *gerE* to determine if this protein is essential for sporulation and insecticidal activity. If wild type *Bt* terminates insects and the GerE knockout strain has no effect on survival, it will be concluded that GerE is essential for the insecticidal properties of *Bt*. This research will significantly contribute to science as this will be the first to determine if the regulation of sporulation is connected with the insecticidal activity of *Bt*.

201 - Phenotype of mitochondrial gene FAM210B knock-out in *Arabidopsis thaliana*

Anastasiya Buryak[1], Sara Cline[2]

[1]Athens State University, Huntsville, AL, [2]Athens State University, Athens, AL

Mitochondrial gene FAM210B is found across eukaryotes. In humans it plays a role in role in metabolic regulation and heme biosynthesis, although the full scope of the functions is still unknown. In this research we are exploring the function of FAM210B in a plant model organism *Arabidopsis thaliana*. *A. thaliana* mutant has been produced through the knockout of the FAM210B gene At2g29040 by T-DNA insertion. Using TAIL-PCR procedure we aim to confirm the location of the T-DNA insertion. Followed by genotyping PCR to confirm the mutants are homozygotes. The second part of this research is focusing on phenotyping the root structure. Through exposure of plants to different media (MS and Iron deficient media), we are monitoring the growth of the wild type, heterozygous, and homozygous mutant plants to see if we can discover any phenotypic differences in the roots. In addition, we will be exposing *A. thaliana* to bacteria, *Paenibacillus endophyticus*. We suspect that FAM210B homozygous mutant might be lethal, so testing such interaction might reveal a phenotype in a heterozygote. Determining the function of FAM210B in plants will provide insight into the role this conserved domain plays in the mitochondria.

202 - Monitering Presence of the endangered Cape Fear Shiner, Notropis Mekistocholas, in the Cape Fear River Basin using eDNA

Gracie Vickery, Megan Rudock-Bowman

High Point University, High Point, NC

The Notropis Mekistocholas known as the Cape Fear Shiner (CFS) is an endangered minnow fish native to the cape fear river basin that commonly schools with sympatric species of notropis. CFS are found in fewer waterways than ever before. Monitoring has traditionally used catch and release netting, which is time intensive and potentially harmful to the CFS. Further, CFS are small and low population numbers may lead to false negative results. Instead, environmental DNA (eDNA) can be collected and analyzedusing custom assays to identify where the CFS are located with improved cost efficiency and accuracy. Sympatric species were identified in the literature and sequences of all COI genes downloaded. MEGA was used to align DNA sequences and create a phylogenetic tree containing CFS. We collected from the Deep, Haw and Rocky Rivers and then filtered on site. Filter paper was preserved in ethanol and on ice until the DNA could be isolated using Qiagen DNeasy PowerWater kit and DNA quality and concentration was evaluated using a NanoDrop. The DNA was amplified using PCR and analyzed with gel electrophoresis. Analysis thus far suggests successful amplification of product that is the desired size inboth unknown and positive control samples. Sequencing of the PCR products is needed to validate the assays and further testing on sympatric species is necessary to rule out false positives.

203 - Identifying potential drug response variants of catechol O-methyltransferase using in silico prediction tools and molecular modeling

Jared Laughlin, Cynthia Stenger, Hanna Joy Jefcoat

University of North Alabama, Florence, AL

COMT is a gene that encodes the protein catechol O-methyltransferase, an enzyme that is involved in the metabolism of catecholamines such as dopamine and norepinephrine. Missense variants of this enzyme have been associated with an altered

response to certain pharmaceutical drugs. In this ongoing study, we are examining potential drug response variants of catechol O-methyltransferase.

204 - Using eDNA to assess the Distribution and Diversity of Native Pollinators in High Point University Campus Gardens

Ellie Ratta, Connor Spitler, Kara Vaartjes, Brian Ragoobir, Megan Rudock-Bowman

High Point University, High Point, NC

The Mariana H. Qubein Arboretum and Botanical Gardens at High Point University is an extensive network of over 30 campus gardens, which include a diverse range of flowering plants. As we look to add pollinator habitats, such as bee hotels, to our campus community it is important to assess the distribution types of native pollinators present so that we may serve them best. The overall goal of this study is to determine if the addition of pollinator habitats to the campus environment has improved the distribution and diversity of native pollinators, by provided safe, easily accessible nesting spaces. In the preliminary study, three gardens were selected based on the availability of flowering plants in the late fall. Flower heads from each of three plants were collected in one liter of water and in a conical tube on ice. Flowers were allowed to soak in the water for a minimum of 2 weeks to allow transfer of eDNA into the water for collection by filtration. Filter paper was cut in half and the DNeasy Powerwater Pro kit (Qiagen) was used for isolation of eDNA from water in duplicate. Frozen plant samples were divided and the DNeasy Blood and Tissue kit (Qiagen) was used for eDNA isolation in duplicate. PCR targeting a partial fragment of the cytochrome oxidase I gene (*COI*) and subsequent metabarcoding analysis (Illumina TruSeq at Azenta) was used detect and identify small arthropods. Further analysis and samples will be necessary to draw conclusions, however we plan to expand this study to the entire HPU Campus Garden system, as well as evaluate how flower species differences and plant locations may impact the amount of eDNA that can be collected.

205 - Characterizing SAMHD1 missense variant R366C and its pathogenic characteristics associated with Aicardi-Goutieres Syndrome

Cynthia Stenger, Andrew Page, Hanna Joy Jefcoat

University of North Alabama, Florence, AL

Aicardi-Goutieres syndrome (AGS), a form of leukodystrophy, is a rare inherited auto-immune disease affecting the brain, immune system, and skin, causing intellectual and physical impairments through white matter damage. The exact prevalence of AGS is unknown, yet 500 people with the disease have been described in scientific literature. SAMHD1, a gene associated with Aicardi-Goutieres syndrome (AGS), encodes a deoxynucleoside triphosphate triphosphohydrolase (dNTPase) enzyme essential for restricting viral infections and maintaining gene stability by regulating dNTP levels. The missense variant R366C of SAMHD1 was studied. Tools such as in-silico predictors, molecular dynamics simulations, ConSurf conservation score, and proximity in relation to known pathogenic variants were used to determine possible variant pathogenicity. Using the tools described above, the R366C missense variant is predicted to be pathogenic, and should potentially be considered in the clinical diagnosis of AGS.

206 - Detection of an Antibiotic-Resistant Gene in Northeast Georgia Water using eDNA

July Morning, Dulce Ruiz, Jeanelle Morgan, Swapna Bhat

University of North Georgia, Oakwood, GA

Bacteria have genetic material in the form of circular DNA, called plasmids. There are regions of the plasmid that contain antibiotic resistant genes (ARGs) that allow some bacteria to withstand antibiotics that would otherwise kill and prevent spread. ARGs exist in nature either intracellularly (iARGs) or extracellularly (eARGs). iARGs are located within the bacteria and are spread through conjugation or transduction, while eARGs are spread through natural transformation and originate from the lysis of dead bacteria (Liang et. al 2021). Recent studies have shown the occurrence of eARGs in water from full-scale wastewater treatment plants and surface water can pose serious health risks due to increased virulence and transmission (Liang et. al 2021). Identification of bacteria with ARGs in wastewater treatment plants in other areas have raised concern as to whether these ARBs and ARGs are present in North Georgia waterways. A previous study identified at least one antibiotic-resistance gene (the *bla* gene) from a local wastewater treatment plant that runs directly into Lake Lanier, a main drinking water source for the Atlanta area (Moua et. al 2024). In this study, the presence of bacteria has been successfully observed in Flat Creek, a stream near a water treatment facility using PCR methods of detection. Conduction of qPCR will provide clearer results for the presence of the antibiotic-resistant gene, *bla*CTX.

207 - Bioinformatics Analysis of POGZ Variants in Relation to White-Sutton Syndrome

Hannah Rollins, Lauryn Staples, Jenna Ridlen

Jacksonville State University, Jacksonville, AL

White-Sutton Syndrome is a neurodevelopmental disease that results in physical abnormalities, intellectual disability, and in some cases, epilepsy. Using Simple ClinVar, two genes were discovered to have genes associated with White-Sutton Syndrome: POGZ and CLI3. POGZ is associated with sixteen missense variants of uncertain pathogenic significance, whereas CLI3 is only associated with a single variant of uncertain pathogenic significance.

POGZ was the gene chosen for this research due to it having a higher association with White Sutton Syndrome. POGZ is a gene that encodes for a protein involved in mitosis- specifically chromosome separation, sister chromatid cohesion, and kinetochore assembly. POGZ plays a critical role by managing different stages of mitosis. Mutations in POGZ disrupts functions of mitosis, which lead to developmental defects commonly leading to neurodevelopmental disorders such as intellectual disabilities, autism, and microcephaly. POGZ is located on loci 1q21.3, which is a region crucial for chromosome segregation and central to brain development and function.

This research will use several bioinformatics and protein modeling tools to ascertain the pathogenicity of variants. The results of this research will determine the pathogenicity of a POGZ variant of uncertain significance in relation to White-Sutton Syndrome.

208 - Comparing the 3D chromatin organization of breast cancer subtypes through Hi-C analysis

Avery Underwood, Jenny DeLustro, Dr. Andrea Perreault

Elon University, Elon, NC

With breast cancer affecting a large portion of the population, finding effective methods of treatment is an increasingly strong demand. Cancer is a result of incorrect gene expression resulting from abnormal 3D chromatin organization. Through breast cancer research, specific targets have been identified to strengthen prognosis and efficacy of treatment. This project aims to find differences between breast cancer subtypes to aid in identification of specific genetic structures and expression for cancer treatments. Through Hi-C analysis, comparisons can be made between the different subtypes to find unique features of genome organization in each subtype. Hi-C is an experiment that identifies interactions between regions of DNA, allowing us to analyze 3D structures and chromatin organization. This data can be used to make contact maps that show where the chromatin interactions are occurring. This can show unique structural elements in the subtypes such as TADs and chromatin loops. This research will identify and explore how the chromatin interactions are similar and different in 2 breast cancer subtypes (ER-positive and TNBC). Contact heat maps will be used to visualize contact frequency from Hi-C datasets and find chromatin loops and interactions. Then, combining this data with RNA-seq data, we can see the expression of genes and what the structure looks like at those areas. Both breast cancer subtypes will be compared against each other to find similarities and differences. The expected results will suggest that TNBC has the most variability compared to normal-like cells. Based on previous results in the lab, we expect that 3D organization of ER+ and TNBC samples will be the most different, contributing to the vast differences in gene expression profiles. Investigating breast cancer subtypes will provide insights for more effective precision medicine therapies for breast cancer patients.

209 - Environmental drivers of microbial community composition in aquatic ecosystems: Insights from the Upper Saluda watershed

Justina Bossa, Jayla Ward, Emily Prince, Melissa Hayes

Lander University, Greenwood, SC

The microbial community composition in aquatic ecosystems varies in part due to environmental factors like nutrient availability and pH. However, it is challenging to directly specify which environmental conditions drive the differences among these communities. The goal of our research is to determine the relationship between environmental characteristics and bacterial communities in the Upper Saluda watershed in South Carolina. As a first step, we measured the physical and chemical properties of the different sites and applied principal component analysis (PCA) to characterize them. We collected water samples from thirty different sites throughout the watershed and categorized them as either lake, ponds, rivers or streams. We measured latitude, elevation, depth, temperature, pH, conductivity, as well as the concentration of nitrate, nitrite, ammonium, phosphate, dissolved oxygen, and chlorophyll a. The PCA established which sites were similar to or different from each other and what properties were driving these differences. PC1 separated sites by habitat type; lake, pond, stream, or river. The division was driven by chlorophyll a abundance, which was higher in both ponds and lakes than river and streams. PC2 separated sites based on nitrogen forms, with some sites characterized by high ammonia concentrations and others by high nitrite. Taken together, PC1 and PC2 account for 79% of the total variance among the sites. As a next step, we extracted DNA from 100 mL of water at each site using Quiagen DNeasy PowerWater Kits. DNA samples will be sent

for Illumina MiSeq high-throughput sequencing to characterize the bacteria in the community. At that point we will be able to determine the extent to which the physical and chemical conditions are related to the microbial community composition at each site.

210 - Investigating Protein-Protein Interactions at the Phage-Host Interface of Bacteriophage Cain

Layla Herndon, Victoria Frost, Kathryn Kohl

Winthrop University, Rock Hill, SC

Bacteriophages (phages), viruses that infect bacteria, have coevolved with their bacterial hosts for 3.5 billion years. Phage biology is a vastly uncharted territory, with little knowledge about the identity of phages, phage genes, and the ways in which they interact with their bacterial hosts. Identifying interactions between individual phage proteins and their bacterial host's proteome helps predict a possible role of those phage genes during infection. Additionally, investigating these interactions allows for connections to be made between different phages that share homologous genes. To initially screen for interactions between a phage protein and its host's proteome, the phage gene can be transformed into the host, and any effects on the host growth following gene induction can be observed. By using this phenotypic approach (termed a "cytotoxic assay"), Winthrop University's SEAGENES students have previously characterized mycobacteriophage Cain: a K6 subcluster phage. Twenty-two percent of Cain's predicted genes appeared cytotoxic when overexpressed in the host. Two cytotoxic Cain genes (*35* and *84*), and one non-toxic gene (*40*), were selected to investigate the protein-protein interactions occurring between Cain proteins and the host bacteria *Mycobacterium smegmatis* in more detail. A Bacterial-2-Hybrid assay has demonstrated that there are true interactions between all three Cain proteins and the host bacteria. Studies to further investigate these interactions, and to identify the proteins involved, are underway to help elucidate the possible role of Cain genes *35*, *40*, and *84*. Overall, identifying phage-host interactions will contribute to a greater understanding of phage biology, which is critical for the applicative use of phages.

211 - *Aeromonas hydrophila* alters growth, biofilm formation, and swimming motility at host and aquatic temperatures in response to polyunsaturated fatty acids

Lydia Byerly, Meredith Grant, Gillian Morton, David Giles

The University of Tennessee at Chattanooga, Chattanooga, TN

Aeromonas hydrophila is an aquatic, gram-negative bacterial pathogen of fish and humans. In humans, the pathology of *A. hydrophila* itself through skin and tissue infections, gastritis, and septicemia. Many treatments for this bacterium are currently ineffective due to antibiotic resistance. It is becoming increasingly evident that gram-negative bacteria utilize polyunsaturated fatty acids (PUFAs) as signaling molecules that can control phenotypes associated with virulence. This study explored the temperature-dependent effects of PUFAs on *A. hydrophila's* planktonic growth, biofilm formation, and swimming motility. Variable growth effects were observed over 12-hour growth curves using PUFAs as either supplemental or sole carbon sources. Several PUFAs caused statistically significant changes in both biofilm and soft agar assays. Collectively, the data revealed PUFA-mediated adaptive behavioral responses at temperatures defining *A. hydrophila's* biphasic lifestyle.

212 - Isolation of Glyphosate-Degrading Microbes from Agricultural Samples and Potential for Future Applications

Savanna Eggenberger, Amber M. Smith, Jamie Champasouk, Rachel E. Diner

University of Memphis, Memphis, TN

Glyphosate (GLY) is the active ingredient in Roundup, a broad-spectrum herbicide widely used in both commercial agriculture and home landscaping. While not currently thought to pose a risk to humans when used as directed, GLY can have a negative impact on aquatic life and beneficial microorganisms even at low levels of exposure. The discovery of novel microbial taxa and the metabolic pathways involved in GLY degradation will enable a deeper understanding of microbial functional diversity and increase the potential for beneficial bioremediation applications. We collected diverse agricultural samples from soil, irrigation runoff water, sediment, and plants and incubated the microbial communities in GLY-enriched Bushnell-Haas media over a period of ~30 days. 39 total isolates were characterized using 16S Sanger sequencing, and, despite being largely unique compared to similar sequences on the NCBI database, many had close homology to known GLY-degraders (e.g., Pseudomonas). Furthermore, of the 39 strains sequenced, 22 demonstrated potential GLY resistance during preliminary growth monitoring. Our ongoing research aims to further characterize these isolates' GLY degradation capacity by looking at factors such as degradation rate and environmental limitations. We also plan to determine the primary active pathways used by the isolates and identify any potential impacts or beneficial applications the microbes may have on crop soil systems and water quality.

214 - The Microbial Ecology of Cold Sulfur Springs in Blount Springs, Alabama

Kevin Drace

Samford University, Birmingham, AL

The former resort town of Blount Springs, Alabama, was built around several sulfur springs. These springs are characterized by a sulfur-rich aquifer that reaches the surface, forming narrow streams that merge before joining additional water sources. Cold sulfur springs are recognized for their distinctive microbial communities, often dominated by sulfur-oxidizing and sulfur-reducing bacteria, which play critical roles in biogeochemical sulfur cycling. The microbial composition of streams in Blount Springs was analyzed by swabbing organic biofilms growing on leaf matter, comparing white-filament-covered leaves, purple-stained leaves, and a nearby control stream. Distinct clustering of microbial communities was observed among the three sample types. As expected, the control stream exhibited high microbial diversity, dominated by *Melosira* (18%), a photosynthetic diatom. Purple-stained leaves were dominated by *Chromatium* (20%) and *Chlorobium* (13%), both sulfur-oxidizing, anoxygenic, photosynthetic purple-sulfur bacteria. Swabs of white-filament-covered leaves showed a dominance of *Halothiobacillus* (30%) and *Sulfurovum* (15%). In contrast, the thick white biofilm collected independently was dominated by *Sulfurovum* (59%) over *Halothiobacillus* (13%). Both species are chemolithotrophs utilizing sulfur compounds as energy sources. Notably, *Sulfurovum* was also prevalent in the purple-leaf samples, underscoring its ecological importance in these sulfur-rich environments. These findings highlight the role of sulfur-utilizing bacteria in structuring microbial communities within Blount Springs and suggest a potential interplay between light availability and sulfur metabolism.

215 - Evaluating the expression of virulence genes essential for glucose metabolizing pathway of *Shigella flexneri*

Daniel Bohler[1], William Garcia[2], Jessica Wade[1], Kingsley Dunkley[1]

[1]Department of Biology-Abraham Baldwin Agricultural College, Tifton, GA, [2]Dental College of Georgia at Augusta University-Oral and Maxillofacial Surgery Department, Augusta, GA

Shigella flexneri (SF) is a gram-negative, opportunistic bacteria that invades the colonic and rectal epithelium. This bacterium is responsible for causing an intestinal infection known as shigellosis, a worldwide human health concern with approximately 164 million cases reported each year. Developing countries experience a high incidence of shigellosis due to the lack of clean water, and the presence of poor sanitation and malnutrition. In this study, SF (ATCC 29903) was grown in Luria broth (LB) at pH 7 with 0.3% glucose. Triplicate samples were collected every two hours, from 0-10 hours and were subjected to various assays including glucose analysis and gene expression. An aliquot (400 µL) of the culture was preserved immediately in 800 µL of RNAlater and stored at -20°C for analysis. We evaluated the relative expressions of virulent genes associated with SF: these include virF, which is a transcriptional virulence activator, and csrA and pfkA genes associated with glucose metabolism. Results determined that the amount of glucose utilized by SF is directly correlated to the growth rate during incubation after 3 hrs. It is assumed that these virulence genes allow the microorganism to flourish and colonize the GI tract during infectious conditions. There is evidence to suggest that csrA, pfkA, and virF genes are induced during exponential and stationary phases, and may influence bacterial growth rate, which aids in its invasion and is possibly one of the causes of shigellosis infection.

216 - *In vivo veritas:* transcriptomics reveals expression patterns driving pathogenicity of hypervirulent *Aeromonas hydrophila* in channel catfish

Dr. Priscilla Barger, Ph.D., Xu Wang, Haolong Wang, Joseph Newton

Auburn University, Auburn, AL

Aeromonas hydrophila, a Gram-negative bacterium ubiquitous in freshwater ecosystems, is a common opportunistic pathogen in Southeastern channel catfish (*Ictalurus punctatus*) aquaculture systems. Typical *A. hydrophila* (tAh) is regarded as a secondary pathogen, causing sporadic disease in stressed fish. However, in 2009, a highly virulent strain, termed hypervirulent *A. hydrophila* (vAh), emerged in Alabama catfish production ponds. This strain caused widespread mortality in healthy, market-sized fish due to peracute motile aeromonad septicemia (vMAS). Epidemic-scale vMAS outbreaks have led to catastrophic losses in the Southeastern catfish industry and remain the leading cause of fish disease mortality in Alabama production systems. While some differences exist, genomic comparisons between vAh and tAh strains found most classes of virulence factors distributed similarly across isolates. Despite this, vAh exhibits significantly greater pathogenicity. The disparity in virulence between these pathovars suggests that vAh hypervirulence may be an adaptive response to its environment, characterized by the differential expression patterns of virulence-associated genes rather than the presence of unique genomic virulence factors. Upon introduction into U.S. catfish ponds, vAh, historically a pathogen of carp, may have evolved different gene expression patterns to optimize its fitness for a new host and environment. This may include upregulation of genes that facilitate colonization, immune evasion, and tissue invasion. To investigate this hypothesis, whole-genome transcriptomic analysis was performed on vAh strain ML09-119 cultured within the peritoneal cavity of

market-sized channel catfish. Our findings revealed significant upregulation of genes and pathways involved in adhesion, toxin production, proteolytic activity, iron acquisition, mucin degradation, immune evasion, reactive oxygen species detoxification, and cell envelope repair. These genes likely play critical roles in vAh invasion and colonization, correlating with severe disease outcomes in catfish. This study provides valuable insights into the genomic adaptive responses of vAh and identifies potential targets for disease prevention and treatment in aquaculture systems.

217 - The Safety of Oyster Consumption: Assessing Bacterial Concentrations and Antibiotic Resistance of *Vibrio* Species in Oysters from Georgia's Coast

Alyssa Pold, Dobrusia Bialonska, Paul Johnson, Nancy Dalman

University of North Georgia, Dahlonega, GA

Some *Vibrio spp.* are commonly found in shellfish and pose threats to consumers of oysters. *V. parahaemolyticus* is the leading cause of seafood borne illness worldwide, while *V. vulnificus* can cause life-threatening necrotizing fasciitis and other serious illnesses. As Georgia expands its oyster mariculture industry, it is imperative to continuously monitor the safety of harvests. To address these concerns, we have begun assessing oyster safety by conducting long-term quantification of bacterial loads present in oysters and antibiotic resistance patterns in samples collected from Sapelo Island, GA and Brunswick, GA. Oyster tissues homogenized in normal saline were plated on CHROMagar™ Vibrio, incubated for 24 hr at 37°C, then colony forming units were counted. Thus far, concentrations of *V. parahaemolyticus* have been seen to reach, or exceed, FDA regulations for safe consumption extending into harvesting season which normally is considered safe for oyster harvesting. Currently, *V. vulnificus* bacterial loads are being evaluated for possible temporal trends. Antibiotic resistance has been assessed by creating a lawn of fresh cultures on MHII agar with Liofilchem® MIC strips, incubating for 24 hr at 37°C, then examining for resistance against Ampicillin and Ciprofloxacin based on CLSI standards for *Vibrio spp.*. Thus far, resistance to both antibiotics has been observed with *V. parahaemolyticus* over multiple time periods and collection sites. Currently, antibiotic resistance in *V. vulnificus* samples is also being assessed. Both the high bacterial loads and presence of antibiotic resistance expose consumers to pathogens that may be more difficult to treat. Data collected and examined, to date, suggests that further research is necessary to draw conclusions about the safety of developing oyster mariculture on Georgia's coast, and this work will hopefully provide a framework for the further evolution of the industry.

218 - Culture and Characterization of Nitrifying Bacteria for Optimized Seeding of Aquaculture Systems

Christopher Bryan[1], DeLacy Rhodes[2]

[1]Berry College, Mt Berry, GA, [2]Berry College, Mt. Berry, GA

Nitrogen is an integral element in the production of biological molecules. In plants, nitrogen is a necessary component of photosynthesis, but for an organism to use it, it must be in a form that the organism can assimilate. Nitrogen in the form of ammonia or nitrite is toxic to most organisms, but some prokaryotes can use this ammonia to obtain energy in a two-part process called nitrification, usually completed by two separate organisms. The first step of nitrification involves ammonia-oxidizing bacteria (AOB) breaking down ammonia (NH_3) into nitrite (NO_2^-) while in the second step nitrite-oxidizing bacteria (NOB) break down nitrites to form non-toxic nitrate (NO_3^-). Understanding the rate and ability of these microbes to carry out nitrification is important, as removal of ammonia and nitrite are necessary for the health of aquatic ecosystems and aquaculture systems. The goal of this project is to culture and characterize a species of both AOB and a species of NOB for the purpose of determining the most efficient way in which to prepare aquaponics tanks. A commercially available AOB species, *Nitrosomonas europea* (ATCC 19718), was first characterized through the establishment of growth curves using florescence microscopy and charting ammonia oxidation rates using colorimetric reactions and spectrophotometry. A single species of NOB is purchasable, but its environmental relevance is questionable; therefore, various NOB were isolated from environmental samples. Isolation was achieved through enrichment over several months, density dependent centrifugation, and serial dilution prior to 16s rRNA sequencing. Growth curves and nitrite oxidation rates were established using the same methods as for AOB. For both AOB and NOB, cell density was correlated with ammonia/nitrite oxidation and will be used to determine future experiments investigating the optimal ratios and seeding timing for both AOB and NOB species for the optimization of creating commercial and household aquaponics systems.

219 - Correlation of oral hygiene and consumption with oral biofilm flora.

Andrew Pettry, David Chambers, PhD

Concord University, Athens, WV

Plaque is an oral biofilm that accumulates on teeth having both positive and negative effects. The bacteria within this biofilm can help to maintain tooth mineralization and protect from acid exposure; however, build-up of plaque can also lead to dental caries and the more severe conditions of gingivitis and periodontal disease. Flora of patients with better oral hygiene tend to contain greater amounts of gram-positive bacteria, while the flora of patients with poorer oral hygiene tend to contain greater amounts anaerobic gram-negative

bacteria. To better understand the possible correlations between oral hygiene factors and oral bacterial flora, we will use MinION 16S ribosomal sequencing of collected samples and correlate them with a completed questionnaire from each donor. This will allow us to evaluate bacterial species that correlate with the different conditions.

220 - Employing ddPCR for microbial source tracking in central Alabama watersheds.

Kellan Hoffman, Julie Olson

The University of Alabama, Department of Biological Sciences, Tuscaloosa, AL

Alabama has over 200,000 kilometers of rivers and streams, a precious natural resource frequently used for recreational purposes and serving as an important source of drinking water to more than one-fourth of the state. Unfortunately, the introduction of unprocessed human wastewater originating from various sources (e.g., overflowing wastewater treatment plants or sewer systems, septic tank failures, etc.) and manure from concentrated animal farming operations are common occurrences throughout the state, putting humans, animals, and the ecosystem at risk. To investigate sources of fecal pollution, the Olson lab partnered with Riverkeeper organizations in the Black Warrior, Cahaba, and Coosa watersheds, who collected monthly river water samples over two years at fifteen locations (ten constant and five variable) within each watershed. Droplet digital PCR (ddPCR) was performed on genetic material extracted from vacuum-filtered river water samples to determine the presence and concentration of Bacteroides, a gut-obligate, anaerobic bacterial genus, an emerging bacterial marker and surrogate for fecal contamination in microbial source tracking studies. To further inform source tracking efforts, a novel multiplex ddPCR assay was designed to discern the host origins of observed Bacteroides concentrations. From these data, the Olson lab was able to identify reaches of the Black Warrior, Cahaba, and Coosa watersheds with potential point and/or non-point sources of fecal pollution. These data will assist Riverkeepers in their efforts to foster community engagement in river conservation and allow for the efficient use of their limited resources as they pursue litigative action against corporate polluters. Monthly precipitation rates, factors that heavily influence movement of fecal material into and through river systems, were also included in the analyses of this ongoing multi-year source tracking study. Additionally, quantitative microbial risk assessments are currently being developed using ddPCR multiplex results to determine risks to human health at sampling sites within the three watersheds.

221 - The Comparative Effects of *Eucalyptus globulus* and *Thymus vulgaris* on Corynebacterium pseudodiphtheriticum Growth

Chelsea Brown[1], Wanda Schroeder[2]

[1]Wesleyan College Department of Biology, Macon, GA, [2]Wesleyan College, Macon, GA

Opportunistic pathogens are growing in resistance as the use and overuse of antibiotics increase. One such organism, Corynebacterium pseuduodiphtheriticum, is a part of the normal skin and upper respiratory commensal flora; however, in immunocompromised individuals, it can cause infections in the lower respiratory system and contribute to pneumonia and chronic wound infections. In these individuals, C. pseudodiphtheriticum is difficult to treat because of its increasing resistance to commonly used antibiotics, such as penicillin and erythromycin. Thus, identifying alternative antimicrobial compounds that can limit C. pseudodiphtheriticum growth is of considerable interest. Examination of the antimicrobial properties of volatile aromatic compounds derived from plants ("essential oils") has become a hotspot for research as an alternative to antibiotics. Previous research in our lab has demonstrated significant antimicrobial affects of white thyme and tea tree oil against opportunistic pathogens such as S. aureus and S. epidermidis. To expand our understanding of aromatic plant compound's antimicrobial activity, the current study tested White Thyme oil, to determine if these extracts might influence the growth of Corynebacterium in contrast to Eucalyptus. Eucalyptus globulus dilutions of 1:2, 1:5, and 1:10 were tested against C. pseudodiphtheriticum and yielded no inhibition zones. Though E. globulus did not inhibit the growth of the bacteria, other oils such as White Thyme, or Thymus vulgaris, are known to have high antibacterial activity because of their different chemical composition. The current study tested the antimicrobial activity of dilutions of T. vulgaris against C.pseudodiphtheriticum, and yielded large zones of inhibition as concentration increased. The differences in the chemical composition between the oils, as well as the genome of Corynebacterium, may have played a role in the change of inhibition.

222 - Characterization of Basic Growth and Virulence Factors of *Ewingella americana*

Abigail Neff, William Penwell

Jacksonville University, Jacksonville, FL

Ewingella americana is a Gram-negative bacteria first discovered in 1983 and is considered to be a rare emerging human pathogen. More commonly seen in brown rot infections of mushrooms; however, this pathogen has been linked with human diseases such as bacteremia, lower respiratory infections, peritonitis, and urinary tract infections. Though human infections are uncommon, previous nosocomial outbreaks, as well as the bacteria's impact in fungi agriculture, demonstrate a need for a better understanding of the bacteria. Little research has been completed on the bacteria's pathogenic potential, other than genetic analysis. Genetic analysis

revealed a number of potential virulence factors, including temperature-related genes similar to *Listeria monocytogenes*, but few actual basic microbiology experiments have been completed. Conflicting reports on its growth temperature range indicate a need to establish optimal growth temperature and its ability to grow at lower temperatures. The focus of our experimentation is to establish the bacteria's growth characteristics, biofilm formation, and production of antimicrobial compounds against other bacterial pathogens. The study is completed on three different strains for *E. americana*, one from a soil sample from Jacksonville, FL, and one from a brown rot mushroom infection, and the ATCC strain which comes from a human infection.. Initial studies indicate *E. americana* produces an antimicrobial compound against *Acinetobacter baumannii, Stenotrophomonas maltophilia,* and *Klebsiella pneumoniae*. Temperature growth experiments indicate the bacteria does grow at 4°C, validating the genetic presence of genes similar to *Listeria monocytogenes.*

223 - Characterization of extracts obtained for *Streptomyces*

Alleigh Ward, Taja Mathews, Richard Watkins

Jacksonville State University, Jacksonville, AL

Bacteria in the genus *Streptomyces* are widely recognized as a source of antimicrobial compounds. *Streptomyces* is also emerging as a promising source of compounds with anticancer properties. In this work, we utilize a crowdsourcing approach to obtain strains of *Streptomyces* from multiple Collaborative Undergraduate Research and Engagement (CURE) labs to evaluate these metabolites. Streptomyces strains were cultivated under optimized conditions to enhance secondary metabolite production, and crude extracts were obtained through solvent-based extraction. The antimicrobial activity of these extracts was tested using the agar diffusion method and minimum inhibitory concentration (MIC) assays against pathogens in the ESKAPE group (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* species).

224 - Variation in genetic structure and parasite prevalence in Northern cardinals (*Cardinalis cardinalis*) and their ectoparasites across ecoregions in Arkansas

Nora Hines, Alexander Worm, Drew Sweet

Arkansas State University, Jonesboro, AR

Variations in climate, landscape fragmentation, and urbanization can influence the dispersal and population structure of organisms, but it is not clear how these factors can impact the dynamics of host-parasite interactions. Here, we seek to better understand how the presence of different ecoregions in Arkansas, and their geographic boundaries, affect stable populations of birds and their ectoparasites. Cardinals are an excellent focus species to address this aim as they are a relatively common bird throughout each ecoregion, carry multiple ectoparasitic species, and individual birds maintain stable territories. We hypothesize that the distinct ecoregions in Arkansas serve as barriers to gene flow among cardinals and their ectoparasites, and distinct populations exist for both organisms along ecoregion boundaries. We collected blood and any lice from 50 cardinals across 4 different sites in Arkansas, representing 3 different ecoregions and urban, natural, and agricultural habitat. With these data, we calculated prevalence and abundance of the lice. We then obtained genome-wide single nucleotide polymorphisms (SNPs) from cardinals and their lice to assess fine-scale patterns of dispersal and relatedness among different ecoregions. Our results show differences in the abundance, diversity, and genetic structure of lice between ecoregions, which could indicate a barrier to dispersal among and between host species. We also found several degrees of relatedness among the lice on different hosts, indicating direct transmission between those cardinals. Bettering our understanding of the mechanisms behind parasite dispersal and host switching can aid in conservation and human health initiatives as these ecosystems change.

225 - The crash of Green Ash (*Fraxinus pennsylvanica*) a six year study (2019-2024) of a piedmont North Carolina swamp forest decimated by the invasive Emerald Ash Borer

Salem Fleming[1], Emma Halstead[1], Arilyn Lynch[1], Madison Kluge[2], Matthew Rodriguez[1], Jay Bolin[1]

[1]Catawba College, Salisbury, NC, [2]University of Kentuky, Lexington, KY

The Emerald Ash Borer (EAB) is an invasive species in the United States. We measured the decline and patterns of change in a Green Ash (*Fraxinus pennsylvanica)* dominated swamp forest in the Catawba College Fred Stanback Jr. Ecological Preserve (FSJEP). In the fall of 2019 we established six, 200 m^2 plots using a nested plot design to measure changes in the canopy, sapling, and herbaceous vegetation in Rowan County, North Carolina. We resampled the plots every fall between 2019-2024. Green ash was eliminated from the canopy layer after 6 years of monitoring. Our data indicated low diversity in the tree canopy, tree importance values in descending order, green ash, sweet gum (*Liquidambar styraciflua*), red maple (*Acer rubrum*), black willow (*Salix nigra*), American elm (*Ulmus americana*), and the American Sycamore (*Platanus occidentalis*). In Fall of 2019 green ash trees were visibly showing signs of EAB infection. In Fall 2019 no ash trees were standing dead, by 2022, 78% of the green ash trees were dead, and

in 2024 were eliminated from the canopy strata. The importance value of the green ash canopy declined from 2019 (IV = 1.61) to 2024 (IV = 0.0). Based on photometric methods canopy coverage declined strikingly from 73.1% to 4.84% from fall 2020 to fall 2023, then slightly increased in fall 2024 to 5.31%, as the composition of the forest shifted. Successional trends based on canopy mortality and sapling dynamics will be presented.

226 - Alligator population structure, movement, and habitat use on Bald Head Island, North Carolina

Allison Polinski, Elizabeth Darrow

Bald Head Island Conservancy, Bald Head Island, NC

American Alligators (*Alligator mississippiensis*) are important apex predators in the Cape Fear River, NC, including Bald Head Island (BHI) at the mouth of the river. BHI is an ideal location to study alligators, with a sizable population in a relatively small (~1,000 ha) and easily accessible area. Alligators have been seen utilizing a variety of environments on BHI, including freshwater ponds, brackish river water, salt marsh, and open ocean ecosystems. Since 2007, the BHI Conservancy has conducted weekly nighttime spotlight surveys of freshwater ponds from May-August to estimate alligator population size and structure. Size class of each alligator is estimated in categories of 0-3 feet, 4-6 feet, 7-10 feet, and 11+ feet total length. Size is used to estimate age, since alligators are considered sexually mature once they reach 6 feet long (10-15 years). The population has increased since 2007, but has been relatively stable since 2021 at approximately 30 alligators. The use of various habitats and resulting exposure to a range of salinities and contaminants has interesting implications for physiology and ecotoxicology studies. In April 2022 we partnered with NCSU to conduct a satellite tagging study to observe movement patterns of adult alligators. Five 8+ foot long alligators (4 males, 1 female) were fitted with iridium satellite tags. Alligators were tracked until tags fell off, 45 - 473 days. Alligators spent the majority of their time in freshwater ponds, with brief forays into marsh, ocean beach, and forested habitats; however, none of the alligators left the island or used the main Cape Fear River during the sampling period. We plan to analyze the data further to document home range and possible interactions between alligators. This satellite tagging effort will provide important data to scientists, managers, and the general public on Bald Head Island.

227 - Investigating Patterns in Breast Cancer Metastasis Using Invasion Ecology Frameworks

Garrett Timmons

Mississippi State University Biological Sciences, Starkville, MS

Metastatic breast cancer, characterized by a 5-year relative survival rate of only 32.4%, remains a leading cause of cancer-related mortality. Despite advances in understanding molecular drivers of metastasis, a holistic framework incorporating ecological interactions of circulating tumor microemboli (CTMs) is necessary to enhance predictive power and therapeutic strategies. This research investigates how circulatory dynamics shape metastatic patterns using the invasion ecology framework developed by Catford et al.

The study focuses on two hypotheses: (1) metastatic success depends on circulating tumor microemboli (CTM) size, and (2) circulatory pathways direct metastatic colonization by influencing CTM distribution among tissues. To address these hypotheses, a network model was constructed that represents CTM pathways, using cross-sectional arterial data and Markov Chain Monte Carlo simulations. A model linking CTM size to metastatic probability will assess hypothesized relationships using beta distributions convolved to a negative binomial CTM size distribution. Finally, these two models will be combined to predict the location and distribution of potential micro-metastases.

Preliminary simulations represented some of the variation the in the distribution of CTMs in head tissues, aligning with clinical data on metastatic patterns in the brain and skull. The integration of circulation-based models with CTM size probability estimates provides a novel approach for predicting metastasis at tissue-specific and sub-tissue levels.

This work advances the understanding of metastatic processes by integrating ecological concepts with oncology. Insights from the study could inform new therapeutic targets, precise interventions, and preventative strategies to combat breast cancer metastasis, marking a paradigm shift in how metastatic mechanisms are studied.

228 - Impact analysis of climate change on localized earthworm populations

Elizabeth Burkey, Jason Ake, Loyd Butcher, Madeline Cecil, Ali Wyer, Jeremiah Dann

Department of Organismal Biology, Ecology, and Zoo Science, West Liberty University, West Liberty, WV

This study is a continuation of work established at West Liberty University, focusing on the earthworm populations in the campus

woods area and the effects of climate change based on comparison data collected over four summers, 2021 to 2024, utilizing equations provided by Byun and Wilhite (1999). The purpose of this study was to analyze the impacts on localized populations of naturalized Lumbricidae and invasive Megascolecidaea species. Since 2020, we have been monitoring a 900 m^2 plot in WLU's campus woods community. Weekly surveys of this site measured worm density, length, and a variety of environmental parameters, including air and soil temperature, precipitation, and soil moisture. These parameters are considered to be the main factors that affect earthworm densities based on previous studies (Eisenhauer et al., 2014; Phillips et al., 2020). Our results conclude that extreme weather conditions, specifically drought, have deleterious impacts on both populations but more so on Lumbricidae species. This suggests that the Megascolecidae species are more hardy and able to endure and survive through extreme events most probably due to their life history, of which little is still known. Continued monitoring of both populations and improved research regarding Megascolecidae life history is needed to provide more conclusive evidence for the fate of naturalized and invasive earthworm populations and the effects of population density fluctuations on native deciduous forests.

229 - Preliminary observations of a well-defined colony of burrowing crayfish (*Distocambarus* species) in a neighborhood

Lee Morris

University of South Carolina Union, Union, SC

A colony of *Distocambarus* species of crayfish has been identified in a neighborhood of the city of Newberry, South Carolina. The species has not been confirmed as only four adult females have been observed. Variations seen in the annuli ventrales suggest two separate species, probably *D. youngineri* and/or *D. carlsoni*. The colony is located at a 0.28 acre corner lot that is mowed twice monthly during the growing season; the area has a perched water table that becomes swampy after periods of heavy rain. Chimneys and turrets are prevalent during the "wet" season (reproductive season, January through May), but have also been noticed in proliferation after high precipitation, notably at the end of June 2023 and the end of July 2024. While crayfish can be actively seen building mounds at night during these times, reasons for the surface irruption of these crayfish outside reproductive season is unknown. Examination of the chimneys and turrets suggest construction by individuals of different sizes at all times of the year when visible. Some turrets (with no observable opening at the apex of the structure) do seem to have working entrance holes in the vegetation immediately adjacent to the mound, blurring the designations of "chimneys" and "turrets". The area is also colonized heavily by fire ants, with fire ant mounds very close to active crayfish mounds. Studies are planned to verify species, examine the relationship between precipitation and crayfish irruptions, and study behaviors external to the burrows.

230 - Insect visitors to oak mistletoe (*Phoradendron leucarpum*) flowers in forested wetlands of eastern Virginia and North Carolina

Isaiah Hudgins, Lytton Musselman, Nicholas Flanders

Old Dominion University, Norfolk, VA

The oak mistletoe (*Phoradendron leucarpum*) is a parasitic shrub found across the southern United States growing on deciduous trees. Among forested habitats of eastern Virginia and North Carolina, mistletoe is most common in forested wetlands despite the widespread occurrence of potential host tree species. Mistletoes are considered keystone resources and, thus, oak mistletoe is likely an important resource for avian frugivores wintering in forested wetlands of the region. It is important to understand processes that maintain mistletoe in forested wetlands, yet the factors most influential in driving oak mistletoe habitat relationships remain unidentified. Oak mistletoe is pollinated by insects in fall and winter, yet little else is known about its pollination biology. In fall 2024 we initiated a study of oak mistletoe pollination in regional swamp forests to identify floral visitors and pollinators. This work represents the first step in determining the role that pollination limitation may play in driving oak mistletoe distribution.

231 - An Analysis of Pheretimoid Earthworm Life History with Regards to Climatic Changes through the Year.

Jason Ake, Elizabeth Burkey, Madeline Cecil, Ali Wyer, Zachary J. Loughman, Jeremiah Dann

Department of Organismal Biology, Ecology, and Zoo Science, West Liberty University, West Liberty, WV

The United States is in the midst of an invasion by multiple genera of East Asian pheretimoid earthworms. These earthworms are ecosystem engineers capable of disrupting nutrient cycling and litter microhabitats in hardwood forests across the United States. Several aspects of pheretimoid biology are understudied, leaving an incomplete understanding of their full invasive range and life history. Existing knowledge regarding pheretimoid life cycles suggests that a single generation hatches in April or May from eggs that have overwintered from the previous fall. In an attempt to track this process, field surveys took place at two sites at West Liberty University beginning on April 1st and continuing biweekly until the beginning of December. However, observations made during field

sampling did not support the general hypothesis, and juvenile pheretimoid earthworms were found during the first sampling event, suggesting flexibility of hatching early depending on winter weather. Hatchling earthworms also appeared throughout the spring alongside all size categories of pheretimoid worms until historic drought led to populations declining too low to be detected by sampling methods. Following the end of the drought and after the first frost in November, hatchling pheretimoid worms were observed once again. These results suggest that climatic changes may have significant impacts on the lifecycle of pheretimoid earthworms, and that there may be a high degree of flexibility in the timing of life history events such as hatching and maturation. Additionally, these results support a pattern of asynchronous hatching that is continuous through the year in pheretimoid earthworms.

232 - Fruit preferences of Eastern Bluebirds during the winter in southwestern Kentucky and northwestern Tennessee

Courtney E. Hutchison, H. Dawn Wilkins

University of Tennessee at Martin, Martin, TN

Eastern Bluebirds (*Sialia sialis*) are nonmigratory cavity nesting birds that overwinter in Tennessee and Kentucky. In the winter, they roost communally in nest boxes. When extremely cold weather is coupled with snow and ice, bluebirds can be found dead in these nest boxes. The causes of death are unknown, however, limited food availability is a likely factor. Eastern Bluebirds are primarily insectivorous but will switch to fruits when cold temperatures and snow cover limit their access to arthropods. Bluebirds cannot digest seeds of fruits and instead will regurgitate the seeds which can then be collected from nest boxes. In 2021, Bob and Judy Peak donated 90 Eastern Bluebirds that were found dead in nest boxes following a severe winter weather event. Our goal was to identify seeds found either on the bodies or inside of the stomachs (proventriculus and ventriculus). We then compared our findings to what was found in nest boxes by Dr. David Pitts during the winters of 1977- 1978 and 1983-1987. For all winters sampled, sumac (*Rhus coriaria*) was the most abundant seed consumed. Privet (*Ligustrum* spp.), an invasive species which has increased its range in Tennessee and Kentucky, was not collected in past samples but was found on the bodies of the bluebirds that died in 2021. Differences in seeds consumed over time may reflect the different locations sampled but may also show an increase in the prevalence of privet. Based on these findings, we encourage landowners to consider planting native plants, such as sumac, in their landscaping to help Eastern Bluebirds survive severe winter weather events.

233 - Breeding biology of Eastern Screech-Owls and Barred Owls in northwest Tennessee

Charles Q. Sands, H. Dawn Wilkins

University of Tennessee at Martin, Martin, TN

There is little known about the timing and sequence of events that take place during the breeding season of Eastern Screech-Owls (*Megascops asio*) and Barred Owls (*Strix varia*) in northwest Tennessee. Both species are secondary cavity nesters and are known to use artificial cavities (nest boxes). The breeding biology of Eastern Screech-Owls has been studied more comprehensively than Barred Owls, however their nesting phenology in northwest Tennessee is not well documented. The breeding biology of Barred Owls has not been well studied and is considered a priority for future research for this species. In the past we have censused Barred Owls and have found them to be abundant in northwest Tennessee. While we know that Eastern Screech-Owls are present, there is little information about their abundance in northwest Tennessee. Our goal is to gain a better understanding of the breeding biology of Barred Owls and Eastern Screech-Owls. To accomplish this goal, we built and deployed twenty artificial cavities for Barred Owls and twenty artificial cavities for Eastern Screech-Owls in various locations around Weakley County, Tennessee. Once boxes are occupied, we will make observations about the sequence and duration of nesting activities. In addition, we will be using playback of owl calls to census Eastern Screech Owls to gain a better understanding of their abundance and habitat use in northwest Tennessee.

234 - Mammal Life History Databases Compared

Ethan Duncil, JR Burger, Kimberly Cook

University of Kentucky, Lexington, KY

Comparative life history data are used widely in the study of ecology, evolution, and conservation. In recent decades, there has been growing numbers of databases containing life history data. Yet it is less clear how these databases compare. We compare six mammalian life history datasets using 8 life history traits: 1) Adult body size, 2) weaning size, 3) litter size, 4) Birth frequency, 5) development time, 6) lifespan, 7) age at maturity, and 8) respiration. We find that the AMNIOTE database (Myhrvold et al. 2015) subsumes 95%-97% of species found in other databases depending on the trait excluding respiration, which is absent in AMNIOTE. Variable estimates among databases are highly correlated. We tested trait and taxonomic biases among datasets. Trait distributions show similar patterns across databases. The overlap in trait distributions is particularly similar in AMNIOTE and PANTHERIA (Jones

et al. 2009), while the other datasets diverge somewhat. Rodentia and Chiroptera made up a higher proportion of total data points in AMNIOTE compared to other datasets, while Carnivora and Artiodactyla comprised a comparatively smaller proportion of AMNIOTE. Notably, the proportion of each taxonomy's representation was similar between AMNIOTE and PANTHERIA. The main takeaway from the comparison of these databases is that AMNIOTE appears to subsume much of the other databases and has the largest number of unique species and most diverse set of taxa.

235 - Managed Populations of Sarracenia spp. at the Highlands Biological Station show higher flowering densities

Jake Thompson[1], Steph Jeffries[2], Mr. Jason Love, M.S.[3]

[1]NCSU, Albemarle, NC, [2]NC State University, Raleigh, NC, [3]Highlands Biological Station, Western Carolina University, Highlands, NC

Sarracenia (pitcher plant) species are key components of North American carnivorous plant communities, with 7 species found in NC. Overcrowding from other species has shown to decrease diversity of carnivorous plants by outcompeting these species for sunlight, nutrients and space. We wanted to learn if vegetative cover played a role in the flowering rates of Sarracenia. My study investigates the flowering density of two species of Sarracenia, Sarracenia purpurea var. montana and Sarracenia jonesii growing at the Highlands Biological Station in Highlands, North Carolina, where S. purpurea is considered a natural population, while S. jonesii was introduced to the Station's Botanical Garden in 1992. Minimal management practices are done at the station, only hand weeding of high traffic sites and periodic removal of woody vegetation using hand saws. Data was collected in two ways: a true count for smaller populations, while larger populations were sampled with 1x1 meter square plots. Results show a considerable difference in flowering density between sites that were managed than that of sites that were not managed. This suggests that Sarracenia requires higher levels of light to effectively flower. Lower levels of light could lead to a lower number of seed production thus decreasing future population sizes.

236 - Fire Effects on Arboreal Vegetation in a Native Prairie Restoration

Micah McNeil[1], Erin Eichenberger[1], Alexander Krings[2], Stephanie Jeffries[1]

[1]North Carolina State University, Raleigh, NC, [2]Department of Plant and Microbial Biology, North Carolina State University, Raleigh, NC

In the not so distant past, the Piedmont physiographic region was a patchwork of open grasslands and woodlands. For millennia, fire shaped these landscapes, sustaining vibrant plant communities that supported diverse wildlife communities. Fire suppression has shifted many plant communities to closed canopy forest. Now, prescribed fire has become a primary tool used in grassland restoration across the United States. The objective of this project is to understand how prescribed fire affects tree density and species composition in a restored Piedmont prairie. Picture Creek is a Piedmont prairie where grassland restoration practices have been implemented, such as timber harvests and prescribed fire. Previous researchers established fifteen 100 square meter circular permanent plots on a randomly placed grid in this restoration project area. In 2022, researchers recorded diameter (cm) at breast height (1.37 meters) and species for each tree within these plots. Managers executed a prescribed fire on the stand in the 2023 growing season, and we resampled the permanent plots in 2024. Preliminary review indicates that the 2023 prescribed fire reduced the density of live stems. Smaller diameter trees and fire intolerant species appear to be most affected. Further analysis will compare changes in the number of trees per hectare in each diameter class using the diameter distribution graphs from 2022 and 2024. This means that fire is effective in reducing the density of small trees in Piedmont prairie restoration. This result is important because it underscores the necessity of prescribed fire for Piedmont prairie restoration. Understanding fire effects on this plant community is beneficial to land managers as they make cost benefit analysis on management decisions.

237 - Do birds of a feather flock together? Habitat-linked avian diversity and community composition

Danielle Langley, Lisa McDonald

Lander University, Greenwood, SC

With more than a century of active citizen science and the constant emergence of new technologies, we understand trends in bird population dynamics particularly well. Despite the popularity of birds among the general public and the many invaluable ecosystem services they provide, bird populations are not well protected and continue to drastically decline. In a previous study using camera trap data, we found that bird diversity was highest in areas with increased habitat heterogeneity, but our estimates of species richness were extremely low. In our current study, we chose a site with high habitat heterogeneity and used acoustic recording units (ARU) to identify environmental factors important to avian community composition. We collected data using 12 ARU stations deployed at a 90-acre camping and recreational area near Waterloo, SC. Using GIS, we assigned each ARU a habitat type (surrounded by forest, on the edge of forest and field, or on the edge of forest and water) and predominant tree community (deciduous, conifer, or mixed forest). We used BirdNET to identify the birds present by song and call and calculated species diversity for each station using the Chao-1

index. We visualized our community-level data using NMDS. To detect differences in diversity and to differentiate between the bird communities found within different habitats and tree community types, we used ANOVA and PERMANOVA. Species diversity did not differ between habitat types or tree community types. However, we did find a difference in the community composition of different habitat types with distinct sets of bird species utilizing each habitat type and its resources. Our results emphasize the importance of protecting a wide range of habitats to maximize the number of bird taxa that are protected and to protect as many unique bird communities as possible.

238 - Medium-to-large bodied mammal diversity at Carolina Wildlands Foundation: Three years of Snapshot USA data compared to national trends.

April Wooten[1], Morgan Warner[2], Jason Doll[1], Travis Knowles[1]

[1]Francis Marion University, Florence, SC, [2]Carolina Wildlands Foundation, Chesterfield, SC

Snapshot USA is an ongoing nationwide camera trapping project designed to monitor the status and spatiotemporal patterns of medium-to-large-bodied mammals in the USA. Recently, a 5-year summary of data was submitted for publication. The Carolina Wildlands Foundation (CWF) manages a large, private conservation property in Chesterfield County, SC, and is one of the subproject sites for Snapshot. This poster summarizes trends in the most captured mammal species at CWF over a 3-year period (2021-2023). Additionally, we discuss intrasite trends at CWF and compare the results to the nationwide 5-year summary. We also explore implications for continued monitoring and conservation efforts.

239 - Autumn Activity of Twig-girdling Beetles (*Oncideres cingulata*) in Georgia: Tree Preferences and Timing of Girdling Activity in Relation to Leaf Litterfall

Muniza Khan, Aliza Ratnani, James Ferrari

Wesleyan College, Macon, GA

Twig-girdling beetles (*Oncideres cingulata*) pose a challenge to trees by severing live twigs in autumn, causing losses of biomass as well as nitrogen, a limiting element. In this study, we examined beetle tree preferences, morphology of girdled twigs, and the timing of girdling in relation to autumn leaf fall in the Wesleyan College Arboretum (Georgia). Ten Mockernut Hickory trees (*Carya tomentosa*), 13 Pignut Hickories (*Carya glabra*), and 4 Winged Elms (*Ulmus alata*), all with dbh ≥30 cm, were located. From October 4 to December 5, 2024, focal trees were visited biweekly and any girdled twigs beneath them were measured for basal diameter and fresh mass. In addition, leaf litterfall was collected weekly from 12 traps (0.25 m² each), oven-dried, and weighed. Finally, twenty 5x5 m plots were sampled for fallen twigs and all trees ≥5 cm dbh were identified and counted. The peak of twig fall occurred on October 16 (38% of twigs), preceding the peak of leaf fall, indicating that twig girdling beetle activity is temporally distinct from natural leaf abscission. The average mass of girdled twigs was 67.1 g with leaves and 44.0 g without, and average basal diameter was 9.6 mm. Twig mass, foliage mass, and twig basal diameter of the two hickory species were not significantly different (t-test, $p > 0.05$), suggesting similar impacts on these trees by *Oncideres*. Girdled twigs on the 20 study plots numbered 660 twigs/ha, and 100% of these were *Carya*, despite hickories making up only 32% of trees ≥15 cm dbh in the plots. Hickory twigs may be preferred due to their decay resistance or some other aspect of their chemistry. These results underscore the potential ecological impacts of twig girdlers in temperate forests and may lend insights into pest dynamics in agroforestry settings such as pecan (*Carya illinoinensis*) orchards.

240 - The role of plant phylogenetic relatedness on community assembly in the undisturbed Cherokee Prairie in northwest Arkansas

Chenoa Summers, Ben Benton, Scott Mangan

Arkansas State University, Jonesboro, AR

Tallgrass prairies are among the most endangered ecosystems in the world with less than four percent of its original area remaining. Cherokee Prairie, an undisturbed tallgrass prairie located in northwestern Arkansas, is home to pimple mounds, a unique geological feature of the late Pleistocene. We know that plant species composition of plants on the mounds differ significantly from those in the surrounding prairie. However, we do not know whether the evolutionary history of plant species contributes to community assembly across distinct prairie habitats. For this study, we determined the phylogenetic relationships among 92 species of tallgrasses and forbs found in Cherokee Prairie. Phylogenetic beta diversity was calculated using mean nearest taxon distance. We found that plant communities among mounds were more closely related to each other than they were to plant communities in the prairie matrix located in close proximity. Likewise, prairie matrix communities were more closely related to each other than they were to mound communities. We then examined whether phylogenetic relatedness of the community could possibly explain the plant species presence or absence. To do so, we calculated the average community phylogenetic distance of select target species of sufficient abundance. Of the 19 species examined, we found that community phylogenetic relatedness was correlated with the occurrence of five plant species. Our

findings that documented habitat-specific phylogenetic patterns in undisturbed ecosystems can help inform decisions when selecting ideal native seed mixes for the restoration of tallgrass prairies.

241 - Assessing Soil Health Indicators and Microbial Communities in Longleaf Pine Versus Loblolly Pine-Hardwood Ecosystems

Crystall Lee, Siren van Leeuwen

Georgia Highlands College, Rome, GA

This study aims to assess soil health and correlate it with microbial diversity in two distinct forest ecosystems: longleaf pine (Pinus palustris) forests and loblolly pine-hardwood (Pinus taeda) forests. To achieve this, we will measure soil respiration, bulk density, and pH across multiple sampling sites within each forest type. Soil respiration will be evaluated as an indicator of microbial activity and overall soil health, while bulk density and pH will provide insights into soil structure and chemical properties, respectively. Microbial diversity will be assessed using DNA sequencing techniques to identify and quantify microbial communities present in the soil samples.

By comparing these parameters between the longleaf pine and loblolly pine-hardwood forests, we aim to elucidate the relationships between soil health indicators and microbial diversity in different forest ecosystems. The findings from this research will contribute to a better understanding of how forest management practices and environmental conditions influence soil health and microbial communities, ultimately informing conservation and restoration efforts in these forest systems.

242 - Pollinator-Mediated Dispersal and Community Coalescence: Linking Pollen Diversity to Nectar Microbiome Assembly in *Hamelia patens*

Jessica Williams, Jake Francis

Florida Atlantic University, Boca Raton, FL

Dispersal is a critical driver of beta diversity, shaping species composition among communities. Understanding how dispersal influences community assembly is especially important in specialized microhabitats, such as floral nectar, where microbial communities can affect plant fitness and ecosystem functioning. In nectar, microbes adhere to pollinators and spread among flowers during foraging. Here, we investigate how increased dispersal impacts the convergence of nectar microbial communities in *Hamelia patens*. We hypothesize that increased dispersal leads to greater homogenization of nectar microbiomes, reducing beta diversity across flowers. To test this, we sampled floral nectar and stigmatic surfaces from 32 flowers, each collected from 8 individuals across 5 populations (n = 1280). Nectar was extracted for DNA analysis, and microbial communities were characterized using nanopore sequencing of the 16S rRNA and internal transcribed spacer (ITS) regions. In parallel, we assessed pollen transfer as a proxy for dispersal by swabbing stigmas with fuchsin jelly and quantifying pollen loads via microscopy. We predict that microbial communities in flowers experiencing higher pollen-mediated dispersal will exhibit greater compositional similarity, indicating coalescence of nectar microbiomes across hosts. Our findings aim to improve understanding of how dispersal shapes community assembly within specialized microhabitats and clarify ecological drivers underlying microbial convergence.

243 - Plant community variation across different fire regimes and hydrologic conditions at the Blackwater Ecological Preserve in Isle of Wight County, VA

Gianna Claude, Muriel Draper, Taylor Sloey, Erik Yando, Nicholas Flanders

Old Dominion University, Norfolk, VA

The Blackwater Ecological Preserve (BEP) encompasses the northernmost extant assemblages of longleaf pine-savanna and longleaf pine-turkey oak communities. Since the acquisition of the property in 1984, regular prescribed fires have greatly increased the population size and quality of the pyrophytic communities. In addition to naturally reproducing longleaf pines (*Pinus palustris*), the area supports numerous state-rare plants. During the growing season of 2024 we sampled understory and mid-story vegetation and canopy composition at nine 20 x 20 m plots across a range of prescribed burn histories and hydrologic conditions at the BEP. We used a perMANOVA to test for differences in understory community composition between fire-suppressed and frequently burned sites with hydrologic condition as a fixed effect. We qualitatively contrasted understory, mid-story, and canopy conditions with results from a similar study conducted over 30 years ago when prescribed burning was first initiated at the BEP. Information on the long-term effects of prescribed burning at the BEP will aid managers in creating restoration goals at other fragments of the longleaf pine ecosystem at the northern edge of its range.

244 - Analyzing the interaction between stem-boring insects and *Spartina alterniflora* reproduction

Ellie McDole, Chloe Robertson

Georgia Southern University, Savannah, GA

Spartina alterniflora, commonly called smooth cordgrass, spans the Eastern seaboard of North America through the Gulf of Mexico to southern Texas. Methods to properly germinate *S. alterniflora*, especially from seed, have become a topic of interest as living coastlines are being implemented along the Atlantic coast to stabilize shorelines. By focusing on the marshland community of Rodney Hall Boat Ramp (RHBR) in Savannah, GA this study aims to analyze the effects of stem-boring insects on seed viability. Incipient flower stalks of *S. alterniflora* were examined for noticeable drill holes along the plant stem and tagged along with a neighboring intact stalk for a paired design. Adult insects found in oviposition and burrowing larvae from within the stalks were collected. Over 10 weeks, these stalks were monitored weekly and seeds from both drilled and undrilled plants were collected once viable. A total of 3,057 seeds were collected and placed into cold, wet conditions for winter stratification. In the spring, a subset of seeds will be removed from storage, washed, and tested for viability utilizing tetrazolium-chloride. We expect to see a decrease in viability in seeds that displayed drill holes along the stem. Any correlation between the presence of stem borers and seed viability or seed set will be examined.

245 - Effects of *Lonicera maackii* Invasion on Native Plant Biodiversity in Mixed-Oak Forests of West Virginia

Emma Crouch[1], Alijah Kuhn[1], Joshua Hamrick[2], Kyle Palmquist[1]

[1]Marshall University, Huntington, WV, [2]Huntington Museum of Art, Huntington, WV

Lonicera maackii (Amur honeysuckle) is a shrub native to East Asia that was introduced to the Eastern U.S. and quickly invaded deciduous forests across the region. This plant has multiple life history traits that give it a competitive advantage over native species. The objective of our study was to quantify the long-term effects of this invasion on native plant biodiversity in mixed-oak forests in Huntington, WV. We hypothesized that plots with higher abundance of Lonicera maackii would have lower plant species richness and diversity, and less tree regeneration than uninvaded plots. From April to October 2024, we established 5 invaded (>20% L. maackii cover) and 5 uninvaded (<20% L. maackii cover) 100 m2 permanent vegetation plots in the forest behind the Huntington Museum of Art. We recorded and estimated cover for all vascular plant species, measured and identified all trees, tallied tree seedlings and saplings, and counted L. maackii stems. Soil was collected in each plot and analyzed for texture and nutrients. We calculated several biodiversity metrics and evaluated whether invaded plots had lower diversity with linear models. We also evaluated whether soil properties differed between invaded and uninvaded plots using paired t-tests. Shannon Diversity, Shannon Diversity of herbaceous species, and species richness did not differ significantly between invaded and control plots ($p > 0.05$). Clay % was significantly higher in invaded than in uninvaded plots ($p = 0.02$), suggesting L. maackii invasion may have occurred preferentially in areas with higher water- and nutrient-holding capacity. In Fall 2025, all L. maackii stems will be removed using herbicide and thus these results will provide baseline, pre-treatment data for this removal experiment. In the future, Marshall University students will monitor these permanent plots, and compare pre-treatment and post-treatment data to better understand the effects of L. maackii invasion on native biodiversity.

246 - Does winter leaf reddening protect *Galax urceolata* from herbivory?

Rebekah Olls, Serene Alshalabi, Nicole Hughes

High Point University, High Point, NC

The leaves of many temperate, herbaceous evergreens turn red in winter in the presence of high light due to the production of anthocyanin pigments. While previous studies suggest that these pigments may function in photoprotection, it is also possible that these pigments function in camouflage, protecting exposed leaves from browsing mammals that forage in winter. Since most mammals lack functional red photoreceptors, red leaves likely appear dull in color to such animals, reducing their visibility within the litter layer. This hypothesis does not preclude the possibility that anthocyanins function in photoprotection, and indeed, both may have positive impacts on plant fitness. However, the second hypothesis has not yet been explored. In the present study, we utilized choice experiments using red and green leaves of *Galax urceolata.* Prior to dusk in an area where deer are known to regularly forage, one red and one green leaf were each tied to a thin (<1cm diameter) primary oak branch using hemp thread, and positioned so that leaves were approximately 5 cm above the ground and 1 m apart, with left/right orientation randomized between trials. Color preference (determined as first leaf eaten) was recorded using a motion-sensing hunting camera placed 2 m away from the leaves, at plant height, during the winter of 2024-2025. The experiment was repeated on multiple dates, with new sets of leaves used each time. Experiments are currently underway.

247 - Canopy Gaps Provide Structural Diversity and Promote Early Successional Vegetation

Jessica Maier, Jodi Forrester

North Carolina State University, Raleigh, NC

Closed canopy, even-aged forests provide many ecosystem services including valuable habitat for species like the eastern gray squirrel and wild turkey. Homogeneous mature forest, however, provides limited complexity for species who thrive under disturbance. Canopy disturbance such as harvested gaps create pockets of early successional plant communities, resulting in a mosaic of uneven-aged forest. The vegetative composition of gaps creates potential habitat for early successional specialist species, including ruffed grouse, eastern cottontail, and indigo bunting. We aim to quantify vegetative vertical structure from gaps to interior forest. Using a point contact method, we measured the vegetative structure and life form composition of the gap-forest matrix and unharvested control areas in a mature mixed hardwood forest in Pisgah National Forest, near Asheville, NC. Calculated cover by life form allowed us to assess the potential to provide habitat for early successional species. Our results showed that *Rubus* spp, maximum height, and structural variability of understory vegetation increased within the gap and decreased to a point resembling control plots as transects approached interior forest. Patterns were similar across large (0.9 ha) and small (0.1 ha) gap sizes. By better understanding the vegetative structural diversity created by canopy gaps, and their impact on early successional species, forest managers can be more targeted in achieving habitat-focused management objectives.

248 - Impact of invasive Chinese privet (*Ligustrum sinense*) removal on woody species recruitment and succession in a residential wetland, seven years later

Lissa Leege

Georgia Southern University, Statesboro, GA

Chinese privet (Ligustrum sinense Lour) is a problematic invasive shrub in wetlands in the southeastern United States, known to reduce light and soil moisture, as well as species richness and abundance of both herbaceous and woody species. Two years following removal of invasive privet in a residential wetland in Georgia, USA, we found almost no native woody species recruitment, despite the presence of non-native woody species in these sites. Here we sought to 1) determine if native woody species recruitment and growth into the shrub layer was limited by deer herbivory or competition with invasive Japanese stiltgrass (Microstegium vimineum), and 2) re-evaluate long term removal and privet plots for woody species recruitment, now seven years after privet removal. To evaluate deer and competition effects, we removed stiltgrass in 1x1 m plots around 10 individual 2-year old saplings of each species (removal) and left stiltgrass in 10 additional plots (control). We then caged the saplings in half the removal and half the control plots and left the rest uncaged. We measured sapling growth, vegetation cover and stiltgrass cover May-November during the first year, and sapling growth again in May of the second year and compared across treatments and years. To evaluate native woody recruitment in permanent plots, we determined the community composition and species abundance of woody species in the shrub layer and compared with data from the same plots from five years prior. Here we present recent findings and ongoing research.

249 - Organic and Inorganic Components of Curcuma longa

Bal Khatiwada, Abigail Farquhar, Pearson Futch

Abraham Baldwin Agricultural College, Tifton, GA

Curcuma longa (Turmeric) powder is widely used as a spice in Middle Eastern and Asian countries. One of the active ingredients of C. longa, curcumin has been widely studied for its role as an anti-inflammatory and an antioxidant properties. In this study, we are interested in profiling coloring agents present in rhizomes of *C. longa* that are grown locally in Georgia versus overseas. The turmeric powder we purchased overseas has a brighter color as compared to the regular organic turmeric powder from local supermarket. The bright color in turmeric powder may have link to lead chromate-based dye found in other samples. We are interested in finding out the active chemical agents that produce the bright color in the turmeric powder and compare it to the rhizomes grown locally. We plan to profile metal ions present in the turmeric powder by smelting and dissolving the ashes in aqua-regia. The concentration of metal ions dissolved in aqua-regia will be determined using the Coupled Plasma-Optical Emission Spectroscopy (ICP-OES) instrument. We are also interested in finding out synthetic dyes that may have link to the bright color in the powder. We have extracted the dye using solvent-solvent extraction and planning to identify the dyes using Attenuated Total Reflection - Fourier Transform Infrared Spectroscopy (ATR - FTIR) technique.

250 - Effects of coexistence between *Lepomis cyanellus* and *Lepomis auritus*

Daniel Martinez

University of Mary Washington, Fredericksburg, VA

Introduced species can cause problems for native species, especially when the introduced species is closely related to a native species or shares a niche that is already being filled. Lepomis cyanellus (green sunfish) was introduced into Virginia lakes and streams as a sport fish, but the species fills a similar niche with Lepomis auritus (redbreast sunfish), which is also a close relative. Both species are considered trophic generalists and use similar resources; this leads to competition in sympatric populations of these fish. To check the effects of coexistence between both species, I sampled both species from streams where they lived in sympatry and streams where they lived in allopatry. From the samples I collected, I compared the morphology and stomach contents of sympatric and allopatric populations of both species. This allowed me to identify any character displacement caused by competition for resources, and the stomach content analysis showed how their diets overlapped. From this, I was able to quantify the effect of coexistence between L.cyanellus and L.auritus for both species.

251 - Interactions Between Floral Traits, Pollinator Preference, and Nectar Microbial Contents

Ethan Hughey, Dr. Grace Freundlich, Foster Campbell, Johannamarie Nwanagu

Furman University, Greenville, SC

Interactions between flowers, pollinators, and microbes create a unique three-way relationship that has been researched extensively and is still being investigated because of the complexity of their interactions. Microbes live within the nectar of flowers, which pollinators consume and then transfer these microbes. These flowers attract pollinators through their physical and chemical traits, such as petal features or nectar content. I wanted to investigate how differences in floral traits influences pollinators, and consequentially, how they affect microbial loads. We predicted that floral species commonly found in pollinator gardens will have different levels of bacterial and fungal density, and that more pollinator visitation will increase microbial density. Furthermore, the physical traits of different floral species likely affect the attractiveness of those flowers to pollinators. Our study finds that in Upstate South Carolina, certain floral species are more often visited than others. In addition, those that were less visited tended to have lower bacterial loads. However, there seems to be little evidence showing significant differences in fungal growth between species, suggesting bacteria is more dependent on pollinator transfer compared to yeast and fungi. Furthermore, there is little substantive evidence that petal size influences bacterial contents. Overall, our findings suggest greater pollinator visitation increases bacterial loads and is worth investigating further. To continue, we will focus onto collecting a greater breadth of data on both floral traits and pollinator observations to better explore this relationship.

252 - Assessment of Stand Age Structure and Fire Dynamics in Longleaf Pine (*Pinus palustris*) Savannas and Pond Pine (*Pinus serotina*) Pocosins in the Green Swamp Preserve, North Carolina

Emily Parker, Monica Rother

Department of Environmental Sciences, University of North Carolina Wilmington, Wilmington, NC

Pond pine (*Pinus serotina*) pocosin wetlands are ecologically significant but understudied ecosystems in the Atlantic Coastal Plain. Fire dynamics play a crucial role in pocosin function and resilience, yet basic characteristics of the natural fire regime remain poorly understood. Our study, focused on the Green Swamp Preserve in North Carolina, examines the stand-age structure and fire history of pond pine pocosins and adjacent longleaf pine (*Pinus palustris*) savannas. We also examine ecosystem response to the 2023 Pulp Road Fire through a survey of tree mortality, tree resprouting, and new tree establishment. We observed that historical fire regimes differed significantly between these two ecosystems. Fires were less frequent and more severe in pocosins in comparison to adjacent longleaf pine savannas which experience less intense more frequent fires. Basal and epicormic resprouting along with new tree establishment facilitated recovery following the Pulp Road Fire. Fire scars in tree rings revealed previously unknown historical fire events that expanded a GIS database of wildland fire. This work has also revealed that higher stand age uniformity often correlates with more severe fire events. Our findings contribute to adaptive land management strategies, including prescribed burning plans designed for restoration and maintenance. By addressing critical knowledge gaps in pocosin fire ecology, this research enhances our understanding of fire-adapted ecosystems and supports effective conservation practices in the face of evolving fire regimes and climate change.

253 - Using Environmental DNA (eDNA) to Understand the Biological Diversity of Soil Microbiomes in South-Central Florida

Tatiana Guerra[1], Elik Esquilin[2], Laura Froberg[2], Dr. Tammy Laberge, Ph.D[2]

[1]Miami Dade college, Miami, FL, [2]Miami Dade College, Miami, FL

Environmental DNA (eDNA) refers to the genetic material shed by organisms into their surroundings, such as soil, water, and air. This technique is used to analyze environmental samples, monitor species distributions, and assess biodiversity by detecting the presence or absence of species within a given habitat. Our study uses eDNA analysis to identify bacterial diversity in soil samples from the Archbold Biological Station's Buck Island Ranch. Specifically, we examined bacterial diversity in soils subjected to different land-use conditions: improved and semi-native ecosystems. This research aims to understand the essential roles of microbial processes in each environment. The semi-native ecosystem is characterized by a mixture of native and non-native species introduced through human activities. Our study seeks to identify specific bacteria that contribute to plant growth in these distinct environments. Soil samples were collected from each environment and stored at -20°C until DNA extraction. DNA yield and purity were assessed, and suitable samples were diluted and sent for sequencing to identify 16S rRNA genes. Metabarcoding analysis was performed using the DNA Subway Purple line. This sequencing data is expected to reveal bacterial diversity and community composition differences across the habitats. Comparative analysis will be used to elucidate variations in bacterial communities between the soil types and their potential benefits to plants in each location. We hypothesize that the semi-native ecosystem will exhibit lower bacterial abundance due to human disturbances compared to the improved ecosystem. Understanding the soil microbiome and its impact is critical for advancing agricultural practices and ecological conservation. This knowledge could facilitate the development of biofertilizers to improve soil health. Additionally, comparing bacterial communities between improved and semi-native areas may provide valuable insights for land-use planning and landscape management. These findings could inform future research on microbial ecology, plant-microbe interactions, and ecosystem dynamics in south-central Florida.

254 - "Moving" mountains: modeling the distribution of southern Appalachian spruce-fir sky islands in space and time

AJ Hopkins, Kimberly Cook, Joseph Burger

University of Kentucky, Lexington, KY

Mountaintops in the southern Appalachians form a "sky-island" archipelago, populated by spruce-fir and northern hardwood forests. The distribution of *Picea rubens* extends from northeastern North America to the southern region of the Appalachians, where high elevation mountaintops provide suitable climatic conditions for the species to persist. We use presence-point data compiled from the Global Biodiversity Information Facility (GBIF) to create a species distribution model for *Picea rubens*. In attempting to correct for spatial bias present in the GBIF database, we use a spatial thinning method based on presence data for *Abies fraserii, Betula alleghaniensis, Abies balsamea,* and *Betula papyrifera*, the species most prominent in the spruce-fir forest types at both the northern and southern ends of *Picea rubens'* distribution. In modeling the differences between species-defined spruce-fir forest types, we can better understand how habitat suitability changes for *Picea rubens* across its range. The resulting models allow us to predict past, present, and future distribution of *Picea rubens*, revealing notable variation in the suitability of high elevation sky islands of spruce-fir forests in southern and central Appalachia.

255 - Evaluating the effects of plant density and garden location on pollinator diversity as assessed by eDNA metabarcoding and pitfall traps.

Kara Vaartjes, Brian Ragoobir, Ellie Ratta, Connor Spitler, Megan Rudock-Bowman

High Point University, High Point, NC

The Mariana H. Qubein Arboretum and Botanical Gardens at High Point University is an extensive network of over 30 campus gardens, which include a diverse range of flowering plants. As we look to add pollinator habitats, such as bee hotels, to our campus community it is important to assess the distribution types of native pollinators present so that we may serve them best. The overall goal of this study is to assess the impact of garden density, plant diversity and overall garden size on pollinator diversity. In the preliminary study, three gardens were selected based on the availability of flowering plants in the late fall. Flower heads from each of three plants were collected in one liter of water and in a conical tube on ice. Flowers were allowed to soak in the water for a minimum of 2 weeks to allow transfer of eDNA into the water for collection by filtration. Filter paper was cut in half and the DNeasy Powerwater Pro kit (Qiagen) was used for isolation of eDNA from water in duplicate. Frozen plant samples were divided and the DNeasy Blood and Tissue kit (Qiagen) was used for eDNA isolation in duplicate. PCR targeting a partial fragment of the cytochrome oxidase I gene (*COI*) and subsequent metabarcoding analysis (Illumina TruSeq at Azenta) was used detect and identify small arthropods. Pitfall traps were also used to collect and identify ground insects. Using plant maps of the 3 campus gardens, the following statistics were calculated: garden

area, % of garden area without plants, plant diversity, and plant density within each garden. Molecular Data and results from pitfall traps were used in this analysis. Further analysis and samples will be necessary to draw major conclusions, as we expand this study to the entire HPU Campus Garden system.

256 - Paralyzed Fruit Flies: A Model System for Studying Human Diseases

Sariah Ocampo, Jo Qian

University of North Georgia, Oakwood, GA

Dynamin, initially discovered in bovine brain tissue as a 100-kDa microtubule-binding protein, plays a crucial role in membrane fission for synaptic vesicle recycling. The function of dynamin was first characterized in *Drosophila* with the temperature-sensitive *shibire* (*shi*^{ts}) mutation, which caused rapid paralysis and synaptic transmission blockade at restrictive temperatures due to defects in vesicle cycling. The fly *shi* was mapped as a homolog of dynamin. Humans possess three dynamin isoforms: dynamin-1 (DNM1), dynamin-2 (DNM2), and dynamin-3 (DNM3). DNM1 and DNM3 are predominantly found in neurons, while DNM2 is widely expressed. Despite dynamin's established role in endocytosis, the specific functions of its isoforms in different tissues, such as neurons and muscles, are still unclear. To explore these functions, we used fruit flies as a model to investigate the physiological and pathological roles of dynamins, which may also aid in developing therapeutic strategies. To study the evolutionary relationships of dynamin from various species, amino acid sequences of human dynamin, fly shibire, and their homologs in classic model organisms were retrieved from Flybase and National Center for Biotechnology Information (NCBI), aligned with Clustal Omega, and formatted for publication. To identify amino acid variants of dynamin that may be potential contributors to human diseases, conserved domains of dynamin across phylogenetically diverse organisms were collected from NCBI's Conserved Domains Database and disease-causing amino acid variants in conserved domains of dynamin were identified using the UniProt database. We identified conserved regions that allow dynamin to perform its essential roles in cellular processes, and amino acid variants in these domains that affect its function, leading to various diseases. In the future, we plan to perform phenotypic analyses of third-instar larvae carrying disease-causing mutations and analyze the expression and subcellular localizations of neuronal and muscle proteins.

257 - Effects of Changes in Fire Management Policy at Pilot Mountain State Park on Fire Frequency and Size

John Guglielmetti, Esprit Cha, Dane Kuppinger

High Point University, High Point, NC

Fire plays a crucial role in shaping southeastern U.S. ecosystems, including the Piedmont's dry forests, where fire-adapted species indicate a historical fire presence. Despite this, fire history studies in the region remain limited. National fire suppression policies (1930-1980) reduced fire frequency, but their long-term effects on community dynamics and fire behavior in the Piedmont remain unclear. This study extends the fire history of Pilot Mountain State Park back to 1826 by incorporating 48 additional samples, documenting 45 fires: 20 in the pre-suppression period (1689-1929), 11 during suppression (1930-1979), and 10 post-suppression (1980-2023).

Fire frequency changed over time, with the Mean Fire Interval (MFI) increasing from 4.22 years pre-suppression to 4.80 years during suppression, then declining to 4.20 years post-suppression. Fire size was also affected, with larger fires pre-suppression (mean: 559,216 m²) compared to suppression (120,237 m²) and post-suppression (125,574 m²). These findings suggest that current fire management policies have not restored historical fire regimes, potentially affecting ecosystem structure and function. Further research is needed to evaluate the ecological consequences of altered fire frequency and size in the Piedmont.

258 - Fishes and Crayfishes of the Troy University Arboretum

Sophie Richards, Jonathan Miller

Troy University, Troy, AL

The Troy University Arboretum is composed of 75 acres of natural area in the middle of Troy, AL. Since the Department of Biological and Environmental Sciences regained management of the facility in 2020, recent measures have been taken to improve the habitat and trail systems to better exemplify the ecosystems of our area. The natural aquatic systems are highly degraded and are much more complicated in relation to restoration abilities, although restoration of one of the headwater streams is underway. A baseline of local biota and stream conditions was needed to better understand the system in its current state, as well as to determine if the improvements allow for colonization by more native species in the future. Through electrofishing, we sampled the fish and crayfish species at six stream and two wetland sites that spanned the entire arboretum. The study resulted in a total of seven species of fish and two species of crayfish across all sites. Of the fish species found, four species were tolerant (*Semotilus thoreauianus*, *Gambusia holbrooki*, *Ameiurus natalis*, and *Lepomis macrochirus*). This study suggests that the streams of the arboretum are in poor condition

overall and future improvements are needed to restore biological integrity.

259 - A Field Investigation of Water Quality Parameters in an Impacted Urban Stream in Central NC Using Stream Invertebrate Community Indices With Implications for the Importance of Protection of Riparian Zone Vegetation to Improve Stream Health

Ashley Ragland, L. Michael Larsen

Campbell University, Buies Creek, NC

Urban streams are negatively impacted by stormwaters, pollutants, and the impacts of channel straightening, removal of streambank vegetation, and destruction of protective riparian zone vegetation. In this study, we compared the physical characteristics and biological structure of a degraded urban stream flowing through W. N. Porter Park in Erwin, (Harnett County) NC with a similar but less impacted reference stream (East Branch, Buies Creek), in the watershed. Sampling of the macroinvertebrate and freshwater fish communities at these two sites was completed in the fall of 2024 through early spring, 2025. Water quality measurements were taken from the sites on each sampling date. Stream habitat quality evaluations, including stream flow, benthic habitat conditions, shoreline conditions, assessment of potential water pollution sources adjacent to the sites, and the existing condition of riparian zone vegetation adjacent to the streams were investigated. Stream Invertebrate Community Indices (SICI) to assess the stream invertebrate community were used to compare the sites. Benthic macroinvertebrate communities in the urbanized stream were less diverse, as compared with the reference site. These data were then compared with riparian zone vegetation patterns at the two sites. Standard water quality parameters, to include pH readings, water temperature and oxygen readings, water hardness, and other chemical measurements were similar between the sites. Though statistical analysis of the direct effects of riparian zone vegetation patterns was not conducted in this preliminary study, it is readily apparent from the initial data that much of the degraded environmental conditions found in the urban stream site can be likely attributed to the destruction of stabilizing vegetation in the floodplain area, and the degradation of stream shorelines in Porter Park through water erosion and urban runoff. Future studies at this impacted stream are planned to investigate the effectiveness of streambank stabilization efforts and restoration of riparian zone vegetation.

260 - An investigation of the effects of stream restoration on aquatic macroinvertebrate assemblages in two first-order tributaries of the Middle Fork Forked Deer River in West Tennessee.

Elizabeth Lattus, Tom Blanchard

University of Tennessee at Martin, Martin, TN

Stream straightening and channelization are known to result in head-cutting, valley plug formation, un-natural sediment transport, and a reduction in the variability of microhabitat types available to aquatic organisms. In West Tennessee, most rivers and streams have been extensively channelized. Because of the known adverse effects of channelization, stream restructuring projects have been implemented by the West Tennessee River Basin Authority (WTRBA) to restore the natural sinuosity to sections of heavily straightened streams of West Tennessee. The stream restructuring projects have been successful in lessening problems associated with excessive sediment load and transport at project sites, but little is known regarding the effects of stream restructuring on aquatic macroinvertebrates in these systems. With this study, we hope to add to the understanding of how macroinvertebrate assemblages respond to stream restructuring and restoration. We used D-frame dipnets to collect aquatic macroinvertebrates along three stream reaches within an un-restored stream (Deloach Creek) and three stream reaches within a recently (5 yrs.) restored stream (Moize Creek). Both streams are first-order tributaries of the Middle Fork Forked Deer River (MFFDR) in West Tennessee. The lower watersheds of both were dedicated primarily to agricultural activities and their confluences with the MFFDR are less than 500 meters apart. We compared between the two streams, taxa richness, Simpson's Diversity Index, and an Index of Biotic Integrity to assess the response of aquatic macroinvertebrate assemblages to stream and watershed restoration.

261 - Microbiome Composition Differences Among Four Species of Freshwater Mussel Found in the Tallapoosa River (Alabama)

Ryley Dykes, Brian Helms, Erin Shelley, Jonathan Miller, Molli Newman

Troy University, Troy, AL

Mussels play a critical role as ecosystem engineers in the freshwater systems where they are found. The state of Alabama, which houses approximately 180 freshwater mussel species, contains the highest diversity of freshwater mussels in North America. Unfortunately, approximately 70% of these freshwater mussel species are imperiled due namely to environmental changes such as pollution, habitat destruction or alteration, introduction of invasive species, lack of fish hosts, and climate change. Microbiome is a term used to describe the particular set of microorganisms living within or on a particular organism, and microbiomes of organisms are known to play a crucial role in maintaining overall organism health and wellness. Environmental conditions can influence an

organism's microbiome, thus aquatic degradation may lead to adverse effects on overall organism health, but this may differ across species with respect to environmental condition affected. This study explores the microbiome composition and diversity of four freshwater mussel species found in the Tallapoosa River (Alabama) to examine species-specific differences in mussel microbiome composition. Mantle swabs were collected from 4 individuals each of *Cyclonaias asperata, Lampsilis ornata, L. teres, and Obliquaria reflexa* at one mainstem site on the lower Tallapoosa River during summer 2023. Genomic DNA was extracted from these swabs, the 16S rRNA gene was amplified, and the resulting amplicons were sequenced using an Illumina MiSeq to identify bacterial community composition within the mantle mucus. Preliminary analysis suggests that microbiome diversity differs across these species. Functional analyses will potentially reveal possible mussel physiological links. Knowing the typical mussel microbiome composition and being able to sample it in a non-destructive manner, can allow for more precise monitoring of mussel populations and the environment around them so that we can better protect this valuable resource.

262 - Characterization of Blackwater Wetland Reference Sites in Alabama

Barrie Sullivan[1], Kathryn Schabron[1], Jon Armbruster[2], Chris Boyd[1], Alban Guillaumet[1], Brian Helms[1], David Laurencio[2], Katelyn M. Lawson[3], Alfred Schotz[2,4]

[1]Troy University, Troy, AL, [2]Auburn University Museum of Natural History, Auburn, AL, [3]Auburn University, Auburn, AL, [4]Alabama Natural Heritage Program, Auburn, AL

Wetlands provide 40% of global ecosystem services despite covering just 1.5% of Earth's surface. However, wetlands are disproportionately threatened by human development, pollution, and climate change, with Alabama's wetlands being particularly impacted. Alabama is home to a variety of wetland types, each harboring unique flora and fauna. Particularly unique are blackwater wetlands. These wetlands are typically floodplain swamps associated with blackwater systems, waters originating below the fall line containing heavy amounts of tannins, iron, and organic matter, with a low pH. The Alabama Department of Environmental Management (ADEM) is responsible for monitoring surface waters, including wetlands, yet full incorporation of wetland monitoring has been difficult. To assist in these efforts, we are establishing baseline reference conditions of water chemistry, flora, and fauna in blackwater wetlands and their receiving streams in southwest Alabama. Five blackwater systems will be compared to five alluvial and five spring-run wetland systems common in the area as points of comparison. Systems will be chosen based on AL Natural Heritage Program database information and scores from the Wetland Ecological Integrity Assessment developed by the Natural Heritage Network, resulting in 30 sites overall (15 wetlands, 15 receiving streams). For each site, we will use standard protocols at the appropriate season and hydroperiod to quantify water quality and physicochemistry, vegetation composition, macroinvertebrate assemblages, fish assemblages, herpetofaunal composition, and avian assemblages. GIS layers and maps will be created as an interactive tool for community-based environmental protection and public outreach. The sampling at selected sites is anticipated to begin spring 2025. Results from this effort will provide water quality and biotic composition to characterize reference condition of blackwater systems, quantify relationships in conditions between wetlands and receiving streams, and ultimately assist ADEM in establishing standard wetland monitoring protocols across Alabama.

263 - Considerations for Utilizing AI Assistance in Macroinvertebrate Identifications

Claire Williams

Tennessee Department of Health, Nashville, TN

A unique and important skill in aquatic biology is the identification of various aquatic macroinvertebrates.

In identifying benthic macroinvertebrates, scientists evaluate the condition of water bodies. One way of doing this is looking at the genus, abundance, and diversity of aquatic larva. Each individual organism has a certain tolerance to pollution, so identification is extremely important to understand the heath of the body of water.

Aquatic biologists rely on dichotomous keys to accurately identify larvae. Keys are constantly changing. Currently, there are no universal keys or databases online with all information needed. Modifying and updating taxonomic keys in literature takes years. There are constant changes with taxonomy, especially when experts do not agree. Consensus in identification is often difficult.

However, society today is in a transitional era with AI and its role in daily life. The question facing nearly all scientific fields is this: What opportunities does artificial intelligence present for the furtherance of science? For aquatic biologist, it is easy to envision an ultimate long-term goal of a universal key or identification database to aid in the taxonomy of macroinvertebrates with quicker, more cost effective, and more accurate results. Aquatic biologists need to become comfortable with the idea of incorporating AI into research. However, there are several things to take into consideration before undertaking this endeavor.

With the help of AI, there could be a universal platform where experts in the field can upload, correct, and change the qualifications among certain groups as they reach a consensus about the organisms. A universal platform or identification database would allow aquatic biologists to be on the same page with taxonomy,and greatly improve their ability to monitor the aquatic environment.

264 - Linking Changes in Common Blood Parameters to Physical Trauma Using Fish as a Model

Blaine Wondemu, Ryan Saylor

Berry College, Mount Berry, GA

Traumatic brain injury (TBI) is caused by external impacts to the head. TBI can result in physical, cognitive, or behavioral symptoms, and outcomes range from complete recovery to permanent disability or death. Various treatments combat TBI effectively, but their success depends on diagnosing the issue after physical or cognitive decline is observed. TBI has a significant impact on human health, especially athletes, yet controlled experimentation to determine a dose and response is not possible. In contrast, fishes are a model species for assessments of traumatic injuries caused by impacts from hydropower turbines during passage events at hydroelectric dams. Thus, we aim to use fish as a model system to test the dose (trauma severity) and response (indicators of stress) associated with impact trauma. Our objective was to determine what blood parameters (e.g., glucose, sodium, etc.) can serve as indicators of traumatic injury. Use of these blood parameters will help determine if common stress metrics can be used to discern head from mid-body injuries in fish as well. We used rainbow trout (Oncorhynchus mykiss) as a model system because it has been used extensively in dose responses studies linked with impacts from hydropower turbines. Traumatic injury was assessed using simulated turbine blade strikes to the head, mid-body, or no impact (control) and sampled blood using the caudal puncture technique. Blood was analyzed for common stress indicators using a VetScan blood analyzer and Avian/Reptile Profile Plus rotors. Blood parameters were compared between treatments to determine if they varied significantly according to strike location. Here, I will describe initial insights from our pilot study to determine if investigating fish blood parameters is a viable way to study sub-lethal impacts from hydropower turbines and model blood biomarkers as correlates for TBI in humans.

265 - Exploring and mapping water quality in the Lumber River watershed

Lillian Matthews, Amber Rock

University of North Carolina at Pembroke, Pembroke, NC

The Lumber River is a culturally, ecologically, and economically important river in Southeastern North Carolina. The Lumber River and its tributary wetlands form a unique, free-flowing blackwater system that supports a high biodiversity of plants and animals. However, the Lumber River watershed has, for decades, been home to a high number of polluting industries, including both manufacturing and agricultural applications. These industries represent both historical pollution discharges and current threats to water quality in this regionally important watershed. Ensuring the water quality of this watershed is imperative to ensuring the good health of the ecosystem and its inhabitants. This study evaluates water quality data collected over the past year and compiles several research and service-learning projects into an ArcGIS map that projects the results alongside land use and topographical data. These projects investigated biological, physical, and chemical metrics of water quality, including fecal coliform bacteria, benthic macroinvertebrate community composition, nitrogen and phosphorus concentrations, and standard physical variables such as dissolved oxygen, pH, and turbidity. Current research is also exploring possible antibiotic runoff resulting from livestock operations within the watershed. Man-made antibiotics in the ecosystem can have a harmful impact on the beneficial bacteria critical to important bioprocesses. Data collected thus far suggest few impacts of agricultural runoff, as nitrogen and phosphorus concentrations were typically low. However, the data suggest marginal impacts of runoff from urban areas, including increased conductivity downstream of the city of Lumberton. The strongest impacts have been associated with industrial runoff, with increased heavy metals and decreased macroinvertebrate biodiversity downstream of historical and current industrial sites. Based on these findings, it is apparent that future research in this watershed should include a more rigorous evaluation of water quality. A more systematic approach could better capture the full complexity and dynamic nature of pollution impacts in this region.

266 - Ecology of Freshwater Sponges in Western North Carolina

Marcus Planck, Zariya Stewart, Raelyn DoByne, Cara Fiore

Appalachian State University, Boone, NC

Freshwater sponges (Porifera: Demospongiae: Haplosclerida: Suborder Spongillina) are pervasive worldwide but with patchy distributions and limited literature on their ecology and distribution. Freshwater sponges typically disperse by sexual reproduction with a planktonic larva and by production of resting bodies known as gemmules. The gemmules are both a dormant stage of the sponge during winter or drought and are considered a propagule that can be transported to other rivers by waterfowl. Here we present the species distribution for freshwater sponges at five sites in western North Carolina and preliminary information on factors that influence hatching gemmules from a subset of these species. Four sponge species were found consistently at the sites, but each site tended to

have just one species, while multiple species at one site was occasional. Hatching of gemmules was inconsistent in the laboratory but generally required longer periods (7-10 days) to initiate hatching compared to the model sponge species used in many developmental biology studies, Ephydatia muelleri. While freshwater sponges tend to be relatively small and cryptic, they are important filter feeders, habitat, and trophic connections in aquatic systems. This work provides preliminary insight into an understudied but ecologically relevant group of animals in aquatic systems and further work is needed to better understand the ecology, functional roles, and factors affecting the distribution of freshwater sponges.

267 - Atmospheric deposition of microplastics is associated with magnitude of precipitation in the southern Blue Ridge Mountains of western North Carolina

Anna Boodée[1], Madison Cleary[1], Erin Flanagan[1], Sofia Friedman[1], Angelina Guerrero[1], Natallie Hammond[1], Mary Catherine Hoover[1], Lucy Kraus[1], Genevieve Marti[1], Casey Meisel[1], Hannah Shepard[1], Edie Sherlock[1], Caleb Tyler[1], Katherine Wadkovsky[1], Annika Willis[1], Reagan Jarrett[2], Jerry Miller[3], Radmila Petric[1], Austin Gray[4], Nathaniel Barrett[3], Robert Youker[5], Mr. Jason Love, M.S.[2]

[1]Institute for the Environment, University of North Carolina at Chapel Hill, Chapel Hill, NC, [2]Highlands Biological Station, Western Carolina University, Highlands, NC, [3]Department of Geosciences and Natural Resources, Western Carolina University, Cullowhee, NC, [4]Virginia Tech, Blacksburg, VA, [5]Western Carolina University, Cullowhee, NC

Atmospheric deposition has been shown to be a primary source of microplastics (MPs) in headwater streams in the southern Blue Ridge Mountains. It is therefore critical to the assessment of MPs in rivers to document spatial and temporal variations in atmospheric depositional rates over the region. We deployed three wet/dry deposition collectors along a precipitation gradient in western North Carolina. Samples were collected weekly from October 2023 through November 2024. We filtered the samples and identified MPs ≥50 µm under a dissecting scope using standard identification protocols. Dry deposition rates ranged from 0 – 1,284 MPs/m2/day; wet deposition rates ranged from 0 – 3,034 MPs/m2/day. Fibers were the most prevalent microplastic, making up >90% of our samples. Blue was the most common color. The highest rates of deposition were associated with Tropical Storm Helene. Total annual deposition for Highlands Biological Station, our wettest site, was 55,589 MPs/m2, with deposition from Tropical Storm Helene comprising 11,518 MPs/m2, representing 20.7% of the annual total. Two weeks following the storm, deposition rates remained elevated, perhaps indicating local or regional re-suspension of MPs into the atmosphere after a period of drying. This is the first study to calculate annual total depositional rates of MPs in the southeastern United States. Our research reveals that microplastic deposition rates in the southern Blue Ridge Mountains are as high or higher than those reported in many European cities.

268 - Analysis of Fauna, Taxa, and Predation Frequency of the Upper Waccamaw Formation

Joseph Suddeth, Jack Vogenitz

Erskine College, Due West, SC

Predator-Prey relationships are vital to the environment because it brings balance to the food chain and shows how organisms interact with each other. This paper outlines the predation of marine organism from the phylum Mollusca in the Waccamaw Formation. The Waccamaw Formation consists of two layers called Upper and Lower Waccamaw formation. The Waccamaw Formation is dated back to the Cenozoic epoch which is around 11,000 to 2.4 million years ago. The samples collected in this study are from western South Carolina. The data supports that the overall average of drill frequencies for Lower Waccamaw Formation equated to 16.79% and the overall average of the Upper Waccamaw Formation drill hole frequencies equated to 21.36%.

269 - Endogenous tidal rhythms in mangrove tree crabs (*Aratus pisonii*) imply larval retention in a coastal lagoon

Savannah Goodwin, Corie Charpentier

Stetson University, DeLand, FL

Endogenous tidal rhythms can facilitate dispersal in estuarine larvae. For example, upward migrations during outgoing ebb tides result in offshore transport. In this experiment, we assessed whether the planktonic larvae of mangrove tree crabs (*Aratus pisonii*) exhibit tidal rhythms that could impact dispersal. Survivorship of larval *A. pisonii* is greater at high salinity (25 – 35 ppt), and larvae lack large protective spines. Therefore, we hypothesized that *A. pisonii* hatchlings would exhibit tidal rhythms that facilitate offshore transport, away from brackish estuaries with high predator abundance. Using larvae that hatched within 24 h of ovigerous female collection from Mosquito Lagoon, FL, we observed larval swimming activity in the dark for 72 hours. We evaluated larval activity by counting the number of larvae in the top third of a 20-cm tall column every 30 minutes. We then identified behavioral rhythms in surface swimming with periodograms and compared activity rhythms to tidal height using cross-correlation analysis. Larval *A. pisonii* displayed endogenous rhythms in swimming behavior that correlated to the tidal cycle. Contrary to our hypothesis, peaks in upward swimming corresponded to the incoming flood tides, not the outgoing ebb tides that facilitate offshore transport. Hence, these larvae may favor

retention in Mosquito Lagoon, which maintains relatively high salinities required for larval survival.

270 - Quantifying success of Bald Head Island's living shorelines through ecosystem service assessment over a three-year period

Joel Davies, Elizabeth Darrow, Allison Polinski

Bald Head Island Conservancy, Bald Head Island, NC

Oyster reefs provide many beneficial services for coastal ecosystems, including water filtration and habitat provision. Restored oyster reefs can provide many similar functions. In 2021, we built three restored oyster reefs in the tidal creek on Bald Head Island, North Carolina. Three years later, we set out to determine success of restored reefs against naturally-occurring ones through an assessment of oyster recruitment and growth, as well as habitat provision for benthic invertebrates. We conducted a survey at low tide in October 2024, sampling the restored reefs, along with paired wild and control (bare sediment) sites in the same stretch of creek. Three 0.25 m^2 quadrats were sampled from each site, with all reef or sediment material from the quadrat collected. All macrofauna present were identified and counted, and all oysters were measured and assigned a size class. The same methods were used at the same sites prior to restoration in 2021, and repeated post-restoration in 2022 and 2023, so we were able to quantify the difference in live oyster abundance through time using a before-after-control-impact design (BACI). The Shannon-Wiener index was calculated for each sample to contrast invertebrate diversity among site types. Live oyster abundance was greater in the restored reefs as they matured, surpassing wild reef abundances by 2023 ($P<0.0001$). The restored reefs showed higher numbers of juvenile oysters than wild reefs, indicating successful recruitment and survival. Faunal abundance and diversity indices increased similarly, with wild reefs being slightly more diverse ($H=1.933$) than restored reefs ($H=1.876$), despite a large proportion of organisms being from two non-native species. Based on our findings, it is clear that the restored reefs have measurable success through time. Future work will involve examining individual site differences and impacts of water quality metrics as they fluctuate temporally.

271 - Olivine Effects on the Salt Marsh Grass *Spartina alterniflora*

Ryan Reid, Taylor Allen, Heather Joesting

Georgia Southern University, Savannah, GA

The carbon dioxide levels in the atmosphere are increasing significantly, greatly contributing to global climate change. To minimize the negative impacts of climate change, innovative strategies to reduce atmospheric carbon dioxide concentration are necessary. Serving as significant carbon sinks, coastal salt marshes serve as significant carbon sinks by storing carbon within sediments and biomass. The mineral olivine has been shown to enhance carbon capture in soils, and the addition of olivine to salt marsh soils may increase their ability to sequester carbon, subsequently removing atmospheric carbon dioxide. Prior to field experiments on the carbon sequestration effects of olivine in salt marsh soils, controlled experiments must be conducted to evaluate the effect of olivine on native salt marsh plant species. This project's purpose was to investigate the effect of olivine on the growth of *Spartina alterniflora*, which is a native grass that plays a crucial role in salt marsh ecosystem function. *S. alterniflora* seedlings were grown into four treatments: topsoil and sand mixture; topsoil, sand, and marsh soil mixture; topsoil and olivine mixture; and topsoil, olivine, and marsh soil mixture. Number of stems, plant height, and leaf chlorophyll content were measured weekly for 12 weeks, after which all seedlings were harvested for the measurement of aboveground and belowground biomass. Results showed that individuals grown in olivine had significantly lower plant height, leaf chlorophyll content, number of stems and biomass. pH levels were significantly higher in the plants grown in the olivine, suggesting that olivine additions created an unfavorable environment for *S. alterniflora* growth.

272 - Characterizing shallow-water estuarine microhabitats and associated early stages of marine fishes

Lexie DelViscio[1], Sydney Bates[1], Antony S. Harold[2]

[1]College of Charleston, Charleston, SC, [2]College of Charleston, Grice Marine Laboratory, Charleston, SC

Microhabitats are composed of characteristic environmental variables usually patchy or restricted. Shallow-water marine fishes may associate with microhabitat patches, although there is relatively little evidence in the literature that early stages of fishes do. Fish species were sampled in two microhabitats in the Charleston Harbor estuary. These microhabitats were located on either side of a sand spit that is exposed at low tide. Collections of fishes were made using a fine-mesh beach seine pulled through a 10 m transect. The microhabitats were characterized by water temperature, salinity, oxygen concentration, algal coverage of the substrate, substrate grain-size composition and chlorophyll-a concentration. These parameters were determined for each sample of fishes. Preserved fish specimens were sorted and identified to the lowest possible taxonomic level. The microhabitats were compared using non-metric multidimensional scaling. The catch consisted of a total of 114 fish specimens, 42 of which were identified as larval or early juvenile. The microhabitat in the shallow channel shorewards of the sand spit had low algal coverage and larger substrate grain sizes (sand). The fish samples were made up of juvenile and adult Atlantic Silversides (*Menidia menidia)* and very few larval or early juvenile fishes. The other microhabitat, on the exposed side of the sand spit, was characterized by more extensive algal coverage and relatively small

grain size (silt/sand). In this exposed microhabitat Atlantic Silversides (*Menidia menidia*) were most common, however anchovies (Engraulidae), mojarras (Gerreidae), and other larval fishes were present, unlike in the channel. In conclusion, although based on a small sample size, the indications are that these two microhabitats exhibit distinct fish assemblages but the causation is yet to be determined. Future research will extend this work to a larger set of samples and additional microhabitats which we predict will lead to a more conclusive analysis.

273 - Fin-tastic Fish Findings: An Investigation on Fish Biodiversity at St. Catherines Island

Deeya Khambhaita, Jessica Reichmuth

Francis Marion University, Florence, SC

Biogeography is one of the key factors for the spatial distribution of many species. Numerous terrestrial and marine species follow the biogeographical pattern of latitudinal diversity gradient, where biodiversity increases closer to the equator. However, this pattern is not true for all locations. St. Catherines Island is a private island off the coast of Georgia. The island is a prime location for research due to the limited human activity and fish diversity. By using the island's diverse fish populations, the purpose of our investigation is to determine how changes in latitude and seasons affect fish biodiversity and abundance at St. Catherines Island. If latitudinal changes along with seasonal differences affect fish biodiversity, then there should be a variation in fish diversity and abundance between the Island's two sampling sites. The investigation collected fish from North Beach (NB) and South Beach (SB) on St. Catherines Island. After using 18m and 30m seines to collect the fish, the species' identities, total abundance, and total length were then reported. North Beach had a higher overall species richness than South Beach, with warmer months also having a higher species richness than cooler months. The Shannon-Weiner Index will be calculated to further support or dispute these findings. Richness differences may be related to sampling site location, current water quality parameters, or low tidal cycle.

274 - Estimate of Biomass and Carbon Storage in Cane Creek Mountains Natural Area

Julia Cunningham, David Vandermast

Elon University, Elon, NC

Photosynthesis removes carbon dioxide (CO2) from the air and in woody plants, the carbon is stored for long periods of time. Forests with long-lived and large trees should store significant amounts of CO2. The purpose of this study was to document the composition and structure of the forest and to estimate biomass and carbon storage in Cane Creek Mountains Natural Area (CCMNA), a local park with a Piedmont monadnock forest type. Data were collected from 46 non-permanent plots in which prism cruising was used to select trees for inclusion in the study. Diameter at breast height (DBH), as well as the species for each tree was recorded. Our results indicate that the size and species of trees in CCMNA are consistent with that of old-growth forests. Oak species are dominant, with 50% of trees being chestnut oak (*Quercus montana*), and 12.6% being white oak (*Quercus alba*). Furthermore, we found that the forest stores between 193.2-214.7 Mg/C/ha (45-50% of biomass), which is significantly higher than that stored in younger Piedmont forests. We examined the relationships between carbon storage and the following values: number of trees (N), species richness (S), Shannon's diversity (H'), % oak, and tree size (DBH). The only significant correlation with carbon storage was tree size. Our results indicate that local parks such as CCMNA are significant carbon sinks so long as they are managed to maintain healthy forests.

275 - Long-term Data Reveals that Precipitation Patterns Influence Nestling Growth of Bluebirds

Noah Williams

Appalachian State University, Boone, NC

In the southern Appalachian Mountains, climate change is causing more extreme precipitation events and increased temperatures. A better understanding of how weather influences detailed reproductive parameters of common bird species can shed light on how more imperilled avian populations will respond to global change. Although weather during the breeding season can impact reproduction, non-breeding season weather can cause carry-over effects and impact reproduction into the following breeding season. A mechanism for such an effect could be that winter weather influences food availability (arthropods) or maternal body condition. Using 14 years of data, we test the hypothesis that extreme variability in weather negatively impacts hatching and fledging success as well as growth of nestling Eastern Bluebirds (*Sialia sialis*). We examined both breeding season and non-breeding season weather metrics including: average precipitation, variation in precipitation, variation in the amount of snowfall, and variation in low temperature. We found that clutch size, the number of nestlings fledged per nest, and hatching success was unaffected by any of the weather variables while only nest success was affected by our weather variables. After non-breeding season weather characterized by higher amounts of precipitation, nests were less likely to fledge offspring. The growth of nestlings was significantly influenced by the amount of precipitation and variation in precipitation during the non-breeding season and breeding season. Nestlings grew more slowly after winters with high precipitation and during summers with a higher variation in precipitation. Bluebirds in our region generally produced two nests per summer and the effects of non-breeding season weather were most strongly felt by those nests that were started during

the early portion of the breeding season.

276 - Scalable Carbon Dioxide Flux Measurements for Ecological Monitoring using Connected Hardware and Cloud-based Software

Brandon Haney[1], Jason Hupp[1], George Burba[1,2], James Kathilankal[1], Doug Lynch[1], Gerardo Fratini[1], John McCoy[1], David Franzen[1], Tyler Barker[1]

[1]LI-COR, Inc., Lincoln, NE, [2]University of Nebraska - Lincoln, Lincoln, NE

Ecological monitoring of the carbon cycle requires accurate characterization of carbon dioxide flux at the Earth's surface, a process that can result in long term carbon sequestration into plant biomass or soil carbon or emissions into the atmosphere. Traditional methods to quantify this exchange over time and space have required complex instrumentation and skills in electronics, data management, sophisticated processing and post-processing algorithms, and networking, before any analysis ready data is available. Scientists in the ecological monitoring domain can utilize a simplified approach to carbon dioxide monitoring to inform their scientific questions related to the carbon and water cycles. This presentation provides an overview of the performance and capabilities of a scalable sensor for carbon dioxide flux monitoring using a simplified form factor, utilizing the eddy covariance method. Processing and post-processing outputs related to temporal accumulations and spatial extrapolation and attribution demonstrate the utility and potential to advance carbon cycle research.

277 - Soil-Based Emissions and Context-Specific Climate Change Planning: A Case Study of Georgia (USA)

Davis Nelson

Clemson University, Clemson, SC

Soil-based emissions from land conversions are often overlooked in climate planning. The objectives of this study were to use quantitative data on soil-based greenhouse gas (GHG) emissions for the state of Georgia (GA) (USA) to examine context-specific (temporal, biophysical, economic, and social) climate planning and legal options to deal with these emissions. Currently, 30% of the land in GA has experienced anthropogenic land degradation (LD) primarily due to agriculture (64%). All seven soil orders were subject to various degrees of anthropogenic LD. Increases in overall LD between 2001 and 2021 indicate a lack of land degradation neutrality (LDN) in GA. Besides agricultural LD, there was also LD caused by increased development through urbanization, with 15,197.1 km^2 developed, causing midpoint losses of 1.2×10^{11} kg of total soil carbon (TSC) with a corresponding midpoint social cost from carbon dioxide (CO_2) emissions (SC-CO_2) of USD $20.4B (where B = billion = 10^9, $ = U.S. dollars (USD)). Most developments occurred in the Metro Atlanta and Coastal Economic Development Regions, which indicates reverse climate change adaptation (RCCA). Soil consumption from developments is an important issue because it limits future soil or forest carbon (C) sequestration potential in these areas. Soil-based emissions should be included in GA's carbon footprint. Understanding the geospatial and temporal context of land conversion decisions, as well as the social and economic costs, could be used to create incentives for land management that limit soil-based GHG emissions in a local context with implications for relevant United Nations (UN) initiatives.

278 - Effects of Increased Temperature on Growth Rates and Survivorship of Longleaf Pine and Wiregrass: Implications for a Warming Climate

Haley Hightower[1], Monica Rother[2]

[1]Department of Environmental Sciences - University of North Carolina at Wilmington, Wilmington, NC, [2]Department of Environmental Sciences, University of North Carolina Wilmington, Wilmington, NC

Previous studies have demonstrated that changing climate conditions may affect the growth and survival of native species in longleaf pine savannas, but further research is needed to better understand how responses will differ across species and locations. The North Carolina Climate Science Report forecasted a temperature increase in North Carolina of at least 1.1 to 2.2 °C by 2050 (Kunkel et al., 2020). We designed a field experiment to examine the effects of temperature increases on juvenile longleaf pine (*Pinus palustris*) and wiregrass (*Aristida stricta*) in a recently burned location in the coastal plain of North Carolina. The experimental area consists of 80 subplots that were each planted with 4 longleaf pine and 3 wiregrass seedlings. 40 of the subplots were warmed using open-top heat-trapping chambers, and the other half were the control subplots. Over a 2.5 year data-collection period, survival and growth rates were compared between the treatment types (warmed and control). Differences in air temperature between warmed and control plots were monitored using dataloggers placed in a subset (n=8) of the plots. Longleaf pine seedlings were more significantly affected by the heat increase than wiregrass seedlings. Several plots (n=7) experienced 75% or more longleaf mortality over the course of the experiment, and of those 7 plots, 6 were in the warming treatment. Our results suggest that forecasted warming climate and associated drought will have a negative effect on these foundational species and may have a significant impact on the range and success of

these species and the longleaf pine ecosystem. Results of this study are applicable to forest restoration and management, endangered species conservation, carbon sequestration, and forest derived resource economics.

279 - Urban Trees Delay and Divert Water During Large Precipitation Events

Jorge Vera[1], Kyle Palmquist[1], Noah Manuszak[1], Elizabeth Moss[2], Shane Welch[1]

[1]Marshall University, Huntington, WV, [2]WVSU Extension Service, Charleston, WV

Many urban areas lack tree cover and are primarily dominated by impermeable structures, which facilitate surface runoff and amplify the effects of precipitation intensity. Urban trees provide ecosystem services, including rainwater retention and flood mitigation, as they increase water infiltration. Thus, they are essential during periods of high rainfall as they can reduce and postpone peak flow. Our objective was to examine how urban trees mitigate the severity of precipitation events. We hypothesized that canopy interception by trees would result in a time lag in surface runoff and reduce the intensity of precipitation events. Our study was conducted in Charleston and Huntington, WV. We chose five native tree species commonly planted in urban settings that vary in bark morphology and mature size: *Acer rubrum*, *Platanus occidentalis*, *Quercus palustris*, *Cornus florida*, and *Cercis canadensis*. We instrumented six individuals of each species to measure stemflow (water that flows down the branches and bole of the tree), throughfall (precipitation that passes through the canopy), and total precipitation using three HOBO rain gauges that automatically record 0.2 mm increments of precipitation. A mass balance equation was used to calculate canopy interception (water intercepted by the canopy) based on precipitation and throughfall. We also calculated the time lag between precipitation start and stemflow start and the end of precipitation to the end of stemflow. Our preliminary results suggest large trees (*Platanus occidentalis*, *Quercus palustris*) have a longer stemflow lag time and may have a more significant role in reducing peak flow than small trees. For example, a *Quercus palustris* tree had a 12-minute delay in stemflow, and stemflow continued for 1.65 hours after the end of precipitation. Our research enhances understanding of how urban trees delay and divert precipitation via canopy interception and stemflow, thereby reducing and postponing peak flow to municipal stormwater drainage systems.

280 - Exploring Ecological Symphonies: Unraveling Shifts in Phenophases of Trees vis-à-vis Changing Temperatures

Diane Diel, Utsav Adhikari, Joydeep Bhattacharjee

University of Louisiana at Monroe, Monroe, LA

Temperature serves as a critical factor in the growth of plants and the progression of ontogenetic stages. Temperate deciduous forests are reliant on the cyclical change in temperature to fulfil the thermal requirements for timely and optimal budburst. As temperatures continue to increase, the phenology of these forests are beginning to shift. Elevated temperatures accelerate budburst leading to earlier shifts into spring phenophases. These phenological shifts introduce stress and cause incomplete spring budburst in our forests. In this study we took 9 years of green chromatic coordinate (GCC) data from PhenoCam imagery alongside high-frequency temperature data collected at the US-ULM Carbon Flux tower in Russell Sage Wildlife Management Area, northeast Louisiana to form the basis of our analysis. Initial trends show there has been shifts in phenology as overall, 2023's canopy green period was 24 days longer than 2014's at 243 days long while 2014's canopy green period was 219 days. This trend was mirrored by the contrast in temperatures for these years. In 2014, the average temperature for the year was 12 degrees C, 8 degrees cooler than 2023's average of 20 degrees C. This research is currently being used to determine the specific critical parts of the year that determine complete budburst in the spring. This includes determining if thermal requirements are being met with these increasingly common warmer years. This research highlights the complex relationship between temperature and forest phenology, shedding light on the dynamics of our forest ecosystem, and its response to increasing temperatures. Characterizing the phenological shifts in our forests give valuable insight into future impacts of rising temperatures and help inform future conservation efforts.

281 - Evaluating Soil Microbial Community in Restored Longleaf Pine Forests versus Loblolly Pine and Hardwood-Dominated Forests

Tabitha Cantrell, Crystall Lee, Siren van Leeuwen

Georgia Highlands College, Rome, GA

The restoration of longleaf pine (Pinus palustris) forests is a crucial ecological effort aimed at revitalizing ecosystems that have been significantly altered by the encroachment of loblolly pine (Pinus taeda) and hardwood species. This undergraduate research experiment seeks to evaluate the soil microbial community composition in restored longleaf pine forests compared to forests that have transitioned to being dominated by loblolly pines and hardwoods. Soil microbial communities play a vital role in nutrient cycling, soil health, and overall ecosystem functioning, making their assessment crucial in understanding the impacts of forest composition changes.

The primary objective of this study is to compare the diversity, abundance, and functional potential of soil microbial communities between restored longleaf pine forests and loblolly pine/hardwood-dominated forests. This will help to elucidate the ecological benefits of longleaf pine restoration on soil microbial health.

Methodology: Soil samples will be collected from three restored longleaf pine forest sites and three loblolly pine/hardwood-dominated forest sites within the MWA. Standard soil sampling procedures will be employed to ensure consistency.

Microbial Community Analysis: DNA will be extracted from 1 gram of soil then serial diluted. Aliquots will then be inoculated on sterile media and incubated. After sub-culturing bacterial isolates will be morphologically biochemically tested including indole testing and nitrogen fixation.

It is hypothesized that restored longleaf pine forests will exhibit higher microbial diversity and abundance of beneficial microbial taxa compared to loblolly pine/hardwood-dominated forests. Understanding these differences will highlight the ecological advantages of longleaf pine restoration and provide insights into forest management practices aimed at enhancing soil health and ecosystem resilience.

282 - Effects of Manipulated Incubation Temperature on Nest Success and Nestling Growth in Eastern Bluebirds

Mallory Hagen[1], Lynn Siefferman[1], Sarah Knutie[2]

[1]Appalachian State University, Boone, NC, [2]University Of Connecticut, Storrs, CT

Climate trends demonstrate more frequent and intense weather fluctuations in the Southern Appalachians including warmer and wetter summer weather. Increased temperatures could reduce the chances of female songbirds successfully completing the energetically expensive incubation stage and incubation temperature may have carryover effects that affect nestling growth and fledging success. These disruptions could lead to reduced reproductive success and long-term population impacts, thus an understanding of temperature fluctuation is important in animal conservation. We manipulated nest temperatures during the incubation period in a Southern Appalachian population of Eastern Bluebirds. This is a high elevation population (~100m) with a relatively cold and rainy climate. Nests were randomly assigned to one of three treatments—cold, control, or heat—for 7 days during the 2nd half of the incubation phase. Next, we monitored hatch success, fledgling success and nestling growth rates. Although hatching success did not differ with treatment, the heated clutches took longer to hatch- especially later in the breeding season and nestlings from heated clutches were more likely to fledge the nest. We also explore whether measures of the mothers' quality interact with treatment to influence measures of nestling growth.

283 - Using Nighthawk, a Machine Learning Model, to Compare 2021 and 2024 Autumn Nocturnal Migration of Birds in Georgia

Nalah Karriem, Shalise Gibson, Samara Alexander, James Ferrari

Wesleyan College, Macon, GA

Bird populations have declined significantly since 1970, with an estimated loss of 3 billion birds in North America (Rosenberg et al. 2019). A cost-effective way to monitor common but declining bird species is to record their nocturnal flight calls (NFCs); audio-processing software can then identify birds down to the species level. In this study, we tested the ability of a recently developed machine learning model, Nighthawk (Van Doren et al. 2023), to identify NFCs of autumn migrants in Macon, Georgia in 2021 and 2024. Recordings were made from a rooftop from 12 to 2 AM each night from September 15 to November 15 using an OldBird 21c microphone. Forty-four bird species were detected, with a total of 4589 and 5600 detections in 2021 and 2024, respectively. We focused on 5 thrush species (Gray-cheeked, Veery, Hermit, Swainson's, and Wood) due to their relatively large numbers of detections compared to other species. There were 673 versus 241 thrushes detected in 2021 and 2024, respectively, and the week of October 6 to October 12 saw the highest numbers of thrushes in both years. Some regional inconsistencies were discovered during our tests of Nighthawk's performance. For example, the model most likely misidentified MacGillivray's Warbler (19 detections) and the American Tree Sparrow (11 detections), given the extreme rarity of both of these species in Georgia. This finding shows that the machine learning model may need to be regionally calibrated to improve its accuracy in the Southeast. Nighthawk will be a useful conservation tool as it is able to quickly process hundreds of hours of audio, thus eliminating the current analysis bottleneck. The monitoring of bird populations via NFCs will permit us to track the numbers of each species, enabling conservation biologists to focus their efforts on particular species and areas that need the most attention.

284 - Citizen Science as a Tool for Conservation Management: An Assessment of an Unstructured Data Platform 1890s-2024

Jasmine Ramey, Gregory Smith

Kent State University at Stark, North Canton, OH

Species monitoring efforts play a vital role in wildlife conservation. Scientists and managers can increase the amount of available monitoring data by using citizen science projects - public participation in scientific research. One popular citizen science platform is iNaturalist. While data collected from iNaturalist can be valuable for tracking invasive or endangered species, or documenting species of management interest, it is important to consider potential biases in the data due to the unstructured and open format of observations (observations of any taxa can be submitted). A comprehensive analysis was conducted on a substantial dataset of "Research Grade" observations from Ohio that were uploaded to iNaturalist. Taxonomic groups and observations made in each season were quantified and observations in the database were compared to actual species lists in Ohio. The focus was centered on charismatic taxa and their potential overrepresentation in the dataset, bias in activity of observers, and frequency of observations of threatened and endangered species. Initial findings indicate that iNaturalist does have biases toward charismatic taxa and toward observations in warmer seasons. However, there are also recorded observations of species of concern throughout the taxa in the database. We also looked at the role of geography in the structure of the data as most observations are clustered around major urban centers in the state. Despite potential biases, these programs still offer value as they support public education and provide usable data that scientists would be unable to gather without the help of citizens. However, in order to be applicable, managers need to understand the limitations of such unstructured platforms.

285 - An Initial Assessment of Restoration Success of the Pictsweet Mitigation Site Using a Floristic Survey of the Vascular Plants

Hettie Peek, Michael Schiebout

Union University, Jackson, TN

A floristic survey was conducted during the spring and summer 2024, comparing the Rossville Farm restoration area to an adjacent natural bottomland hardwood forest reference area. Nearly all the specimens from both collections were successfully identified to species level and catalogued. Of the 409 total specimens collected, 141 species were identified from the restoration site, while 92 species were identified from the reference site. Of the 186 total unique species collected from both sites, 47 were shared between both areas. Results showed that 50% of the restoration site species were wetland indicators, while 40% of reference species were wetland indicators. The restoration site had a higher percentage of non-native species (28%) compared with the reference site (26%). These results indicate that the restoration site is progressing towards a functional bottomland forest and is currently composed of many wetland herbaceous species.

286 - Multi-Dimensional Assessment of Species Composition and Vegetative Health Via Aerial Imagery and Machine Learning

Grant Erbelding

University of Louisiana Monroe, Monroe, LA

As the effects of global climate change continue to intensify, consistent monitoring of valuable and vulnerable ecosystems is vital to their preservation. To this end, remote sensing via satellite, and increasingly, via Unmanned Aerial Vehicles (UAVs) has continued to grow as an effective tool for high-resolution ecological monitoring. This project focuses on leveraging time-series aerial multispectral photogrammetry, Machine Learning (ML), and intensive ground validation to develop a comprehensive methodology for monitoring the old-growth Bottomland Hardwood Forest ecosystem native to Northern Louisiana.

Using a multi-temporal and multi-dimensional approach, this project has two major goals. First, the automation of identification of canopy-contributing tree species via ML model developed in the R programming environment. This model will delineate and isolate canopy extent, as well as identify the eight dominant tree species within this ecosystem. Second, spectral indices and vegetative health markers will be used to detect indicators of stress in trees across the forest, providing insight into how this ecosystem is responding to changes in temperature and precipitation patterns. Preliminary results demonstrate promise in aerial stress detection, and ground-truthing through phenological and cellular analysis of stressed individuals will aid in corroborating signs of biotic and abiotic stress factors.

The aim of this project is to produce a scalable and automated ecosystem monitoring system capable of providing actionable insights into forest health, and inform forest management in a changing climate.

287 - Passerines: Which are more likely to be admitted to an avian rehabilitation center in North-Central Alabama

Kristin A. Bakkegard, John Matthew Erickson

Samford University, Birmingham, AL

Birds in the order Passeriformes (perching birds) comprise approximately one third of all bird species in Alabama and nearly 60% of all bird species worldwide. As with most vertebrate groups, they are in decline. A resource to reduce declines is wildlife rehabilitation centers. The Alabama Wildlife Center (AWC) is a wildlife rehabilitation center located in Shelby County, AL primarily serving the north and central counties of Alabama, specializing in the rehabilitation of injured and orphaned birds. To assess whether some families within the Passeriformes are more likely to require care at the AWC than others, we compared AWC's intake data (which also included cause of injury if known) to Alabama Audubon's spring and fall bird count data for the years 2013-2021. Our null hypothesis was that the proportions of birds (by family) entering AWC for care should reflect the proportions of those birds (by family) observed in the wild during the bird counts. We found that this was not the case. Of the 21 families of Passeriformes in this dataset, eight families were more likely to be taken to the AWC than their proportions in the bird counts. The three most impacted families were Fringillidae (4 species; most common– House Finch), Cardinalidae (6 species; most common– Northern Cardinal) and Turdidae (7 species; most common– American Robin). In the Fringillidae, disease (conjunctivitis/salmonella) was the leading cause of admission. For the other two families, it was window strikes, followed closely by cat attacks. Understanding which and why specific families of birds are sent to wildlife rehabilitation centers is important not just for rehabilitators, but also for educating the public and promoting implementation of known mitigation methods that reduce the risk of harm to birds.

288 - A Spatial Analysis of Conservation Easement Characteristics and Biodiversity

Logan Snodgrass, Dr. John Quinn

Furman University, Greenville, SC

Conservation easements are vital tools for protecting biodiversity on private lands, but their effectiveness is influenced by factors like size, location, and shape. This study investigates the spatial distribution and conservation function of easements, focusing on the relationship between easement shape and conservation value. Using data from the National Conservation Easement Database (NCED), we analyzed easements across eight counties in the United States, representing diverse biomes. Landscape metrics such as area, perimeter, shape, core area index (CAI), contiguity, and fractal dimension were calculated using R and the landscapemetrics package. Our analysis revealed significant correlations between several metrics, including perimeter and shape, CAI and perimeter, and CAI and contiguity. Furthermore, easements with exclusive public access exhibited higher contiguity, fractal dimension, shape complexity, and CAI values compared to those with open access. These findings suggest that easement shape and access restrictions play a crucial role in maximizing their conservation potential. This research contributes to a deeper understanding of how easement characteristics can be optimized to enhance biodiversity and inform future conservation efforts

289 - Assessing Biodiversity Attrition From Invasive Species and Herbivory at Lake Raleigh Woods, an Urban Forest in Wake County, NC

Benjamin Warfield[1], Steph Jeffries[2]

[1]North Carolina State University, Winston-Salem, NC, [2]NC State University, Raleigh, NC

With expanding urbanization and deforestation, natural spaces with healthy ecosystems are becoming more important to protect. While creating and protecting parks and open spaces are a high priority in city planning, more action might be needed to offset site degradation from invasive species and herbivory. Lake Raleigh Woods at NC State University is a forested natural area that NC State considers a "Hallowed Ground." It was also deemed a high quality site, with higher biodiversity than any site of comparable size in Wake County, by the NC Natural Heritage Program. However, the forest has not been surveyed recently, and invasive species and increased herbivory may have reduced biodiversity and caused habitat degradation. This study aims to understand how forests like Lake Raleigh Woods experience biodiversity loss without human management and intervention. We seek to learn if Lake Raleigh Woods has experienced significant habitat degradation or loss in biodiversity since its last inventory in 2002. We will compare previous inventory data and Natural Heritage Program forest type characterizations to the composition currently found at the site. This research also presents an opportunity to survey for herpetofauna in the site, to create a baseline that we can compare with a 2006 environmental assessment. That assessment listed 16 potential amphibian species, and 24 potential reptile species. A herpetological survey would provide a good measurement of habitat quality, as reptiles and amphibians are very sensitive to their environment. This research will provide a biodiversity snapshot of Lake Raleigh Woods that can help guide future management. It will also serve as a case study on threats depleting natural spaces in urban areas, even if they are protected from development.

290 - Forest soil microbiome dynamics after *Lonicera maackii* removal in central Kentucky

Marvin Ruffner[1], Carlos Rodríguez López[2], Gretchen Ruschman[2]

[1]Asbury University, Wilmore, KY, [2]University of Kentucky, Lexington, KY

Non-native, invasive plants are known to alter the above- and below-ground structure and function of ecological communities. *L. maackii* (Rupr.) Herder (Caprifoliaceae) is a highly invasive species in Kentucky (KY) and surrounding region. While *L. maackii* invades a variety of environments, it often forms dense understory populations within woodlands and forests altering the structure and function of forest plant communities. Moreover, invasive plants are known to alter soil microbiomes in environments they invade; yet little is known how *L. maackii* impacts forest soil microbial communities. The objective of this research was to characterize forest soil microbiomes in areas dominated by *L. maackii* compared to areas where *L. maackii* has been removed. We hypothesize *L. maackii* invasion alters forest soil microbial communities. Thus, we predict if *L. maackii* is removed then we expect forest soil microbial communities to differ significantly between the "restored" forest compared to the unrestored forest (i.e., *L. maackii* dominated). To test our hypothesis, we collected five soil cores (upper 10cm) from each of three different experimental restoration treatments: 1) untreated (*L. maackii* dominated); 2) *L. maackii* removal + cut-stump herbicide treatment; and 3) *L. maackii* removal + cut-stump herbicide + restoration plantings, from two different *L. maackii* restoration studies initiated in spring 2019 and 2022 in central KY. A total of 45 soil cores (5 soil cores x 3 treatments x 3 replications) were collected from each restoration study (total n = 90). Soil DNA extraction, PCR cDNA library production, meta-barcode sequencing, and bioinformatics are in progress to analyze the forest soil microbiomes from experimental treatments of the two restoration studies. Results from this research will contribute important knowledge regarding the effect of *L. maackii* and subsequent *L.maackii* removal along with the influence of native plant restoration on forest soil microbial community structure and function.

293 - Bridging Conservation Ethics and Bird Diversity: A Reflection on the Values of Managed and Unmanaged Habitats

Jackson Lehmann, Dr. John Quinn

Furman University, Greenville, SC

This project combines avian research with broader questions about conservation ethics and public access. Over the summer, we compared across two types of landscapes: sites implementing "ClimateSmart" timber management practices and unmanaged public lands. Building on this experience, and the ethical implications of conservation, we consider the implications of management funded through public dollars. How do taxpayer-supported conservation initiatives affect biodiversity outcomes? Are these practices reflective of values and rights in terms of public access? Are funds allocated in a way that ensures equity, prioritizing ecological need or potential impact? Who is informed about these opportunities, and is there sufficient outreach to include underrepresented groups, rural communities, or smaller-scale landowners? Additionally, how transparent is the allocation process, and are there mechanisms to ensure accountability and effective use of taxpayer dollars? By exploring these questions and using ClimateSmart as a model for ethical publicly funded management strategy, this work seeks to connect field biology with the larger ethical frameworks of land stewardship, ownership, and public access. In this poster we present both the ecological insights and the philosophical considerations of this work, exploring how field biology can inform diverse conservation models. By bridging scientific analysis with ethical discourse, this study aims to advocate for conservation practices that prioritize both biodiversity and equitable public engagement

294 - *Persicaria perfoliata*'s Dissemination in Boone, North Carolina

Evan Curth, Noah Rokoske, Annkatrin Rose

Appalachian State University, Boone, NC

Persicaria perfoliata is a class B noxious weed that has been present in North America since the 1930s. It was first introduced in Pennsylvania, mixed into Holly (*Ilex*) seeds. Since its introduction it has dispersed to eighteen states, and a method of biocontrol using a monophagous weevil, *Rhinoncomimus latipes*, has been active since 2004. The species was first reported east of Boone in 2008, and weevils were dispersed on individuals of *P. perfoliata* at the Boone Greenway in June of 2021. Populations of both species have persisted since, and the invasive plant continues to spread even with biological control mitigation present. A total of 674 individuals were observed, and most of these (498) had weevils or evidence of weevils (leaf damage) present. The locations where weevils were present had a slightly lower individual average per population, though this was not statistically significant. The spread of the invasive species continues with these biocontrol measures in place, though it is likely reduced as a result of herbivory.

295 - Seasonal Identification and characterization of Shining Clubmoss (*Huperzia lucidula*) Fungal Endophytes

Drew Ellis[1], Erica Campbell[2], Annkatrin Rose[2]

[1]Department of Biology, Appalachian State University, Boone, NC, [2]Appalachian State University, Boone, NC

Huperzia lucidula (shining clubmoss) is a native species of the Appalachian Mountains that contains endophytic fungi that produce a selective and reversible acetylcholinesterase inhibitor, Huperzine A. Endophytic fungi are organisms that spend a significant portion of their life cycle internally within the plant. The project aims to isolate and identify culturable fungi that H. lucidula experiences symbiosis with in different seasons, and compare to the in planta endophyte community in different seasons and tissues. The endophytic fungi will be isolated on potato dextrose agar plates, and sub-cultured in potato dextrose broth. The fungi will be identified by DNA barcoding analysis by amplifying and sequencing the major ribosomal internal transcribed spacer (rITS), and tested for acetylcholinesterase inhibition. It is expected that the observed fungi will be most diverse during the spring and fall seasons when fungal diversity is supported by cool, moist climates. The project's goal is to build upon previous research and determine the level of fungal diversity in each growing season, indicating when the best time to sample endophytes for cultivation would be. By documenting the culturable fungi H. lucidula associates with, this research aims to determine reliable and sustainable methods of culturing the fungus. Future research can utilize this information for possible alkaloid isolation, and clinical research.

296 - Using the NatureServe Climate Change Vulnerability Index to assess risks to rare plant species within Chesapeake & Ohio Canal National Historical Park

Mrs. Clara Thiel, M.S.

Frostburg State University, Frostburg, MD

The NatureServe Climate Change Vulnerability Index (CCVI) is a tool for assessing species risk and vulnerability to climate change-related impacts. Such assessments are useful for land managers as they can be used to inform conservation initiatives for a given species or area. Because many species have different life histories, distributions, and adaptive potentials, it is important that species-specific risk factors be identified to most effectively manage sensitive natural resources with regard to a changing climate. To inform management and conservation initiatives within a small suburban park, climate change vulnerability assessments will be completed for the 106 rare plant species found within Chesapeake and Ohio National Historical Park. Use of the CCVI will allow park managers to identify taxa of greatest conservation concern while also recognizing trends and knowledge gaps related to species resilience and risk factors. Preliminary findings and analyses from assessments completed thus far will be presented.

297 - Application of microsatellite markers in the conservation of *Helianthus schweinitzii* (Torr. & A. Gray)

Zofia Gordon, Gwendolyn Tomlin, Kunsiri Grubbs

Winthrop University, Rock Hill, SC

Helianthus schweinitzii, a federally endangered sunflower, is native to the Carolina Piedmont. This tetraploid hybrid, derived from *H. microcephalus* and *H. giganteus*, reproduces both sexually through pollination and asexually via tuberous rhizomes. Asexual reproduction is beneficial for survival, particularly in response to habitat loss. However, this dependence on asexual reproduction might contribute to reduced genetic diversity within the species. Therefore, understanding the genetic composition of different populations is crucial for its conservation. This study examines genetic diversity within and between populations of *H. schweinitzii*. We have utilized simple sequence repeat (SSR) methods with a universal M13 tail and 19 potential molecular markers, enhanced with various phosphorescent dyes for increased efficiency. The resulting information will reveal insights into clonality, genetic diversity, and population structures of *H. schweinitzii*. Consequently, we can develop tailored conservation plans addressing the specific genetic diversity needs of each population.

298 - Expansion of Surveying for the Eastern Hellbender Across Northwest North Carolina Using eDNA

Holley Lowe, Gracie Vickery, Dominick Latta, Michael Wright, Megan Rudock-Bowman

High Point University, High Point, NC

The Eastern Hellbender (Cryptobranchus alleganiensis alleganiensis) is an aquatic salamander that is listed as a species of special concern. They are commonly found in rivers and tributaries along the Appalachian Mountains from New York down to Georgia. Hellbenders inhabit microhabitats on the downstream side of rocks where they catch food as it floats by. The Hellbender is remarkably rare and withdrawn making them difficult to spot and assess in the wild. Currently, intensive surveying is used to determine the Hellbender population. However, the utilization of environmental DNA (eDNA) and quantitative PCR (qPCR), could significantly cut

down on the time, invasiveness, and cost of these surveys. Our goal is to greatly expand the surveying region in collaboration with an ongoing study by the North Carolina Wildlife Resources Commision (NCWRC). We have collected water samples along the New River and its branches in the northwestern part of North Carolina, in areas suspected to be Hellbender habitats by the NCWRC. Samples are filtered within 24 hrs. DNA is isolated using Qiagen DNeasy PowerWater kit and the concentration and purity analyzed using NanoDrop. The Eastern Hellbender's presence or absence can be determined via qPCR using primers/probes currently used by the NCWRC and Tangled Bank Conservation (TBC). Results from duplicate samples will be validated by TBC. With this knowledge and through these methods it is possible to better monitor population sizes and location of the decreasing number of Eastern Hellbenders across a much larger region of their documented habitat.

299 - Stickier Than Expected: Optimized DNA Isolation in Southeastern *Drosera* Species

Laci Coker[1], Niklas Plath[1], Jeremy Rentsch[2]

[1]Francis Marion University, Florence, SC, [2]Francis Marion University, FLORENCE, SC

Several species of *Drosera*, commonly called sundews, inhabit the wetlands of the southeastern United States. These perennial carnivores are characterized by mucilaginous trichomes covering sections of their leaves that help to attract, capture, and digest prey. Insects, like mosquitoes and gnats, land on the trichomes and become stuck while the leaf curls around the insect to begin digestion. These plants do not use carnivory to replace energy garnered from sugars produced in photosynthesis, but rather to supplement the plant with additional nutrients such as nitrogen, potassium, phosphorus, and trace elements that cannot be found in the poor, acidic soils where they normally grow. Plants already have an abundance of polyphenols, polysaccharides, and secondary metabolites in their cells, but the trichomes of *Drosera* species introduce several more tricky polysaccharides into the plant's chemistry. These substances make isolating DNA and performing downstream enzymatic applications, such as PCR, quite challenging. Oftentimes, DNA that has been isolated, if any is able to be isolated at all, has either poor yield, poor purity, or both. To address this, we screen, troubleshoot, and refine several methods of DNA isolation of varying efficacy to create an optimized protocol with a focus on temperate *Drosera* species native to the southeastern United States, such as *D. capillaris* and *D. filiformis.* The ultimate goal of this work is to formulate an optimized approach that consistently and reliably produces a pure, high yield of genomic DNA that can be used for downstream molecular analysis.

300 - Genotyping an ex-situ collection of *Spiraea virginiana* for Potential Augmentation Work in Great Smoky Mountains National Park

Anthony Mills, Matt Estep

Appalachian State University, Boone, NC

Spiraea virginiana (Virginia meadowsweet) is a rare, clonal shrub in the family Rosaceae. It is restricted to riparian habitats and is endemic to the Southern Appalachian Mountains. Spiraea is rare even in its natural habitat, and is considered federally imperiled (S2, G2) in North Carolina and Tennessee. Populations of Spiraea within Great Smoky Mountains National Park (GSMNP) are declining, but cuttings from these populations have been held in an ex-situ conservation garden for decades. The purpose of this study is to genotype samples of Spiraea virginiana from the ex-situ garden to ensure they are suitable for subpopulation augmentation within GSMNP. DNA was extracted using a standard CTAB protocol and seven microsatellite loci were amplified and genotyped. Each sample genotyped will be compared to existing data from natural populations within GSMNP.

301 - Fecal DNA Analysis of *Sylvilagus aquaticus* Samples

Kate Kaminsky[1], Stephen Harris[2], David Jachowski[2], Michael Hook[3], Laary Cushman[1], Carrie Koenigstein[1]

[1]Anderson University, Anderson, SC, [2]Clemson University, Clemson, SC, [3]South Carolina Department of Natural Resources, Clemson, SC

Sylvilagus aquaticus, more commonly known as the swamp rabbit, is facing endangerment through habitat loss and hunting, but their cryptic nature makes it harder to observe their behavior and help sustain them. With the lack of observational data, another method is needed to gain insight about their diet, health, and genetics; we hypothesize that the use of non-invasive environmental DNA may be a promising option. In our research, we have purified the DNA from various samples of putative swamp rabbit fecal pellets from across South Carolina. Next we searched the literature for effective rabbit cytochrome b amplification primers and selected three sets: Cytb_Lag primers creating a 115 bp amplicon (Rodrigues et.al., 2019), RabSeq R and RabCytb F primers creating a 400 bp amplicon (Adams et.al., 2011), and MVZ05 and MVZ26 primers creating a 733 bp amplicon (Smith and Patton, 1993). We have run multiple PCR reactions to determine which primers work best for our fecal DNA samples. Following selection of the best primer pair, the next stage of this project is to perform sequence analysis of the cytochrome b gene to confirm that it matches the swamp rabbit genome. This is part of a larger project that aims to learn more about the local swamp rabbit species through environmental DNA without directly observing them.

Adams et.al., (2011). Rapid species identification of pygmy rabbits (*Brachylagus idahoensis*) from fecal pellet DNA. Molecular ecology resources. 11. 808-12.

Smith and Patton., (1993).The diversification of South American murid rodents: evidence from mitochondrial DNA sequence data for the akodontine tribe, Biological Journal of the Linnean Society, Volume 50, Issue 3, Pages 149-177.

Rodrigues et.al., (2020). DNA mini-barcoding of leporids using noninvasive fecal DNA samples and its significance for monitoring an invasive species. Ecol Evol. Jun 5;10(12):5219-5225.

302 - Development of an eDNA Assay to Monitor the Endangered *Moxostoma sp. Carolina* (Carolina Redhorse) in North Carolina Waterways

Ms. Catherine Summerrow, Dominick Latta, Megan Rudock-Bowman

High Point University, High Point, NC

Moxostoma sp. Carolina, also known as the Carolina Redhorse, is a threatened species of suckerfish native to the Pee Dee and Little River Systems. Current monitoring methods, including catch and release, and PIT tagging are unreliable, often ineffective, and are stressful to the fish. To better monitor *Moxostoma sp. Carolina*, the Rudock Lab as designed an eDNA assay to monitor presence of the species. This method is cheaper, faster, and generally has a higher throughput than tagging, without the downsides of potentially stressing or harming the endangered fish. Fishmap was used to to identify all sympatric *Moxostoma* species present in documented waterways inhabited by the Carolina Redhorse. The Cytochrome B gene sequence for each species was downloaded from BLAST as a fasta file. MEGA was used to compare sequences, and identify areas of unique sequence for primer/probe design. An ideal area for probe design was identified between base pairs 771 and 899. The Cytochrome B gene was then uploaded to IDT PrimerQuest to generate a primer and probe for this region. Samples were collected from the Pee Dee and Little rivers, which were filtered before DNA isolation using a Qiagen DNeasy PowerWater kit. DNA was analyzed using Real-Time qPCR and PCR to amplify target sequences. A positive result produces DNA fragments of 128 bases, visible via gel electrophoresis and a positive reading in the qPCR presence/absence analysis.

303 - Monitoring the Atlantic Pigtoe in North Carolina using eDNA applications.

Michael Wright, Gracie Vickery, Holley Lowe, Dominick Latta, Megan Rudock-Bowman

High Point University, High Point, NC

The Atlantic Pigtoe, *Fusconaia masoni,* is a freshwater mussel designated as threatened by the US Fish & Wildlife Service. The Pigtoe plays an important role in maintaining North Carolina's unique and diverse river systems. They are also a direct measure of the river system's health, warranting strong conservation efforts. The Pigtoe mussel population is currently being surveyed by traditional catch and release methods which can be time consuming, highly inaccurate, and even harmful. The use of environmental DNA (eDNA) may provide a more efficient and cost-effective method for monitoring this species. eDNA is DNA shed into the water by the Pigtoe that can be collected and analyzed using custom-made assays. To create an effective primer set specific for the Atlantic Pigtoe, we used BLAST to find sequences of all sympatric species, MEGA to create a phylogenetic tree and a DNA alignment of those species, and IDT PrimerQuest to create the primers and probe. Water samples from the Tar River were collected and filtered on site. In the lab, DNA was collected using a Qiagen PowerWater Pro DNA Isolation kit and analyzed for quality and quantity using the NanoDrop. PCR, qPCR and gel electrophoresis were used to determine the presence of Pigtoe DNA in each sample. Our results thus far suggest that our assay is successful in amplifying target sequences. Further evaluation in the presence of positive control samples and assay validation by sequencing will be needed to confirm the accuracy of this assay.

304 - The Effects of Secondary Contact on Tellico Salamanders (*Plethodon aureolus*)

Hunter Shaw, Benjamin Holt

Baylor School, Chattanooga, TN

Secondary contact occurs when previously isolated species occur sympatrically due to changes in geological or geographical conditions. Four possible outcomes of secondary contact are: hybridization, competitive exclusion, stable coexistence, or a mix of the three. This study aims to measure secondary contact and establish ranges for three species of salamanders of the genus *Plethodon* native to the Unicoi mountains of Tennessee and North Carolina. *P. aureolus*, *P. teyahalee*, and *P. shermani* live in proximity with niche overlap, making secondary contact difficult to analyze. Physical similarities and hybridization result in less distinction between species. *Plethodon* salamanders are useful for hybrid research due to their relatively recent time of divergence and similar niche requirements. Tissue samples were collected from individuals of each of the three species in the Bald River Gorge Wilderness, the

Citico Creek Wilderness, and the Cherokee National Forest. Representative DNA sequencing using both nuclear and mitochondrial DNA markers and phylogenetic analyses are then used to further determine the areas in which hybridization may occur. With these data we hope to develop a better understanding of the genetic makeup of Tellico salamanders (*P. aureolus*) and establish the hybrid zones of *Plethodon spp.* in the mountainous regions of Tennessee and North Carolina. The results will evaluate the historical, current, and future effects of secondary contact on salamanders in Southern Appalachia. *Plethodon* salamanders are a key part of the food chain in Southern Appalachian ecosystems, making it crucial to understand the complex morphologies of each species in order to properly protect and conserve them.

305 - Herbaceous vascular plants of Blue Springs State Park and Forever Wild Tract, Barbour County, Alabama

Joshua Bailey, Tyler Parrish, Hailey Williamson, Michael Wayne Morris

Dept. of Biological and Environmental Sciences, Troy University, Troy, AL

Blue Springs State Park and Forever Wild Tract is located in the Southern Hilly Gulf Coastal Plain level IV ecoregion of the Southeastern Plains level III ecoregion in southeastern Alabama. The study area covers 82 ha and is drained by the West Fork of the Choctawhatchee River. The state park was formed in 1963, and the Forever Wild Program of the State of Alabama purchased a contiguous tract in 2013 to add natural habitats to the state park. Natural communities in Blue Springs State Park and Forever Wild Tract include hardwood swamp forests with *Nyssa biflora*, bottomland hardwood forests along the Choctawhatchee River, southern mixed hardwood forests along streams and on slopes above the river, bay swamps, springs, and seepage areas, and upland successional mixed pine-hardwoods. Ruderal habitats range from mowed lawns and roadsides, to picnic areas and sandy fields, to powerline rights-of-way. Trips to document herbaceous vascular plant taxa started in February, 2024, and continued through November, 2024. Herbarium specimens were prepared for deposit in The Alabama Natural Heritage Section Herbarium (ALNHS). Voucher specimens of the woody plant taxa had been made in fall, 2023, and were reported in spring, 2024. To date, 319 herbaceous species as well as 297 genera and 118 families have been documented; currently, 467 species of both herbaceous and woody plants have been vouchered for Blue Springs. Noteworthy species of regional conservation concern according to the Southeastern Plant Conservation Alliance include *Crataegus pulcherrima, Iris brevicaulis, Platanthera flava, Sceptridium lunarioides, Sideroxylon thornei,* and *Stewartia malacodendron*. Families with the most taxa present are: Asteraceae (55), Poaceae (48), Fabaceae (29), Cyperaceae (25), Rosaceae (15), Rubiaceae (14), and Fagaceae (13). Non-native species account for approximately 17% of the flora.

306 - Exploring the usability of iNaturalist BioBlitz data as a means for monitoring invasive plant species

Polly Ciesla[1], Will Bennett[2], Annkatrin Rose[1]

[1]Appalachian State University, Boone, NC, [2]Town of Boone, Boone, NC

The spread of invasive plant species poses a significant threat to the biodiversity of Watauga County and surrounding areas. Monitoring the expansion and presence of species is important in reducing their ecological impact. This study explores the utility of iNaturalist, a citizen science platform, in monitoring invasive plant species and compares the efficacy of student-collected BioBlitz data with more targeted invasive species monitoring approaches. Data was collected from three sources; (1) Appalachian State BioBlitz projects, submitted by students and researchers, (2) independent invasive species monitoring projects, and (3) other web based invasive species mapping tools. Each method was assessed for the quality of data collected, the area of coverage and observation bias to determine the best approach for monitoring the spread and density of invasive plant species. Through comparing these approaches our study emphasizes the strengths in citizen and academic led programs and how they can be used as a resource to complement official invasive species monitoring approaches.

307 - The flora of Roundabout Meadow Wildlife Management Area (Loudoun County, Virginia): five years of research, education and community partnership in a living lab.

Anna Sophia Cline[1], Cameron Pierce[1], Dalia Aguilar[1], Andrea Weeks[2]

[1]George Mason University, Fairfax, VA, [2]George Mason University, Department of Biology and Ted R. Bradley Herbarium, Fairfax, VA

Demonstrating why floristic research is still needed in the 21st century - even in reportedly well-studied areas - is a perennial challenge for accessing research funds, for training the next generation of field botanists and for persuading our local communities that regional plant biodiversity has value in its conservation. To address this complex challenge, we established a living lab in 2020 at Roundabout Meadow Wildlife Management Area (RMWMA) in partnership with Piedmont Environmental Council (PEC), a land conservation non-profit based in northern Virginia. RMWMA is a 2.8 ha upland wetland and former cattle pasture managed for grassland restoration by PEC that is publicly accessible. It is part of a highly visible 120 ha tract that preserves agricultural land in a transition zone between

historic, rural landscapes and rapidly expanding, high-density residential areas in the Inner Piedmont of Loudoun County. PEC is leveraging the location of this tract to demonstrate and promote habitat conservation in the region. Here we report results from five years of an ongoing student-led floristic checklist project at RMWMA and the learning objectives of place-based activities that we developed for upper-division undergraduate students in three courses at George Mason University: Plant Ecology, Plant Diversity and Evolution, Introductory Botany. Future plans include creating a public information kiosk that highlights student discoveries about the RMWMA flora. Based on the success of this living lab collaboration, we encourage other botanical educators to consider establishing community partnerships that combine opportunities for long-term floristic research by undergraduate students with public outreach and education.

308 - An Overview of Section 6 Funding for At-Risk Plant Species in Alabama

Wayne Barger

Botanist Natural Heritage Section, AL-DCNR, Montgomery, AL

Alabama's rich plant biodiversity, along with its numerous critically imperiled plant taxa, has been well documented. Despite this, Alabama was not eligible to receive Section 6 funding through the U.S. Fish and Wildlife Service (USFWS) until 2018. Section 6 is a federal program that annually allocates funding to states for the oversight of conservation projects directly involving "at-risk species" as identified by the USFWS. Provided here is an overview of the Alabama plant taxa eligible for funding under this program, selected projects which were completed as a result, and the outcomes achieved. Eligible species needing further study to assess and mitigate the loss of state/regional biodiversity are also discussed.

309 - Tomato Microbe Abundance in Relation to Trichome Density

Foster Campbell, Ethan Hughey, Johannamarie Nwanagu

Furman University, Greenville, SC

This study investigated the relationship between trichome density and microbial abundance on Solanum lycopersicum, the tomato leaves and the effects of different microbial isolates on larvae development. We Collected trichome counts by making casts of the S. lycopersicum leaves and compared these counts between different S. lycopersicum varieties. We also collected colony counts of different cultivars on YM and R2A nutrient agar and compared these as well. We found that trichome density did not significantly correlate with microbial abundance across different cultivars. However, we observed differences in larvae head capsule width and body length of Trichoplusia ni and Spodoptera frugiperda and mortality rates when exposed to different microbial isolates. This suggests a potential role for specific microbes in influencing insect development and provides a foundation for further research into natural pest management strategies. Future research could explore the mechanisms by which these microbes impact insect development and the potential for using them as biocontrol agents.

310 - Evaluating Bottomland Hardwood Forest Restoration in West Tennessee After 10 Years

Emma Sanborn, Michael Schiebout

Union University, Jackson, TN

Restoration projects are continually being developed and implemented to restore wetlands and the valuable ecological functions they provide. This study investigates how a restoration plan is progressing following restoration work implemented in 2013 on a lowland agricultural site located in Carroll CO, Tennessee. The study specifically compared changes in vegetation composition over the restored area and an adjacent reference bottomland site from a floristic survey of the site conducted in 2016. To determine these changes, a second floristic survey of the site was conducted in the spring, summer, and fall of 2024. Initial results indicate an increase in water tolerant woody plants in the restoration site and a decrease in graminoid species. The site appears to be moving toward an adequately functioning, mature bottomland hardwood forest. Based on the documented progress, we also are provided with a tentative restoration trajectory, as well as insight related to the effectiveness of these restoration methods on similar sites.

311 - Conservation Genetic Analysis of Ozark Milkvetch (*Astragalus distortus*; Fabaceae)

Emily Poindexter[1], Madeleine Gagliano[1], Ashley Morris[2], Andrea Weeks[3]

[1]George Mason University, Fairfax, VA, [2]Furman University, Greenville, SC, [3]George Mason University, Department of Biology and Ted R. Bradley Herbarium, Fairfax, VA

Ozark Milkvetch (*Astragalus distortus* Torrey & A. Gray; Fabaceae) is a small, herbaceous perennial that is native to the south-central United States and Maryland, Virginia, and West Virginia. Across the south-central U.S. the species is commonly found in sunny glades

and grasslands, whereas in the mid-Atlantic states it grows exclusively on shale barrens and is Imperiled (Maryland, West Virginia) and Critically Imperiled (Virginia). Presently, two taxonomic varieties of Ozark Milkvetch are recognized. *Astragalus distortus* var. *engelmannii* can be found in Texas, Louisiana, and Arkansas, overlapping with *A. distortus* var. *distortus,* which spans the species' entire range.

Preliminary data indicates the mid-Atlantic metapopulation may warrant separate taxonomic recognition, which brings the validity of the two existing varieties' circumscriptions into question. Moreover, ongoing conservation efforts for the species in the mid-Atlantic could be aided by precise measures of genetic diversity within and among its populations.

To answer these questions, we utilized 21 microsatellite loci, originally developed for *Astragalus bibullatus,* to genetically fingerprint over 330 individuals of *A. distortus* from 20 populations across its US range. Here we report results from that study and outline future work that will evaluate, in the context of field study and common garden experiments, the reproductive biology and morphology of *A. distortus* individuals from across the species' geographic distribution. These combined studies will resolve the circumscription of varieites within *A. distortus*, update state conservation rankings, and inform future conservation actions.

312 - Investigating the distribution of the poorly understood narrow endemic, *Chelone obliqua* var *erwiniae*.

Aster Ayer

Western Carolina University, Cullowhee, NC

Chelone obliqua var. erwiniae Pennell and Wherry (Erwin's Turtlehead, Plantaginaceae) is a member of the Chelone obliqua complex, a group of three morphologically similar taxa that arose from independent polyploid hybridizations. The other two C. obliqua taxa are both hexaploid, whereas var. erwiniae is tetraploid. While there is research being done on the taxonomy of this whole group by another botanist, I am focusing on the issues of var. erwiniae such as delineating the distribution of this poorly understood, narrowly endemic taxon and establishing more reliable means of discerning vegetative polyploids from sympatric or nearby populations of diploid species. Within the literature, var. erwiniae is usually described as a narrow endemic of the North and South Carolina Blue Ridge known from several counties. However, plants within a somewhat broader, contiguous range that are morphological matches for var. erwiniae can be found well into Northeastern Georgia and more widespread in the South Carolina Blue Ridge Escarpment. The cytotypes of most of these populations have never been examined, and have often been assigned simply at species rank, leading to a confusion that hexaploid taxa may occur within the range of var. erwiniae and a likely underestimation of the extent of this taxon's distribution. Despite this, hexaploid cytotypes have not been documented in the Southern Appalachians. To accomplish this, I am sampling populations throughout the entire range in a more intensive manner than has been attempted in the past. Using flow-cytometry I intend to identify tetraploid populations and thus map the distribution of Chelone obliqua var. erwiniae in order to more appropriately inform potential conservation actions for this endemic plant.

313 - Examining Disparities in the Use and Access of Health Technology

Nwanneka Udolisa

Notre Dame of Maryland University, Baltimore, MD

As time goes on, health technology continues to improve. This technology is available on a number of devices, which increases its ease of use in areas like gathering and storing information. Patients can use mobile applications on their phones to monitor their health conditions at home. For example, a journal published by the American Heart Association (AHA) found that employing at-home health technology to take blood pressure measurements can provide more accurate predictive information about cardiovascular risk and organ damage than clinical examinations. Providers can then read the data transferred from applications to track and improve their patients' health conditions. This poster will look at the intersection of health technology and its impact on social equity and healthcare. Despite these examples of how technology in medicine can be used as a resource, there still exist barriers such as cost, accessibility, education, and so on. The goal of this project is to identify barriers relating to access and health literacy through a series of survey questions. These questions have already been Institutional Review Board (IRB) approved as a part of the LINKED-HEARTS study being conducted at Johns Hopkins. The survey data will be from those survey questions, most of which were asked on a yes-or-no basis or on a Likert scale. To build on that, we will further break down the data by analyzing the demographic percentages of the survey takers, who in this specific case are composed of Eastern Shore, MD, residents. As health technology applications continue to be utilized, it's important to understand which populations are benefiting from them more than others and any kinds of disparities that emerge between different populations.

314 - Updates on Culturally Responsive Environmental Science Program Building at Johnson C. Smith University, Charlotte's only and North Carolina's Premier Private HBCU.

Mark Dugo, Rashawna Huntley, Erika Dugo

Johnson C. Smith University, Charlotte, NC

Last year in Chattanooga, we gave three presentations concerning our environmental curriculum and programming at JCSU, including "*A Culturally Responsive Ecosystem Services Based Framework to Engage African American Undergraduate Students in Sustainability, Ecology, and Environmental Sciences*," "*Introducing a Course Based Undergraduate Research (CURE) Special Topics Environmental DNA (eDNA) Course: with a Report on the Detection of Rare Mussels from the Little Tennessee River of North Carolina*", and "*Reflections on Water Monitoring Strategies in the Irwin Creek Watershed of West Charlotte*." Herein, we provide an update of efforts that are projected to enhance our academic offerings in environmental science for years to come. Specifically, we have two water resource grant opportunities that align with our curriculum's focus on the relationship between land-use and water quality. These activities complement our 1-acre Sustainability Village urban agriculture operation outfitted with hydroponics, aquaponics, and living soil raised beds. One of our collaborations, "From Blue-Gray to Blue-Green: Facilitating the Transition to Non-Plastic, Natural Material Use Within the Coastal Zone Economy" is a NOAA-Sea Grant Marine Debris collaboration with the University of South Carolina, Clemson University, and the University of Ohio-Dayton that is exploring alternatives to plastic for marine coastal use to reduce the accumulation of plastic-based debris in the coastal environment. This collaboration emerged from three previous years of summer engagement at the Baruch Marine Field Lab in the Lowland Country of South Carolina. Locally, we have officially united with the Charlotte Mecklenburg Stormwater Services to formalize a collegiate water monitoring program for the Irwin Creek Watershed. Expected to begin in 2025, we will engage JCSU students and local citizens as stakeholders collecting quality-assured and controlled water quality data to identify hotspots of contamination in Irwin Creek. Both of these initiatives undergird our capacity to provide research and workforce training opportunities for our students.

315 - Immersion learning: Experiencing the major ecoregions of Alabama through a new Biogeography Field Study course at Troy University

Michael Wayne Morris

Dept. of Biological and Environmental Sciences, Troy University, Troy, AL

In spring, 2024, a new Biogeography Field Study course was taught at Troy University so that undergraduate and graduate students in the class could enhance their knowledge of natural communities and biodiversity across the level III ecoregions of Alabama. Among all fifty states, Alabama ranks in the top five regarding total numbers of plant and animal species. Representative sites visited and studied in each ecoregion included the following: Joe Wheeler State Park and the Tennessee Valley Authority trails in the Interior Plateau, Natural Bridge Park in the Southwestern Appalachians, Oak Mountain State Park and unique Ketona dolomite glades along the Little Cahaba River in the Ridge and Valley, the Pike County Pocosin and Conecuh National Forest in the Southeastern Plains, and Weeks Bay National Estuarine Reserve and Bon Secour National Wildlife Refuge in the Southern Coastal Plain. Immersion in habitats at these sites as well as student presentations helped participants gain perspective on the climate, geology, soils, natural communities, and adaptations of representative species of flora and fauna relative to other regions and in comparison with similar environments on other continents. In this era of study abroad courses, which are extremely beneficial to the educational growth of individuals taking these courses, it is emphasized here that academic travel within the United States is equally important in the development of scientists, especially field biologists and educators.

316 - The Impact of Birding on Mental Health In Middle School and High School Students

Gayatri Kedar[1], Deepta Ghate[2], Tom Painting[1]

[1]The Paideia School, Atlanta, GA, [2]Emory University, Atlanta, GA

Introduction

Mental health in adolescents continues to worsen due to school-related stressors. Prior work has demonstrated a positive impact of outdoor activities including birding and forest bathing on mood states in children and adults. The Paideia Bird Club in Atlanta, GA leads school-sanctioned teacher-led bird walks every 2-3 weeks during the school year. This pilot study was designed to test our hypothesis that birding has a positive impact on middle and high school students' mental health.

Methods

Middle and high school members of the Paideia Bird Club in Atlanta, GA were asked to complete the revised Profile of Mood States (POMS) questionnaire before and after a two-hour birdwalk. The abbreviated POMS scale is a widely used tool to determine acute changes in mood state. Participants also completed a clinical research form before the birdwalk to collect age, gender, race, previous birding experience, time spent outdoors and time spent on social media in the past month, and prescribed medication.

Results
23 participants (3 male, 16 female, 3 nonbinary, 13.4 years ±1.5, 13 new to birding) enrolled in the study from September 2023 to October 2024. Birding experience for the 10 experienced birders ranged from 1-4 years. POMS total mood disturbance score (TMD) improved positively in 70% of the birders and the average score changed significantly from 8.6±13 to 0.4±8 (paired t-test, $p<0.001$) after the bird walk. There was significant (paired t-test) improvement in POMS subscale scores of anxiety, depression, anger, fatigue and confusion among the birders. The change in subscale and the TMD scores was not significantly different among the experienced and new birders.

Conclusion
After a school sanctioned 2-hour bird walk in Atlanta GA, adolescents reported being in a more positive mood state. These findings call for better access to birding expertise and equipment for middle and high school students.

317 - From "I have a great idea" to project completion through experiential, undergraduate service-learning projects as part of Tree Campus USA

Stephanie Jeffries

North Carolina State University, Raleigh, NC

Experiential service-learning is an excellent way to engage undergraduate students in their education. Through the annual service-learning and Arbor Day event requirements of NC State's Tree Campus USA designation, I have enjoyed numerous opportunities to involve students in hands-on projects. Positive outcomes include real-world engagement, skill-building, and positive feelings of success, all while contributing meaningfully to campus sustainability goals. I explore attributes of what makes a project successful, outline strategies for designing projects, and share best practices for successful outcomes. Starting with the project outcomes, I consider the type and scope of the project, student skill levels needed, opportunities for collaboration, and leveraging resources for support. Several projects, ranging from large-scale removals of invasive species in a large introductory class, to year-long sustainability internships developing campus tree tours, to senior capstone projects to map and strategize Bradford pear removals on campus, are explored as models that all began as ideas to enhance campus sustainability. Despite the planning effort involved, these projects are a worthwhile time investment, given positive feedback from students and the fun and rewarding collaborations sparked among faculty and staff involved.

318 - Evaluating Sexual Health Knowledge Among Incoming College Students

Kalina Abaturov, Dave Wessner

Davidson College, Davidson, NC

To evaluate the sexual health knowledge of incoming college students, we conducted a longitudinal assessment of the contraceptive knowledge and sexual behavior of incoming freshmen at Davidson College. Latest CDC estimates from 2018 reveal nearly 68 million STIs in the U.S., and 26 million new infections. In 2021, the CDC found that nearly half of these new infections occur among the nation's youth: ages 15-24. To decrease the burden of sexual health issues and combat the growing rate of STIs, public health experts have advocated for the implementation of comprehensive sexual education. In 2019, we investigated the sexual knowledge of the incoming Davidson College Class of 2023, the last pre-pandemic class. The large-scale interruption to learning due to the COVID-19 pandemic has had severe consequences, including disruptions to sexual education programming. In 2024, we administered a questionnaire to collect data from the incoming Davidson College Class of 2028 in order to gain a better understanding as to how sexual education may have shifted pre- and post-pandemic. Responses from 84 participants revealed that the mean Contraceptive Knowledge Assessment (CKA) score did not dramatically shift from 2019 to 2024, with approximately 54% and 52% of questions answered correctly, respectively. Preliminary analyses show that female respondents had significantly higher mean CKA scores than male participants, as was the case in 2019, however, there were no significant differences in mean CKA scores across other demographic variables including race, sexual orientation, and religious affiliation. Additionally, only half of the students who received virtual sexual education responded that online learning impacted their sex education experience. Though our results did not reveal dramatic differences in contraceptive knowledge between these two incoming classes, these findings underscore the importance of evaluating the effectiveness of online learning and prioritizing holistic, comprehensive sexual education programming in schools.

319 - Learning at UNC Pembroke Through Summer Training Programs: Stroking Scientific Inquiry Through the NC Louis Stokes Alliance for Minority Participation STEM Pathways and Research Alliance (NC LSAMP SPRA)

Velinda Woriax

University of North Carolina at Pembroke, Pembroke, NC

The U.S. Census Bureau projects that by the year 2040, the nation's population will be majority minority and by the year 2060, 57% of the US population will be members of minority groups, with no one group being the majority (US Census). To remain at the forefront of scientific discovery and innovation, it is incumbent upon the US to ensure the diversification of the STEM workforce. Since 1997, the North Carolina Louis Stokes Alliance for Minority Participation (NC-LSAMP) has worked to address the complex challenges by collectively leveraging the alliance's strengths and capabilities. The work here highlights evidence-based approaches to recruit and retain underrepresented minority students in STEM. Strategies that facilitate the successful transition into graduate degree programs and the STEM workforce as well as broaden STEM pathways through innovative, knowledge-generating research are being employed through this program.

ASB Lightening Talks

9950 - Bringing native marshelder crop (*Iva annua* L.) back to the farm

Slavko Komarnytsky[1], Peter Schafran[2], Jay Bolin[3]

[1]North Carolina State University, Kannapolis, NC, [2]Boyce Thompson Institute, Ithaca, NY, [3]Catawba College, Salisbury, NC

The increasing global demand for sustainable agriculture and climate-resilient crops has sparked renewed interest in wild and underutilized native plants. Among these is marshelder (Iva annua L.), a herbaceous annual native to North America that was historically cultivated by Indigenous communities, including the Caddo, Osage, and Cherokee nations, for its highly nutritious seeds. Once a vital food source, marshelder faded from agricultural systems with the rise of domesticated grains like maize and wheat. This presentation examines archaeological evidence of its ancient cultivation and explores efforts to understand its current wild phenotypes and genetic diversity. The journey to revive marshelder is not only about cultivating a forgotten crop but also about reshaping our approach to farming and food systems for a sustainable future.

10148 - Investigating the predatory behavior of the bumblebee Assassin Snail (*Anentome helena*) and the potential ecological implications in invaded freshwater systems.

Kathleen Madden, Lori Tolley-Jordan

Jacksonville State University, Jacksonville, AL

The bumble-bee assassin snail, *Anentome helena*, native to freshwaters of Malaysia, is one of only a few freshwater species in the marine lineage, Neogastropoda, that includes predatory snails such as whelks and cone snails. This snail is widely available in the aquarium trade, tolerant of a wide range of water temperatures, survives adverse transport conditions, and readily reproduces in captive conditions. To date, no invasive populations are reported, and the invasion threat is not-well understood. While anecdotal evidence from hobby aquarists suggest that these snails are voracious, generalist predators of snails; the importance of prey size, prey type, and behavior of predator and prey is insufficiently examined . Visual analyses of assassin snail predation of operculate snails were restricted to aperture widths of less than 10 mm , regardless of snail species. Feeding trials also showed that assassin snails are generalist molluscivores as they readily consumed Asiatic clams. This is a significant finding, as prior to this study, no reports of assassin snails consuming non-snail taxa are documented. Finally, regardless of prey type, time-lapsed filming showed that assassin snails aggregate when hunting, although the association among snails (positive or negative) is unknown. Further research describing assassin snail life-history, environmental constraints, and feeding niche breadth are needed to determine potential injurious impacts on invaded systems.

10180 - Developing *Corbicula fluminea* as a Model to Study Microbiome Responses to Cyanotoxin Exposure

Champagne Cunningham, Rachel E. Diner

University of Memphis, Memphis, TN

Corbicula fluminea (*C. Fluminea*) is a prolific species of freshwater clam that is highly invasive in North America. Its presence within the freshwater systems of Tennessee is well documented. The natural history/behavior of *C. Fluminea* directly exposes them to harmful algal blooms (HABs) and their toxins. HABs are capable of negatively affecting water parameters and are considered environmental stressors. When present in freshwater environments, cyanotoxins such as microcystin or anatoxin can directly affect the physiology of *C. Fluminea*. *C. Fluminea* is frequently found in waters with high levels of pollution and/or algal toxins and has been used as a model organism for ecotoxicology studies. While the physiological responses of corbicula to toxicants are well-studied, little is known about the impacts on *Corbicula* microbiomes and host-microbe interactions. To address this knowledge gap, we have developed *C. Fluminea* as a model to study the impacts of harmful algal toxins in aquatic host-microbe systems. In initial baseline studies, we are determining tissue-specific microbiome variability in *C. Fluminea* and establishing an environmental time-series to determine exposure to HAB toxins and environmental impacts on the microbiome. Future laboratory studies will experimentally test the impacts of HABs on *C. Fluminea* microbiomes and physiology, examining both acute impacts and microbiome resilience.

9776 - Host-Pathogen Interactions and Genetic Susceptibility: Investigating the Role of Immune Gene Mutations in Reproductive Tract Infections and Fertility Outcomes.

Selina Ahilon-Calmo

Georgia Highlands College, Cartersville, GA

This research project investigates the role of genetic mutations in immune -related genes and their influence on susceptibility to bacterial infections in the reproductive tract, with a focus on fertility outcomes. Bacterial pathogens such as Chlamydia trachomatis and Neisseria gonorrhoeae are known to cause reproductive damage and are often linked to infertility. This study aims to explore how mutations in genes like TLRs and HLA affect the host's immune response, leading to chronic infections and reproductive complications such as pelvic inflammatory disease (PID) and fallopian tube scarring. Understanding these host-pathogen interactions may provide insights into fertility preservation and potential therapeutic interventions.

9710 - An unexpected journey into invertebrate data from herbarium specimens - a portal to cross-disciplinary, integrated data through a new protocol

Avery Browning

University of South Carolina; A.C. Moore Herbarium (Position: Assistant Curator), Columbia, SC

Delving into herbarium cabinets can produce more than botanical data. While digitizing various specimens, additional information can be seen in the inclusion of unintentionally collected organisms, for example, copepods, crustacean molts, and damselfly larvae.

Beyond general intrigue, presence of these organisms indicates additional associated taxa beyond plants, and information about the organisms, such as using the plants as a possible nursey habitat or reproduction site. It may indicate a snapshot in time of a changing locality, or the dispersal of one species and migration of another. This visual data is easy to miss, (especially unless actively searched for) and may be underutilized as a result.

In the Symbiota portals that we use at USCH, we maintain additional notes of this data. We have also created an iNaturalist project for these findings, as a way to share information and crowdsource determinations in citizen science, with posted observations as microscopic images of the invertebrates. This can be included digitally in records as a 'linked resource,' while the iNaturalist records themselves also include the botanical collection information and link back to the Symbiota portal records. When the iNaturalist record reaches a research-grade level of determination, we also add annotations to the physical specimen.

This new protocol pushes a deeper dive in citizen science into seeing that there is more information to be understood than initially meets the eye and promotes further study into both the botanical specimens and the invertebrates.

10358 - Modern approaches to studying plant-pollinator networks

Jacob Francis

Florida Atlantic University, Boca Raton, FL

Understanding plant-pollinator interactions is critical for conserving the South East's unique and diverse ecosystems, particularly in plant communities at the urban-rural interface. We are developing a comprehensive pollen image database for South Florida, utilizing high-throughput automated microscopic photography, advanced image annotation tools, and computer vision models to identify pollen from co-flowering species. In this talk, I will discuss our methods for collecting, annotating, and managing these data, showcasing our current collection of ~105 plant species common to these communities. I will highlight how these tools are being used to investigate co-flowering species interactions via shared pollinators, with a focus on the role of non-native plants. Preliminary data suggest non-native species such as *Richardia grandiflora* and *Sphagneticola trilobata* may influence pollination dynamics and resource use by native pollinators, potentially impacting native weedy species like *Bidens alba* and *Phyla nodiflora*. Our long-term goal is to expand this database to encompass the full diversity of Southern Florida's flora, providing a valuable resource for researchers, land managers, and conservation practitioners. This project integrates modern machine learning techniques with traditional botanical approaches, offering insights into plant community dynamics and supporting efforts to conserve native plant biodiversity in increasingly disturbed habitats.

9673 - Analysis of heavy metals and oxidative stress in the Atlantic nurse shark (*Ginglymostoma cirratum*) in southern Florida

Ciera Johnson, Dr. Gretchen Bielmyer-Fraser

Jacksonville University, Jacksonville, FL

Heavy metals enter the ocean from a variety of sources and accumulate in aquatic organisms. Antioxidant enzyme production serves as a natural physiological defense to low levels of metal exposure in many organisms. Sustained oxidative stress may result in effects on growth and reproduction. Atlantic nurse sharks (*Ginglymostoma cirratum*) are top predators with resident behavior, therefore, contaminant concentrations in the tissues of these animals may be indicative of the pollution level in a particular area. Also, given that mercury biomagnifies up the food chain, *G. cirratum* may serve as a good bioindicator species for metal exposure. This study will be the first to analyze *G. cirratum* muscle tissue from southern Florida for mercury (Hg), cadmium (Cd), lead (Pb), selenium (Se), rubidium (Rb), silver (Ag), and copper (Cu), as well as antioxidant enzyme activity to determine reference levels and to ascertain if a relationship between tissue metal accumulation and antioxidant enzyme activity exists in this species, as has been shown in other shark species. Comparisons will be made between sampling locations, seasons, sexes, and age classes.

9908 - Using Environmental DNA (eDNA) Analysis to Explore Soil Microbial Diversity in South-Central Florida

Tatiana Guerra[1], Elik Esquilin[2], Laura Froberg[2], Dr. Tammy Laberge, Ph.D[2]

[1]Miami Dade college, Miami, FL, [2]Miami Dade College, Miami, FL

Environmental DNA (eDNA) refers to the genetic material shed by organisms into their surroundings, such as soil, water, and air. This technique is used to analyze environmental samples, monitor species distributions, and assess biodiversity by detecting the presence or absence of species within a given habitat. Our study uses eDNA analysis to identify bacterial diversity in soil samples from the Archbold Biological Station's Buck Island Ranch. Specifically, we examined bacterial diversity in soils subjected to different land-use conditions: improved and semi-native ecosystems. This research aims to understand the essential roles of microbial processes in each environment. The semi-native ecosystem is characterized by a mixture of native and non-native species introduced through human activities. Our study seeks to identify specific bacteria that contribute to plant growth in these distinct environments. Soil samples were collected from each environment and stored at -20°C until DNA extraction. DNA yield and purity were assessed, and suitable samples were diluted and sent for sequencing to identify 16S rRNA genes. Metabarcoding analysis was performed using the DNA Subway Purple line. This sequencing data is expected to reveal bacterial diversity and community composition differences across the habitats. Comparative analysis will be used to elucidate variations in bacterial communities between the soil types and their potential benefits to plants in each location. We hypothesize that the semi-native ecosystem will exhibit lower bacterial abundance due to human disturbances compared to the improved ecosystem. Understanding the soil microbiome and its impact is critical for advancing agricultural practices and ecological conservation. This knowledge could facilitate the development of biofertilizers to improve soil health. Additionally, comparing bacterial communities between improved and semi-native areas may provide valuable insights for land-use planning and landscape management. These findings could inform future research on microbial ecology, plant-microbe interactions, and ecosystem dynamics in south-central Florida.

9861 - NEON: utilizing technicians and technology to provide open data for all!

Margaret Cumberland

National Ecological Observatory Network (NEON), Oak Ridge, TN

The National Ecological Observatory Network (NEON), funded by the U.S. National Science Foundation and operated by Battelle, provides free and open ecological data for anyone to use. With more than 180 NEON data products to choose from and over 500,000 samples available to use at the NEON Biorepository, there are many opportunities to use NEON data and samples for research, curriculum development, or management decisions. NEON data cover a wide range of subject areas within ecology and are collected from 81 field sites, 21 of which are located in the Southeast. This lightening talk will provide a brief look at how NEON field technicians use drone technology to provide quality samples for chemical analysis of sunlit foliage and connect that to remote sensing data collected at the same location. This is just one example of analyses taking place with NEON data in the research community, with more to come.

10446 - The use of stable isotopes in understanding the effects of trematode infections on their host snails.

Abby Reed[1], Lori Tolley-Jordan[2]

[1]Jacksonville State University, Talladega, AL, [2]Jacksonville State University, Jacksonville, AL

Digenean trematodes are flatworms with complex life cycles where adult worms and larvae are obligate endoparasites within their respective hosts. In these life cycles, larval worms are produced in freshwater snails in which a swimming stage (cercariae) exists to infect the next host. As gonads and/or intestines of freshwater periwinkles *(*Pleuroceridae spp*)* and pond snails (Physidae *spp*.) are often infected by trematode parasites, and as these larval parasites shed in large numbers, this creates an ideal model for understanding the significance of parasites in food webs. Here, we used δ13 Carbon (δ13 C) and δ15 Nitrogen (δ13N) isotope concentrations to determine if differences in basal food resources and trophic level positions occurred between trematodes and their snail hosts. In fall 2024, we collected individuals of *E. godwini* infected with a fish parasite Opoecilidae: *Plagioporus spp*. and individuals of *Physella sp.*, infected with a frog parasite Haemotoloechidae spp. and non-infected individuals of each snail species. For infected snails, shed cercariae and infected tissues were collected along with tissues from non-infected snails. All samples were dried, weighed and analyzed for amounts of δ13C and δ13N. Results showed a clear separation of *Physella* and *E. godwini* in δ15N signatures (4 and 8, respectively) while δ13C signatures were similar (-23 and -25, respectively). Cercariae and infected tissues of *E. godwini* had similar signatures of both δ13C (-23 to -24) and δ15N (~8) while δ15N signatures of non-infected *E. godwini* slightly less (7). These preliminary results suggest that stable isotopes are an effective technique in evaluating both the position of trematode parasites and their snail hosts in food webs. Future studies will include larger sample sizes of all categories with refined techniques to understand the relevance of these endoparasites in food webs.

9591 - The Dynamic Nature of Sunflecks Beneath a White Pine Forest

Howard Neufeld, Beka Davis, Ethan Smith

Department of Biology, Appalachian State University, Boone, NC

Using time-lapse photography, we monitored the spatial and temporal patterns of sunflecks beneath a white pine canopy in late summer. Using a Go-Pro camera attached to a tree, we photographed an area of approximately 10 m x 10 m from early morning to mid-afternoon, taking photos every 10 seconds. These photos were then collated into a time lapse video which shows how the pattern of sunflecks moves in a wave-like manner as the sun both rises in elevation and moves westward in its course over the day. Tree trunks were particularly effective in blocking the sun when the solar angle was low, while later in the day sunflecks were more dependent on breaks in the overhead canopy. The interaction of clouds, canopy structure and tree trunks created a complex dynamic of light and shade impinging on understory plants, which in this case consisted almost entirely of the exotic invasive shade-tolerant C4 grass *Microstegium vimineum*. Such dynamics suggest that more realistic approaches are needed in our ecophysiological studies of sunflecks on plants.

9946 - The Cure for Someone's Blood Cancer Could Be Inside YOU!

Matthew (Matt) Kroeger

NMDP. Find Cures. Save Lives., Minneapolis, MN

NMDP is a global leader in cell therapy that is mobilizing everyday people--including college students, faculty & staff--to save lives. With our partners, we drive groundbreaking research, treatment and support to cure blood cancers, disorders and beyond. Many attendees may not be aware that 70% of patients diagnosed with a blood cancer/disease/disorder do not have a fully matched donor in their family, and the cure for a stranger's blood cancer or disease could be located inside them—in their healthy peripheral blood stem cells (PBSC) or bone marrow. For more than 35 years NMDP has operated the most diverse and effective registry in the world, comprised of more than 9 million individuals who have committed to answering the call if they are a genetic match for a patient in need of a life-saving treatment. Through advances in science and health care, 90% of the donations for patients today are now non-surgical. Sadly, a large disparity gap still exists and the odds of finding a match for some individuals. Our vision is to create a world in which EVERY patient can receive their life-saving cell therapy. Spreading awareness and growing the registry by joining our movement is something that college students, faculty and staff can participate in a variety of ways. The national partnership with Beta Beta Beta (TriBeta) Biological Honor Society that launched in the fall 2023 provides low-lift and high-impact opportunities to be part of our life-saving educational and service activities.

9763 - LL-37's Impact on Prostate Cancer Cell Growth and Immune Interaction

Amiyah McCoy, Maria Craig, Paul Deeble

Mary Baldwin University, Staunton, VA

LL-37, an antimicrobial peptide, plays a dual role in promoting and suppressing tumor growth, making it a compelling target for prostate cancer immunotherapy. This project explores the paracrine effects of immune-cell-derived LL-37 on the prostate cancer cell lines LNCaP and PC-3, which represent androgen-dependent and androgen-independent prostate cancer, respectively. The goals are to determine LL-37's impact on cancer cell proliferation and migration, evaluate the effect of alpha-1-antitrypsin (A1AT) on LL-37 expression, understand how immune-cell-derived LL-37 influences prostate cancer cell behavior, and determine whether LL-37 is produced by prostate cancer cells or primarily by other components of the tumor microenvironment (TME). We conducted cell culture experiments using LNCaP, PC-3, and THP-1 cells to assess the effects of LL-37. Undifferentiated THP-1 cells were co-cultured with LNCaP and PC-3 cells to assess whether prostate cancer cell lines express endogenous LL-37 that could induce monocyte differentiation, indicated by THP-1 cell adhesion. Proliferation and migration assays were conducted on the prostate cancer cell lines to characterize their growth and migratory behavior. These assays included trypan blue proliferation assays to measure growth rates and wound-healing scratch assays to evaluate migration. We plan to use rtPCR to quantify LL-37 mRNA production in the cell lines before downregulating LL-37 with A1AT to determine if its inhibition reduces tumor-promoting behaviors. This study aims to determine if LL-37 enhances prostate cancer cell proliferation and migration, particularly in the aggressive, androgen-independent PC-3 cells, and whether downregulating LL-37 with A1AT can mitigate these effects. The results of this research will provide insights into the role of LL-37 in prostate cancer and its potential as a target for future therapies. These findings could help inform the development of immunotherapies that modify the tumor microenvironment to limit cancer progression.

10098 - (Re)ranking the rare sunflowers (*Helianthus*) of upstate South Carolina

Samantha Tessel[1], Eric Ungberg[2]

[1]South Carolina Department of Natural Resources, Clemson, SC, [2]South Carolina Department of Natural Resources, Georgetown, SC

A data-driven approach to assigning state ranks to the flora of South Carolina has resulted in a better understanding of the current distribution of rare sunflowers of the Upstate. Taxonomic complexity and intergradation in *Helianthus* are frustrating to the even best botanists of the Southeast, so a close look at specimens is imperative to assess rarity status. Recent examinations of specimens have indicated that two species of tracked sunflowers, *Helianthus porteri* and *Helianthus glaucophyllus*, are more rare than previously thought, and that several other species are in need of careful evaluation.

9912 - The Significance of Marine Amphipod Taxonomy

Kristine N. White

Georgia College & State University, Milledgeville, GA

The naming, describing, and classification of organisms has always been vital to human survival; for example, allowing early humans to avoid the consumption of poisonous flora. Today, this practice is formally known as taxonomy, which serves as the foundation of all scientific research. Taxonomy allows us to document diversity, providing fundamental knowledge of which study sites might best serve research projects. Despite the significance of taxonomy, emphasis on the subject is in decline. Relatively few scientists with taxonomic expertise remain, which has led to a decrease in the number of students learning taxonomic techniques. This is especially true regarding often understudied, less charismatic organisms. Marine amphipod crustaceans are a prime example. Amphipods are the basis of marine food webs and can be used in ecological and conservation-based studies, both of which are crucial to conserving marine biodiversity. Amphipods dominate marine seascapes in their size range, yet only seventeen amphipod species were previously reported from Bocas del Toro, Panama. A project designed to document the amphipod diversity of the area has trained three students in traditional taxonomic methods and revealed over 150 morphospecies to date. Without morphological identification, DNA sequencing is uninformative due to the lack of DNA sequence data available online for most amphipod species. This project illustrates the need for trained taxonomists to document diversity so marine habitats can be studied and conserved.

10362 - Investigating selective toxicity of targeted DNA-damaging compounds on prostate cancer cells

Logan Boyet, Tiffany Bonn, Mackenzie Custer, Sarah Faragher, Kai Smith, Maura Schoppa, Sridhar Varadarajan, Arthur Frampton

University of North Carolina Wilmington, Wilmington, NC

Globally, prostate cancer (PCa) is the second leading cause of cancer-related death in men. Current chemotherapeutics lack the

ability to selectively target PCa cells. One common form of treatment is androgen deprivation therapy (ADT), which reduces androgens such as testosterone that function as primary growth signals. A drawback is that mutations within the androgen receptor (AR) can lead to aberrant signaling and activation of AR in the absence of testosterone, a condition termed castration-resistant prostate cancer. Our current strategy is to develop compounds that specifically target the overexpressed AR in PCa cells. This study follows previous research conducted in our labs where we showed the efficacy of similar compounds developed to target the estrogen receptor in breast cancer cells. These targeted compounds will be more effective at specifically destroying PCa cells while minimizing toxicity to normal prostate epithelium. The compounds contain a targeting ligand, a DNA-binding domain, and a methylsulfonate that will form toxic DNA adducts in the targeted cells. There are various forms of these AR-targeted compounds that will be tested on PCa cells. The cell lines include AR-negative PC-3s and AR-positive LnCaps and C4-2Bs. LnCaps are early-stage androgen-dependent, while C4-2Bs are late-stage androgen-independent. Our preliminary data suggests the control testosterone methylsulfone compound displays minimal toxicity that is similar on the three PCa cell lines as expected due to the methylsulfone unit lacking the ability to damage DNA. We will next assess the toxic analog of the control compound, where the only difference is the presence of a DNA-damaging methylsulfonate group. We hypothesize that the methylsulfonate-containing compound will exhibit selective toxicity on the AR-expressing cells (LnCap and C4-2B).

9865 - Introducing the Coastal Carolina University Herbarium (CCUH)!

Michelle Barthet

Coastal Carolina University, Conway, SC

The Coastal Carolina University Herbarium (CCUH) is a little-known gem in the coastal region of South Carolina. We, in collaboration with Clemson University, the University of South Carolina, and the South Carolina Division of Natural Resources (SCDNR), recently initiated efforts to digitize the collection of this historic herbarium. The CCUH collection includes over 6,000 vouchers of land plants collected over the past 50 years from Central Mexico to Canada. Vouchers, thus far, incorporate specimens from over 200 plant families, 649 genera, and 1,480 species including several at-risk, threatened, and endangered specimens. All vouchers have been photographed with collecting information entered into SERNEC (SouthEast Regional Network of Expertise and Collections) database with corresponding international access through Index Herbariorum. In addition to the land plant collection, CCUH holds a marine botany collection documenting the impact of infrastructure, storm, and other changes in the marine environment along the South Carolina coastline over the past several decades. We will present a short introduction of some of the most impressive specimens in the CCUH collection identified so far, as well as current and future directions for the collection.

9834 - Don't Forget the Little Guys: Why Parasites Deserve a Bigger Role in Ecology

Mr. Nicholas Tsangarides

Kennesaw State University, Kennesaw, GA

All organisms have parasites. If we want to understand how communities respond to change over time, we must understand how the parasites are affected too. Parasite prevalences can hint at hidden patterns in an ecosystem. Future research should attempt to expand the breadth and reach of their research by simply preserving a small percentage of hosts. Later parasitological study could allow for a greater understanding of the natural environment.

10336 - Assessing mussel assemblage change in the Upper Chipola River

Gabrielle Chartier, Jonathan Miller, Dr. Kaelyn Fogelman, PhD, Brian Helms

Troy University, Troy, AL

Freshwater mussels are among North America's most imperiled groups and the southeastern United States is a key region for their conservation due to its rich mussel diversity. Many federally-protected species face critical threats from habitat degradation linked to increased runoff associated with road crossings and land cover changes, particularly in headwaters. To address these issues, in summer 2024 we evaluated mussel assemblage change (since 2007) and current habitat conditions in Big and Cowarts Creeks, the 2 primary tributaries of the upper Chipola River in SE Alabama. We surveyed 14 sites quantitatively by excavating 20–30 1 m^2 quadrats along cross-sections in representative 100–300 m reaches. Additionally, qualitative surveys were conducted in all habitats within the same reaches. We quantified physicochemical conditions (temperature, conductivity, and pH) for each reach and estimated habitat stability for each quadrat based on a semiquantitative firmness scale. Sediment cores were collected in each quadrat to characterize organic matter and particle size profiles. We encountered a total of 1940 individual mussels representing 15 species. Quantitative methods resulted in 185 specimens representing 12 species and an overall average density of 0.34 mussels / m^2. Qualitative surveys resulted invealed 1,755 freshwater mussel specimens in total, with the highest abundance observed at two sites on Cowarts Creek, yielding 465 and 793 specimens, respectively. Our observed species richness was lower than historical richness as *Medionidus penicillatus* and *E. crassidens* were present historically yet undetected in this effort. However, all other species of conservation concern

(*E. chipolaensis, Pleurobema pyriformes,* and *Hamiota subangulata*) were observed. Ongoing analyses of habitat data suggest that mussel abundance is positively associated with fine and stable benthic sediments. These results ultimately will provide valuable information for the continuous monitoring of temporal trends and ultimately conservation efforts supporting freshwater mussel populations in the Chipola River.

9864 - Using ArcGIS StoryMaps to Document the Growth of the SCDNR Botany and Plant Conservation Program

Mikayla Radek, Keith Bradley, Csilla Czako

SCDNR Botany and Plant Conservation Program, Columbia, SC

The South Carolina Department of Natural Resources Heritage Trust Program was first established in 1974. It was the first program of its kind in the nation, created to conserve and protect cultural and natural resources of the state. These are critical to honoring the heritage and history of South Carolina. Over the past 40 years, the program has dedicated 75 properties covering 95,661 acres as Heritage Preserves. Land acquisition is only one facet of growth that the Heritage Trust Program has experienced. Biodiversity data, including botanical data, has always been a key part of deciding which properties to establish as Heritage Preserves. The increasing utilization of digital technologies has dramatically changed the way the Heritage Trust Program uses and processes data. Over time, the use of the Southeast Regional Network of Expertise and Collections (SERNEC) and other iDigBio Portals, and citizen science platforms such as iNaturalist were key components of improving the efficiency of tracking species populations. Based on SERNEC data records, roughly 3,500 botanical occurrences have been recorded and digitized with locality data from the years 1700-1900. In 2001-2020, roughly 43,000 botanical occurrences have been recorded and digitized with locality data within South Carolina. With greater technologies and access to organization data and public records, conservation efforts within the Heritage Trust Program have reached new heights. Visualizing this growth of the program and the supporting data in an engaging and understandable way allows for communicating our growth and working with the general public. This was done through the ArcGIS StoryMaps platform. ArcGIS software has vast mapping capabilities, and the StoryMaps platform allows users to add a narrative to enhance readers' understandings. Through a combination of interviews and data compilation a visual story was created to be shared on our public website.

9785 - Deprogramming and Desegregating Racial Inequities in Healthcare

Preethi Sriram

Clinical Research, NC

While the Tuskegee syphilis study and other egregious examples of unethical medical experimentation are often cited as reasons for minority distrust of the medical community, there are less well known incidences of concepts that have been created within the past 150 years that are still being utilized in healthcare for diagnoses and treatment within a present day context that need to be reexamined. This talk will provide examples with special attention to body mass index (BMI), acute kidney injury (AKI), the spirometer, and the advent of therapies to targeted to specific racial groups to explore how prior concepts of race and flawed scientific formulas are still used in healthcare that has real world consequences.

Tri-Beta Presentations

9704 - On the Taxonomy of *Didianema* (Gastropoda: Vetigastropoda: Skeneidae *s. l.*)

Timothy Campbell

Gardner-Webb University, Boiling Springs, NC

Skeneidae *s. l.* is a polyphyletic wastebasket for minute, generic gastropods. The only reliable feature for assignment to Skeneidae *s. s.* is reproductive anatomy, but many genera are known only from shells. *Didianema* is an obscure skeneimorph genus, with, as currently classified, one named extant and about seven named fossil species (plus one extant and three fossil undescribed species). It was originally assigned to Vitrinellidae, and later moved to Skeneidae. Recent examination of the holotype of the type species, *Didianema tytha* Woodring, 1928, from the Bowden Formation (mid Pliocene) of Jamaica has prompted a revision of the genus and species previously assigned to it. Based on protoconch morphology of *D. tytha*, *Didianema* is redescribed and transferred to the heterobranch family Cornirostridae, close to the Oxfordian to Tithonian *Heteronatica* Guzhov, 2019. Examination of the other species assigned to the genus indicates the following novel generic assignments *Didianema duplinensis* (Dall, 1890), *Didianema pauli* Pilsbry & McGinty, 1945, and *Didianema carolinae* Gardner, 1948 (*Diagonaulus*); *Didianema ? waltonia* Gardner, 1947, *Didianema?* sp. of Perrilliat Montoya, 1972, *Didianema* sp. of Campbell, 1993, and *Didianema orthorhytis* of Campbell, 2023, *non* Pilsbry (*Cirsonella*); *Didianema* sp. of Lee, 2009 (*"Skenea" sensu* Campbell, 2023); *Didianema chavani* Le Renard, 1994 (juvenile solariellid or areneid?); and *Didianema orthorhytis* Pilsbry in Olsson & Harbison, 1953 (*Xyloskenea*). *Didianema errata* (Guppy in Dall & Guppy, 1896) from the Miocene (?) of Trinidad is retained with *D. tytha* in *Didianema*.

9723 - The Role of Adenovirus Protein E4 11k in P Body Protein Relocalization

Heather Vincent[1], Sarah West[2], Kasey Karen[1]

[1]Georgia College & State University, Milledgeville, GA, [2]Georgia College and State University, Milledgeville, GA

Adenovirus (Ad) can cause the common cold and conjunctivitis. E4 11k is an important viral protein that regulates late gene expression. E4 11k has been shown to disrupt cellular function by relocalizing processing body (p body) proteins to cytoplasmic aggresomes. Aggresomes are sites of misfolded protein storage and only arise when there is cellular stress. The scaffolding p body protein, Ddx6, has been shown to colocalize with E4 11k in aggresomes during a wild-type Ad infection. Ddx6, however, was not relocalized to cadmium chloride (CdCl2)-induced aggresomes. This suggests that E4 11k is necessary for the relocalization of Ddx6. We observed the localization of additional p body proteins, Lsm1, Edc3, and Pat1b, in human lung (A549) cells, following wild-type Ad infection and CdCl2 treatment. Lsm1 and Edc3 were relocalized to both infection and chemically induced aggresomes. Pat1b, however, was not relocalized to either infection or chemically induced aggresomes. Additionally, we infected A549 cells with three E4 11k-expressing viruses: E4 11k, L103A, and DL mutant viruses. The L103A mutant cannot oligomerize but has the ability to dimerize, while the DL mutant virus has some form of multimerization. Current observations indicate that E4 11k is necessary and sufficient to relocalize Ddx6 and that protein folding may affect certain functions of p body relocalization; in particular, the lesser protein folding of the mutants lowered the percentage of Ddx6 that was relocalized to aggresomes compared to E4 11k only. Using these mutant viruses, we hope to determine if the oligomerization from E4 11k is required for aggresome formation. In addition, we want to observe the different p body proteins to determine if their localization during mutant virus infection is altered. We hope to understand better the dynamics of p body and aggresome formation in human cells.

9734 - Investigating the interplay between TLR4 signaling and AHR activity in small intestinal epithelial cells: implications for necrotizing enterocolitis

Arlo Colvard

Lipscomb University, Nashville, TN

Necrotizing enterocolitis (NEC) is a gastrointestinal inflammatory disease that primarily affects premature infants. In NEC, bacterial factors are thought to elicit an excessive response by the immature immune system. In the gastrointestinal tract, this robust inflammatory response leads to excessive apoptosis of the epithelial cells comprising the barrier between the lumen of the gastrointestinal tract and the underlying tissue allowing for bacterial invasion of the underlying tissue, leading to ischemia, necrosis, and potentially sepsis and death. Activation of the aryl hydrocarbon receptor (AhR), an immune system modulator, has been shown to be preventative against the pathogenesis of NEC in a murine model. However, no research has been conducted on the potential benefits of AhR activation *following* pathogenesis. As such, we focused on the effects of AhR activation following pathogenesis within

a model system: rat small-intestinal epithelial cells treated with lipopolysaccharide (LPS), a bacterial endotoxin implicated in NEC. qRT-PCR revealed a decrease in AhR expression following LPS treatment. In this model, AhR activity, assessed by expression of the AhR target gene Cyp1a1 following treatment with the ligand indole-3-carbinol (I3C), was comparable to no LPS control. MTT assays indicated that treatment of the cells within our model with I3C rescued cytotoxicity. Surprisingly, scratch assays revealed a decrease in wound healing ability in the LPS + I3C treatment group, while no differences were observed with either treatment alone. These results may reflect the ability of I3C to rescue relatively mild insults (LPS) but not more significant injury (LPS+Scratch). Our continued research has sought to determine the potential for another AhR ligand, indole propionic acid (IPA), to rescue LPS-induced cytotoxicity. Currently, our findings do not suggest that IPA is capable of ameliorating LPS-induced metabolic deficits. Overall, our research indicates that I3C treatment, and potentially AhR activation, rescues LPS-induced cytotoxicity but not wound-healing ability.

9768 - Implications of Memory Performance on Cerebellar Vermis Activation

Gretchen Lutz

Mary Baldwin University, Staunton, VA

A highly conserved brain region, the cerebellum, was traditionally believed to serve exclusively a motor role but has been recently redefined as having a role in higher brain functions, including cognition and emotional regulation. Studies have implicated alterations in cerebellar size or structure in numerous psychiatric and neurological disorders.

The vermis, the structure connecting the bilateral hemispheres of the cerebellum, has demonstrated consistent activation across cognitive domains and is associated with structural changes in multiple neurodegenerative disorders. However, it has been overwhelmingly neglected in directed research, especially in relation to memory. This study aims to address this gap by investigating the cerebellar vermis in spatial memory in a well-studied rat model.

Memory was measured via a cue test, where rats were acclimated to a track and then subjected to a cue misalignment to prompt spatial memory. Brain tissue was collected after the experiment, and c-Fos immunohistochemistry was used to assess neuronal activation in the vermis.

Thus far, rats have been run and tissue sections have been processed. Quantification of activation and behavioral measures of memory are underway. Results are hypothesized to reveal correlations between higher vermis activation and increased memory performance.

By focusing on neuronal activation rather than volumetric analysis (utilized in most cerebellar studies), this research provides a more direct assessment of the cerebellum's role in memory processes. Findings have potential implications for understanding cerebellar involvement in memory-related disorders and could inform therapeutic strategies targeting the cerebellum.

9769 - MIG6 as an Inhibitor of the Alternative Resistance Mechanism of EGFR/HER2 Heterodimerization in HER2+ Breast Cancer

Ada Bozikov

Mary Baldwin University, Staunton, VA

Breast cancer is currently the most common type of cancer in the United States and the fourth most deadly. One of the most aggressive types of breast cancer, characterized by high mortality, recurrence, and resistance rates, is HER2 overexpressing (HER2+) breast cancer. However, targeting HER2 in treatments has been difficult due to its mechanism of action, namely its ligand-free partnering up with other like receptors (dimerization). Effective therapies exist today, such as antibodies to block dimerization sites (Trastuzumab), but rapid genetic mutation frequently leads to resistance against these treatments. HER2 dimerization with other partners, such as EGFR, is a potential mechanism of resistance. This study intends to test if inhibiting EGFR via overexpression of a naturally occurring inhibitor in human cells (MIG6) can slow Trastuzumab-resistant HER2+ cell growth. MIG6 will be overexpressed through a mammalian expression vector containing GFP as a tag. An empty vector (lacking MIG6) will be used as a control to measure transfection efficiency. Gene cloning through PCR and insertion into the vector through a double digest is underway. After successful vector transfection into the HER2+ cells, cell growth and migration will be measured through cell counts and scratch assays to assess the effects of MIG6. If MIG6 acts as observed by promoting the degradation of EGFR along with its partner (HER2), cell migration and growth are expected to be decreased in MIG6-transformed cells compared to the control cells.

9808 - Using principal component analysis to understand spatial distributions of terrestrial mammals across sites in Upstate South Carolina

Mille Elsborg, Lisa McDonald, Emily Prince

Lander University, Greenwood, SC

The rapid decline in biodiversity due to habitat fragmentation and climate changes necessitates comprehensive monitoring of terrestrial mammal communities to assess the role of individual species in differentiating mammal communities. However, it can be challenging to determine which factors, including habitat type, human infrastructure, and human presence, are driving changes in community composition. Using mammal community data collected from more than 20 camera stations in Upstate South Carolina from 2018-2024, we used principal component analysis (PCA) to characterize similarities and differences between these communities. PCA allowed us to reduce the dimensionality of our data and visualize key environmental and biological factors driving community composition. The first two principal components explain 35.9% of the variation. PC1 is explained by geographic variation in community composition. Stations located in more mountainous northern sites (Pickens County) are characterized by wildlife such as wild hogs, black bears, coyotes, and bobcats, compared to the more southern counties of Greenwood and Laurens, which are situated closer to the Midlands and feature species like gray foxes and fox squirrels. PC2 is explained by variation in community composition due to proximity to water source. The species responsible for distinguishing communities along PC2 are associated with water and include beavers, otters, muskrats, and raccoons. These results highlight that the most important contributors to the structure of mammal communities in Upstate South Carolina are geographic location and habitat type. By identifying these environmental pressures, this study provides a foundation for targeted conservation strategies in rapidly changing ecosystems.

9874 - *S. cerevisiae* Genetic Screen: Identifying Novel Interactors of Sec6

Kun Yuan Chu, Ellen France

Georgia College & State University, Milledgeville, GA

Polarized protein secretion is crucial for the proper delivery of various proteins and lipids in eukaryotic cells. Comprised of four steps: vesicle budding, trafficking, tethering, and fusion, our research focuses on Sec6 protein, a component of the exocyst complex which facilitates vesicle tethering to the plasma membrane. Previous work (Sanger and Munson 2009) introduced new Sec6 mutant proteins with altered the amino acids located on the surface of the protein. Sec6-49 mutant cells displayed severe growth and secretory defects when cells are grown at 37°C while normal growth is observed at 25 °C. However, despite the poor growth of these cells at 37°C, the assembly of all 8 exocyst components was not affected, the complex simply is mislocalized. Our current hypothesis is that Sec6 plays an important role in anchoring the exocyst to the plasma membrane, and that the mislocalization of the exocyst in sec6-49 cells stems from disruption of surface amino acids which may be engaged in interaction with an unknown factor(s) on the plasma membrane. Utilizing a yeast genetic screen with a plasmid based genomic library, The screen employed the transformation of genomic library plasmids into sec6-49. Transformants were grown and selected based on survival at 37°C, andyeast colonies that survived were subjected to plasmid extraction. Currently, we have successfully isolated plasmids that allowed sec6 mutant cells to survive the temperature shift and are working on validating growth via spotting assay at 37° C with the intent to sequence the genomic insert. Isolation and characterization of novel anchoring interactors will allow us to make forward steps in understanding the specific roles of Sec6 and exocyst functions, which is known to play diverse roles in several different organisms including humans.

9947 - TriBeta and NMDP: A Life-Saving Partnership

Matthew (Matt) Kroeger

NMDP. Find Cures. Save Lives., Minneapolis, MN

In Fall 2023, TriBeta and NMDP (formerly Be The Match and the National Marrow Donor Program) launched a new national partnership—the first ever for TriBeta—to help provide a low-lift and high-impact educational service opportunity to all TriBeta chapters across the country. TriBeta chapters and students have the ability to be an integral part of our life-saving movement by spreading awareness of the need for donors and the NMDP Registry on their campuses and within their community circles. This partnership has already led to potential matches for patients who may need a blood stem cell donation as a treatment or possible cure. Information on how the matching process works, what the donation process entails, and how chapters can get involved will be shared in this upbeat, enthusiastic and enlightening session.

10158 - Characterizing the signaling pathway for intrinsic photoresponses in the vertebrate iris

Drew Tobin

James Madison University, Harrisonburg, VA

All light detection for visual function in vertebrate animals such as humans occurs in the eye. The iris is a muscular tissue in the anterior of the eye which controls the amount of light entering the eye. The size of the iris aperture (i.e.-pupil) is controlled by neurological signals initiated in the retina and transmitted to the brain, which signals the iris muscle to constrict during pupillary light reflex. The iris helps to improve visual sensitivity and acuity, it can also protect the retina against light-dependent stress and photoreceptor degeneration. Non-primate vertebrates have an additional intrinsic pathway to drive light-dependent iris constriction. This additional pathway requires intrinsic iridial photoreceptors (IIPs) that initiate light responses. The mechanism by which IIPs communicate with the iridial sphincter muscle cells is still unknown. Some research studies suggest that gap junctions are required for intercellular signaling in the intrinsic signaling pathway. We hypothesize that gap junctions are required for cell-to-cell communication in the intrinsic iridial signaling. We have identified a set of putative gap junction proteins (connexin) expressed in mouse, rat and chicken irises. To test vertebrate irises for the expression and distribution of connexin proteins we used quantitative PCR and immunohistochemical staining. Our results show that connexin expression is evolutionarily conserved in vertebrate irises and is the signaling conduit for the light-driven signaling pathway in the iris.

10281 - Adenoviral Protein E4 11k's Role in the Inhibition of the DNA-PK-dependent DNA Damage Response

Heather Vincent, Kindle Reeves, Kasey Karen

Georgia College & State University, Milledgeville, GA

Adenovirus (Ad) can cause upper respiratory infections, gastroenteritis, and conjunctivitis. The linear, double-stranded DNA Ad viral genome can be broken up into early and late phase genes. Our protein of interest, E4 11k, is a product of one of the early genes that works to disrupt normal cellular function to enhance the viral replication cycle. One of the mechanisms E4 11k uses to achieve this disruption is through the inhibition of the DNA damage response (DDR). The DDR is responsible for repairing double-stranded DNA breaks (DSBs) through non-homologous end joining (NHEJ). During DDR, DNA-dependent protein kinase (DNA-PK) becomes activated via phosphorylation. During an infection, Ad's genome triggers the DSB repair pathway due to the genome's structural similarity to a cellular DSB. The DDR tries to "repair" the viral genome by ligating the viral genomes into concatemers, disrupting viral DNA replication. Ad, however, has evolved mechanisms to prevent activation of the DDR. Previously, E4 proteins have been shown to regulate the activation of DNA-PK. In this study, we aim to determine E4 11k's ability to inhibit DNA-PK phosphorylation in response to cellular DSBs. HeLa (cervical cancer) cells were treated chemically with different combinations of either etoposide (drug that induces DSBs), Nu771 (inhibitor of DNA-PK phosphorylation), or an Ad E4 11k only viral infection. The phosphorylation status of DNA-PK was analyzed through immunoblotting. In addition, we want to characterize DNA-PK localization during an Ad infection. Immunofluorescence microscopy was also used to visualize protein localization. Our results indicate that E4 11k is a novel inhibitor of DNA-PK activation. It has also been shown that etoposide treatment combined with the inhibition of DNA-PK activation result in cancer cells that have less adherence. These findings suggest a potential mechanism for which E4 11k can be used as a novel chemosensitizer for therapy-resistant cancer cells.

10301 - New Records of Spider Wasps (Hymenoptera: Pompilidae) of Great Smoky Mountains National Park

Aiden Starry[1], Mackenzie Cooper[1], Georgia Jinks[1], Danielle Lowe[1], Grace Orewiler[1], Alexander Shoemake[1], Jacob Taylor[1], Will Kuhn[2], Jeremy Blaschke[1]

[1]Union University, Jackson, TN, [2]Discover Life in America, Gatlinburg, TN

The All Taxa Biodiversity Inventory (ABTI) of Great Smoky Mountains National Park (GSMNP) is an initiative devoted to cataloging every kind of life present in the park. Spider wasps (Hymenoptera: Pompilidae) are a diverse taxon of spider ectoparasitoids whose presence significantly impacts numerous ecosystem services. To document the diversity of spider wasps from GSMNP, specimens collected in the park over the past three decades were sent to Union University, sorted to morphospecies, and DNA barcoded. Barcoding mitigates the challenges associated with identifying specimens from diverse taxa by relying on molecular characters instead of solely morphological characters. In total, 190 specimens representing 70 species were barcoded, resulting in 176 sequences useful for species identification (>200 bp in length). One new genus record (*Anoplochares*) and nine potential new species records (*Ageniella obscura delicata*, *Anoplius illinoensis*, *A. lepidus*, *Arachnospila arcta*, *Auplopus caerulescens*, *Entypus magnus*, *Evagetes parvus*, *E. proximus*, and *Minagenia osoria*) are added to the ATBI pending morphological verification. Barcoding also revealed cryptic genetic diversity within several species (*Aporus niger*, *Psorthaspis mariae*, and *Ceropales longipes*) that may indicate the presence of undescribed species in the park. These results contribute significantly to the ATBI by adding new park records for an understudied

taxon and demonstrate the effectiveness of using DNA barcoding to identify spider wasp species.

10325 - Preliminary Survey of Insect Biodiversity at Cypress Grove Nature Park, TN

Mackenzie Cooper, Georgia Jinks, Danielle Lowe, Grace Orewiler, Alexander Shoemake, Aiden Starry, Jacob Taylor

Union University, Jackson, TN

Insects provide numerous ecological services within forests, including pollination, decomposition, and nutrient cycling through parasitoid-host-plant interactions. High insect biodiversity signals a healthy ecosystem. The insect biodiversity present in the bottomland hardwood forest ecosystem of Cypress Grove Nature Park (CGNP) (Jackson, TN) has never been formally surveyed. To begin studying the insect biodiversity of CGNP, a Gressitt-style Malaise trap was set up within the forest. Collections were made ~4 days from Aug. 18 – Oct. 22, 2024. Insects were counted and sorted to order. Specimens within order Hymenoptera were further sorted to family. In total, 19,304 insects were collected, representing 11 different orders. The four most abundant orders were Diptera (91.6%), Hemiptera (26.3%), Hymenoptera (8.4%), and Lepidoptera (4.1%). Fungus gnats (Diptera: Sciaroidea) and planthoppers (Hemiptera: Fulgoroidea) were especially numerous. Within Hymenoptera, 18 families were identified, with the greatest abundance within Ichneumonidae (19.2%), Braconidae (13.2%), and Formicidae (12.78%). Several uncommon species were discovered, including 51 specimens of cricket assassin wasps (*Rhopalosoma* cf. *nearcticum*), three forcepflies (*Merope tuber*), one pelecinid wasp (*Pelecinus polyturator*)—representing a relict morphology from the Jurassic, and one rarely encountered gnat bug (*Systelloderes biceps)*. This study represents the first attempt to catalog the diversity and abundance of insects at CGNP.

10342 - Two Invading Ant Species Affect Biodiversity in Longleaf Pine Ecosystems

Erika Rivera

University of North Carolina at Pembroke, Pembroke, NC

Longleaf pine savannas are unique and diverse ecosystems, therefore establishment by invasive Red-Imported Fire Ants (RIFA, Solenopsis invicta) and Asian Needle Ants (ANA, Brachyponera chinensis) may have a significant impact on biodiversity. The goal of our research is to survey invasive ant nests and ant diversity to identify changes in nest density, richness, and abundance over time. Surveys of RIFA nests were conducted along belt transects in 2014, 2017, and 2022 in three longleaf pine savannas. Pitfall traps were used to measure the abundance and richness of ants along the transects in 2017 and 2022. Our 2017 findings showed that RIFA was clearly the most abundant species of ant. In 2022 we resurveyed the same sites and our data revealed that 1) the ANA was now the most abundant ant species across sites, 2) RIFA abundance and nest densities decreased, 3) there was a sharp decrease in native ant abundance and richness, 4) soil texture impacted ANA and RIFA nest locations 5) and total ant abundance increased by 65% overall, but this was due to large increases in the ANA population. The ANA may be outcompeting other ants including RIFA, suggesting it may have a big impact on the community. These savannas are some of the most diverse in terms of fauna and flora in North Carolina, so it is paramount to understand the impact of these invasive ants to mitigate any environmental effects of the species.

10416 - Establishment of the Invasive Zebra Mussel (*Dreissena polymorpha*) in Multiple Alabama Reservoirs.

Liz Farley

Samford University, Homewood, AL

The zebra mussel (Dreissena polymorpha) has been ranked among the world's worst invasive species. Adults settle on hard substrate and pose substantial threats not only to power and water infrastructure (by clogging pipes, increasing corrosion rates, etc.), but also to biodiversity of native taxa (through competition for limited resources and settling on native mussels). D. polymorpha was originally detected in the Great Lakes during the 1980s and has since become established in many states across the US. Though the species was first observed in Alabama in the 1990s and occurrences have been noted in multiple reservoirs, limited sampling for D. polymorpha has been conducted in our state. Because of this, a zebra mussel working group (composed of members of the Alabama Department of Natural Resources, USACE, and various other individuals) has been established to address the invasion of Alabama waters through monitoring, education, etc. This work aimed to compile and summarize existing data from multiple agencies / individuals, to sample reservoirs for zebra mussel veligers (planktonic larval stage) and other zooplankton to verify where established, reproducing, populations exist, and to conduct a risk assessment for Alabama reservoirs. Veliger and zooplankton sampling was conducted in summer 2024 in Pickwick, Wilson, Wheeler, Guntersville, Smith, Bankhead, Holt, and Oliver reservoirs. Veligers were observed and enumerated from all reservoirs except Bankhead and Smith, leading to the identification/confirmation of multiple active, reproducing, populations of D. polymorpha in our state.

10448 - Examining the Antimicrobial Activity of Azelaic Acid Against ESKAPE Pathogen Relatives as a Mono- and Combination-therapy

Karen Gonzalez

Catawba College, Salisbury, NC

Azelaic acid (AzA), a naturally occurring dicarboxylic acid, exhibits antimicrobial, anti-inflammatory, and anti-keratinizing properties, making it a promising alternative to conventional antibiotics[1,2]. This study evaluates the antibacterial activity of AzA against ESKAPE pathogen relatives; non-pathogenic relatives to species associated with antibiotic resistance and significant clinical challenges. Using a Zone-of-Inhibition (ZOI) assay, various concentrations of AzA (5%, 10%, 20%) were tested alongside controls (DMSO, Penicillin, Tetracycline) on bacterial lawns of *Bacillus subtilis*, *Klebsiella aerogenes*, *Staphylococcus epidermidis*, and *Escherichia coli*. Results demonstrated that AzA exhibited concentration-dependent inhibition, with 20% AzA achieving significant growth suppression across all tested species. Remarkably, AzA inhibited the growth of *S. epidermidis* to a greater degree compared to standard antibiotics tested, highlighting its potential in addressing skin-associated infections. Statistical analysis via ANOVA with Dunnett's post-hoc test supported the significance of these findings. This research emphasizes AzA's low risk of resistance development and its suitability as a novel therapeutic candidate, particularly for dermatological conditions like acne and rosacea. Future studies will investigate combination formulations of AzA to enhance skin permeability.

10486 - Investigating the Role of FOXI3 and EMT in Advanced Prostate Cancer

Emily Hyman

Troy University, Troy, AL

Prostate cancer affects approximately 1 in 8 men and is the second leading cause of cancer-related death in men. When detected early, noninvasive forms of prostate cancer can be treated successfully, but treatment and detection for aggressive, metastatic forms of prostate cancer are still needed. For prostate cancer to effectively metastasize, it must first undergo a process known as epithelial-to-mesenchymal transition (EMT). It has been shown that FOXI3, a transcription factor from the Forkhead box family, plays a key role in EMT during embryogenesis. This study aims to investigate whether FOXI3 similarly influences the EMT process within the context of cancer metastasis.

Specifically, advanced prostate cancer cell lines, PC3 and C42B, along with FOXI3 knockout versions of each cell line will be treated with Zerumbone, a phytochemical that is known to inhibit TGF-β1-induced EMT. Following this, the levels of FOXI3 and e-cadherin expression will be evaluated. The expression will be investigated at many different levels, including RNA, protein, and localization, using PCR, western blot, and immunofluorescence. By analyzing the expression and localization of FOXI3 and e-cadherin, we attempt to establish a connection between FOXI3 and EMT within the context of advanced metastatic prostate cancer.

This study may provide insights into the molecular mechanisms underlying prostate cancer progression and potentially identify FOXI3 as a novel therapeutic target for aggressive forms of the disease. The findings from this research could contribute to our understanding of prostate cancer metastasis and potentially guide the development of new treatment strategies for advanced stages of the disease, addressing a critical gap in current prostate cancer management.

10492 - FOXI3 Regulation of Prostate Cancer Cell Behavior in the Bone Microenvironment

Mario Robledo

Troy University, Troy, AL

Introduction:
Prostate cancer (PCa) is a leading cause of cancer-related deaths in men, with bone metastasis significantly contributing to morbidity and mortality. The bone microenvironment is a fertile "soil" for metastatic "seeds." Understanding the molecular mechanisms governing PCa bone metastasis is crucial for developing effective therapies. This study investigates the role of FOXI3, a member of the Forkhead-box (FOX) family of transcription factors, in PCa bone metastasis. While the functions of some FOX proteins in cancer are well-established, the specific role of FOXI3 in PCa remains largely unexplored. Recent studies suggest FOXI3 is involved in bone development and homeostasis.

Methods:An indirect co-culture experiment using a transwell plate will be used to examine the interaction between PCa cells and bone marrow stromal cells. PCa cell lines will be seeded in the bottom chambers of 6-well plates (100,000 cells/well, 2mL media). Bone marrow stromal cells will be cultured in upper chambers (100,000 cells/1mL media). After a 24 and 48-hour co-culturing, gene expression will be assessed using RT-PCR and qRT-PCR for FOXI3. Protein analysis will be measured using Western blot.

Additionally, we will repeat co-culturing and investigate the effects of bone-derived factors (FGF8 and TGF-β) on FOXI3 expression and PCa cell behavior.

Results: As this is a research proposal, results are pending. We anticipate exposure to bone marrow stromal cell-conditioned media will increase FOXI3 expression and other pro-tumorigenic factors in PCa cells. We expect that FOXI3 removal will reduce prostate cells' invasive and metastatic potential in the simulated bone microenvironment.

Conclusion: This research aims to elucidate the interplay between FOXI3 and the bone microenvironment, potentially uncovering new therapeutic targets for PCa bone metastasis. Understanding these mechanisms could lead to improved treatment strategies and better outcomes for patients with advanced prostate cancer.

10496 - A Bioinformatics Approach for the Identification and Study of Novel Genes in Alzheimer's Disease, Using Zebrafish as a Disease Model

Tanner DeCuir

Union University, Jackson, TN

Alzheimer's Disease (AD) is the most common form of dementia, affecting millions of people in the U.S. Large-scale genetic analyses indicate that AD predisposition may be the result of a multitude of genetic factors, many of which have not yet been thoroughly studied or characterized. As a result, the potential pathologic effects of many of these factors is unknown. This study proposes a bioinformatics-based protocol for the identification of novel AD-associated genes and the elucidation of the effect of variants of unknown significance (VUSs) on AD pathology. In this study, a promising AD-associated gene, GRID2IP, containing an AD-associated VUS was identified from a genetic database. An okadaic acid-induced AD model was then performed in zebrafish (*Danio rerio*) and the expression of a zebrafish ortholog of GRID2IP in healthy and AD-induced zebrafish was analyzed by real-time polymerase chain-reaction (RT-qPCR). The activity of delphilin, the protein product of this gene, was also analyzed using ELISA. Lastly, the wildtype and AD-associated variant human delphilin proteins were analyzed with YASARA computational protein modeling to assess the potential pathological effects of the variant. From these data it was determined whether GRID2IP is likely to have a role in AD pathology and whether its AD-associated VUS is likely to contribute to increased AD risk.

10514 - Investigating the Effects of Extracellular Potassium Concentration on the Expression of Inflammatory Signaling Pathways by Microglia

Elijah DeCuir

Union University, Jackson, TN

Microglia are the immune regulators of the central nervous system. They maintain the brain by expressing either pro or anti-inflammatory signaling molecules. Microglial phagocytosis of dead cells has an anti-inflammatory effect on brain tissue by sequestering cellular toxins and by stimulating the microglia to release molecules that promote the longevity of surrounding neurons and glia. In Alzheimer's disease a substantial upregulation of pro-inflammatory signaling is seen in microglia while at the same time their phagocytic response is impaired. The efflux of potassium from injured cell membranes or from dedicated channel proteins in immune cells serves as a cellular signal to activate inflammation. Given the fact that extracellular potassium levels are elevated in the brains of Alzheimer's patients and potassium channel polymorphisms have been associated with the development of Alzheimer's disease, this begs the question of how extracellular potassium concentration affects the microglial inflammatory response. Despite this, research on the role of potassium as a modulator of inflammation in microglia is significantly lacking. In this study, we use quantitative polymerase chain reaction assays to determine the expression of several pro and anti-inflammatory signaling proteins in SIM-A9 andex vivo mouse microglia exposed to varied concentrations of extracellular potassium in the presence of LPS to determine the effect on the inflammatory response and amyloid-β to simulate the conditions of Alzheimer's disease. Additionally, we will conduct a phagocytosis assay at varied potassium concentrations to determine whether elevated extracellular potassium impairs the phagocytic response of microglia to cellular debris. The results of this study will offer insight into the role of potassium released from diseased neurons as an immunomodulator in Alzheimer's disease and its potential contributions to disease pathology.

10527 - Activation of CCKLR-17D1 Neurons in the *Drosophila* Antenna in Response to Odorant Exposure

Hope Nitsche

Wake Forest University, Winston-Salem, NC

Neuropeptides are essential for the modulation of behavior, development, and homeostasis in animals. Many neuropeptides are evolutionarily conserved and homologs retain similar functions across taxa. Drosulfakinin (Dsk) is the Drosophila homolog of the

vertebrate neuropeptide cholecystokinin and has been shown to play an important role in aggressive behavior and hunger/satiety cues. Previous work has demonstrated the expression of the Dsk receptor, CCKLR-17D1 (17D1), in olfactory receptor neurons (ORNs) within the antenna suggesting a role for Dsk signaling in olfaction and related behaviors. In this study, we sought to characterize the functional activation of Dsk receptor-expressing neurons after odorant exposure using the calcium sensor GCaMP. 17-D1 expressing neurons were visualized via fluorescent confocal microscopy and their activity was recorded before and after the addition of a diluted odorant as indicated by changes in GCaMP fluorescence. We found that a subset of 17D1 neurons within the antenna showed activation in response to food and methyl salicylate. This finding suggests that Dsk activity may play an important role in olfactory processing in Drosophila. Future studies should continue to characterize 17-D1 neurons and the odorants they respond to, to more fully understand the role Dsk plays in olfaction and other behaviors closely linked to smell.

Tri-Beta Posters

BBB1 - The Effects of Resistance Training on Muscle Strength and Muscle Metabolism in Caloric Restricted Rats

Justin Roberts

Lander University, GREENWOOD, SC

Fasting and other caloric restriction diets have been utilized for weight loss by countless individuals and have been successful for many. One problem that exists with weight loss via caloric restriction only is that it tends to be indiscriminate leading to significant losses in both fat and muscle. Short term, this has little downside, but reaching an advanced age with lesser muscle mass is detrimental. The purpose of this study is to identify the amount of resistance training necessary to preserve muscular strength during a caloric challenge. Two groups of Fischer CDF rats were subjected to resistance training via a lifting apparatus; one group was fasted and the other was fed ad libitum, and the diet ran concurrently with the training program. Maximal lifts were performed at the beginning and end of the diet and training program. The fasted group had an initial mean max of 218 grams and a final mean max of 226 grams. The non-fasted group had an initial mean max of 216 grams and a final mean max of 236 grams. Mean body mass change was also measured; the fasted group had a -3.88 gram decrease in body mass and the non-fasted group had a +5.4 mean increase in body mass. Analysis of cross-sectional diameter of the rat flexor digitorum profundus muscle showed no significant differences between groups. This study shows that minimal amounts of training is necessary to preserve strength in fasting populations.

BBB2 - Paracrine effects of LL-37 on Prostate Cancer and Immune Cell Behavior

Amiyah McCoy

Mary Baldwin University, Staunton, VA

LL-37, an antimicrobial peptide, plays a dual role in promoting and suppressing tumor growth, making it a compelling target for prostate cancer immunotherapy. This project explores the paracrine effects of immune-cell-derived LL-37 on the prostate cancer cell lines LNCaP and PC-3, which represent androgen-dependent and androgen-independent prostate cancer, respectively. The goals are to determine LL-37's impact on cancer cell proliferation and migration, evaluate the effect of alpha-1-antitrypsin (A1AT) on LL-37 expression, understand how immune-cell-derived LL-37 influences prostate cancer cell behavior, and determine whether LL-37 is produced by prostate cancer cells or primarily by other components of the tumor microenvironment (TME).

We conducted cell culture experiments using LNCaP, PC-3, and THP-1 cells to assess the effects of LL-37. Undifferentiated THP-1 cells were co-cultured with LNCaP and PC-3 cells to assess whether prostate cancer cell lines express endogenous LL-37 that could induce monocyte differentiation, indicated by THP-1 cell adhesion. Proliferation and migration assays were conducted on the prostate cancer cell lines to characterize their growth and migratory behavior. These assays included trypan blue proliferation assays to measure growth rates and wound-healing scratch assays to evaluate migration. We plan to use rtPCR to quantify LL-37 mRNA production in the cell lines before downregulating LL-37 with A1AT to determine if its inhibition reduces tumor-promoting behaviors.

This study aims to determine if LL-37 enhances prostate cancer cell proliferation and migration, particularly in the aggressive, androgen-independent PC-3 cells, and whether downregulating LL-37 with A1AT can mitigate these effects. The results of this research will provide insights into the role of LL-37 in prostate cancer and its potential as a target for future therapies. These findings could help inform the development of immunotherapies that modify the tumor microenvironment to limit cancer progression.

BBB3 - Characterizing ORF090 as a Putative Latency Factor in *Helicoverpa zea* Nudivirus 2 (HzNV-2)

Madeline Bryan

Clemson University, Clemson, SC

Helicoverpa zea, also known as Corn Earworm, is a common pestiferous moth that affects crops such as corn, cotton, tomatoes, and soybeans. *H. zea* is responsible for upwards of $2 billion of crop damage in the United States annually. *Helicoverpa zea* Nudivirus 2 (HzNV-2) is a sexually transmitted insect virus capable of infecting *H. zea*, which causes sterility in approximately 30-70% of infected individuals. Literature suggests that modification of the virus could increase these rates to 90-100% sterility, providing an efficacious method of population control. The most advantageous modification would be a disruption in the latency of wild-type HzNV-2– which

could be accomplished through the mutation of persistence associated portions of the transcript. HzNV-2 has a circularized genome that codes for 113 open reading frames. Previous studies suggest that ORFs 090, 091, and 092 may be associated with increased latency in the HzNV-2 lifecycle. The goal of this study is to characterize ORF090 as a putative latency factor in HzNV-2 and determine the localization of the protein. This will be tested by cloning HzNV-2 into the pIZT/V5-His plasmid and observing the impact of viral replication using TCID50, as well as visualization of the localization of ORF090-S-tag fusion protein using fluorescence microscopy. Results are expected to show that HzNV-2 ORF090 protein localizes to the nucleus and alters the HzNV-2 replication state.

BBB4 - A Comparison of the Effects of Enzalutamide and HC-1119 on the Proliferation and Migration of Hs578T Cells

Thalía Paiz, Paul Deeble

Mary Baldwin University, Staunton, VA

Triple-negative breast cancer (TNBC) is an aggressive subtype with high recurrence, poor prognosis, and limited treatment options due to the absence of estrogen, progesterone, and HER2 receptors. Targeted therapies for TNBC are needed to improve outcomes and reduce the adverse effects of chemotherapy. The androgen receptor (AR), expressed in up to 55% of TNBC cases, represents a promising therapeutic target. Enzalutamide (ENT), a second-generation AR antagonist, has been shown to reduce proliferation and migration in AR-positive TNBC cell lines. HC-1119, a deuterated form of ENT, demonstrates improvement in metastatic castration-resistant prostate cancer (mCRPC), showing faster metabolism, higher cytoplasmic concentrations, and fewer central nervous system-related side effects. Overlapping metabolic and signaling pathways between mCRPC and TNBC indicate these treatments may be effective in TNBC, with HC-1119 potentially demonstrating greater efficacy than ENT in reducing cell proliferation and migration in the AR-positive Hs578T TNBC cell line. Previous research has established a therapeutic dose of HC-1119 in Hs578T cells; however, no published data exists regarding therapeutic concentrations of ENT in this cell line. This project aims to determine whether HC-1119 shows superior efficacy to ENT in Hs578T cells and identify an effective therapeutic concentration for ENT in Hs578T cells. Both treatments will be assessed with and without the addition of dihydrotestosterone (DHT) to evaluate their inhibition of DHT-induced AR nuclear translocation, a key distinction between first and second-generation AR antagonists. Proliferation will be measured using a trypan blue exclusion assay, and migration will be evaluated using a scratch assay. Preliminary scratch assay results indicate a baseline untreated closure rate of 18–21 hours. This study highlights the importance of novel AR-targeting strategies in treating TNBC and possibly suggests the broader applicability of HC-1119 in other AR-dependent cancers.

BBB5 - Understanding the Evolutionary Co-Variation of the Pectoral and Pelvic Girdles in Rodents

Megan Cronje

Life University, Marietta, GA

Rodents exhibit diverse locomotor behaviors, yet the relationship between these behaviors and the evolution of their pectoral and pelvic girdles remains underexplored. This study hypothesizes that variations in locomotion among rodent species are associated with specific morphological adaptations in their girdle structures. To test this, we analyzed microCT scans of various rodent species representing different locomotor groups. Geometric morphometric landmarks were employed to quantify shape variations, and partial least squares analysis alongside phylogenetic comparative methods assessed evolutionary covariation between girdle morphology and locomotor modes. Consistent with findings in other vertebrate groups, we anticipate that our results will reveal significant correlations between locomotor behavior and girdle morphology, with specialized locomotor groups exhibiting distinct morphological adaptations. These insights will enhance our understanding of the evolutionary interplay between form and function in vertebrate skeletal structures.

BBB6 - Using Bi-Weekly 24-Hour Intermittent Fasting to Create a Model to Study the Effects of Caloric Restriction on Longevity

Jenny Le[1], Jordyn Deason[1], Justin Roberts[2]

[1]Lander University, Greenwood, SC, [2]Lander University, GREENWOOD, SC

Research has shown that caloric restriction has a positive influence on lifespan and health span by reducing common risk factors for many diseases. Intermittent fasting (IF) is a type of caloric restriction that involves cycling between eating and fasting. It is generally thought that it is easier for someone to adhere to IF than conventional diet plans that require people to monitor what they eat. Several studies of caloric restriction in rodents support the extension of lifespan seen in other research models. We hypothesized that a 24-hour IF regimen implemented twice a week would lead to reduced body weight and increased lifespan in rats ($n = 6$) compared to an ad libitum-fed control group ($n = 6$). The IF group had a significant decrease in body weight ($p < 0.05$) and increase in lifespan ($p < 0.05$). Intermittent fasting, applied in this way, provides a practical framework to study the effects of caloric restriction on longevity and

the risk factors that lead to many of the diseases associated with poor metabolic health and aging. Using this IF model, our lab is currently investigating some of these diseases such as metabolic health and glucose sensitivity, age related cognitive decline, and the potential risk of muscle loss in an aging population.

BBB7 - A Search for Pathogenic Protists and Viruses in Tarballs Collected from the Alabama Gulf Coast

Gillian Bailey, Victoria Zlotea, Madilyn Webb, Elizabeth McMahan

Troy University, Troy, AL

Anthropogenic oil spills or natural oil seeps can generate tarballs, which are sticky and dark oil masses solidified by weathering process in marine environment. Because of their peculiar nature, these marine tarballs are able to serve as a habitat for various microorganisms that are not normally found in seawater. For example, previous research reported that tarballs sampled from the Gulf of Mexico contain high numbers of the human pathogen Vibrio vulnificus. Our lab has conducted a research project funded by the 2023-2024 TriBeta research grant to detect pathogenic bacteria in tarballs sampled from the Alabama Gulf coast. In this project, we extended our previous study to detect pathogenic protists and viruses in the tarballs. DNA samples of tarballs collected from two Alabama Gulf beaches were used to investigate the presence of pathogenic protists and viruses by PCR analysis. Our PCR data suggest the presence of pathogenic Adenovirus in our tarball samples, while no pathogenic protist was detected.

BBB8 - Two genes encoding nicotinic acetylcholine receptor subunits, *acr-6* and *acr-7*, are required for nicotine and ethanol state dependent learning in *Caenorhabditis elegans*

Argo Fredericksen

Emory & Henry University, Emory, VA

Substances such as ethanol and nicotine can alter internal states in a variety of organisms, including *Caenorhabditis elegans*. These states can affect learning behaviors. State dependent learning (SDL) is a phenomenon in which a behavior learned in one state is recalled best when in a similar state during recall. We use *C.elegans* to determine the molecular and neuronal mechanisms of this phenomenon. Previous research has shown that *C. elegans* demonstrates state dependency to ethanol and nicotine. We have found a number of molecular components that are shared between ethanol SDL and nicotine SDL, namely *hen-1* and *scd-2*. Dopamine is also required for both mechanisms. This project investigates the alpha acetylcholine receptor subunits *acr-6* and *acr-7* for their requirement for both mechanisms. These findings indicate more similarities between nicotine and ethanol state dependent learning.

BBB9 - Modeling species distributions of select colubrid snakes in South Carolina

Lilly Atkins, Kerry Hansknecht, Lisa McDonald

Lander University, Greenwood, SC

Modern remote-sensing and GIS technologies have significantly simplified the process of modeling species distributions and identifying potentially suitable habitat across large geographic areas. Here, we are building models to predict areas of potentially high snake abundance and diversity throughout South Carolina. Our ultimate goal in this project is to identify local areas of suitable habitat for various snake species to improve coverboard functionality in projects monitoring snake diversity, as well as collection efforts for radiotelemetry research, in a poorly studied area of the South Carolina piedmont. We downloaded all research-grade occurrence records from GBIF for Agkistrodon contortrix, Carphophis amoenus, Nerodia erythrogaster, N. sipedon, N. taxispilota, Pantherophis alleghaniensis, Storeria dekayi, and S. occipitomaculata in the southeastern US. We extracted environmental data from the 19 bioclimatic layers available in the WorldClim database. Using R and QGIS, we clipped relevant layers to include only the southeastern US and built GLM species distribution models for each taxon (with a priority on maximizing the proportions of true positives and true negatives). We built the models using an equal number of presence and pseudo-absence points, trained the model on 80% of these points, and used the remaining points to evaluate the model. We then generated new raster layers to illustrate the habitat suitability predictions of the models. Future refinement of these models will come from incorporation of data from USGS 10m DEM files and from NLCD land cover, US EPA NHDPlus HR and ECOREG, USDA SSURGO databases.

BBB10 - Broadening the Role of Oncogenic ERG in Diverse Cancer Types

Logan Baker

Mercer University, Macon, GA

Ets family transcription factors control genes involved in many important cellular processes, such as cell proliferation, apoptosis, and differentiation. ERG encodes one member of this family required for platelet adhesion and subsequent vascular cell remodeling. The

ERG gene is abnormally expressed in approximately 50% of prostate tumors due to chromosomal translocations, resulting in more than two dozen transcript variants. These variants are linked to the development of different forms of prostate cancer (TMPSSR2-ERG and NDRG1-ERG), Ewing's sarcoma (EWS-ERG), and acute myeloid leukemia (FUS-ERG). Despite being a known oncogenic gene in prostate cells, ERG has not been well characterized in other cancer types. This study surveyed various cell lines to determine their expression of ERG and found the transcription factor in diverse cancer types, including a HeLa cell line. Gene knockout revealed that ERG expression is correlated to the growth rate and gemcitabine survivability of HeLa cells. Bioinformatic data of potential oncogenic mutations to ERG were assessed to better understand the development of chromosomal rearrangements leading to tumor formation. Results suggest that ERG has a broad role in the development and function of cancer in various cancer types.

BBB11 - Community ecology of an anoxygenic phototrophic mat inhabiting a sulfidic hot spring in Yellowstone National Park: predominant populations and their functional potential

Carter Henderson, Eric Becraft

University of North Alabama, Florence, AL

Microbial mats in sulfidic Yellowstone hot springs constructed by filamentous anoxygenic phototrophic bacteria, termed green *Chloroflexus* mats (GCF mats), were first described by the late Dick Castenholz in 1973. They occur in sulfidic hot springs of the Mammoth Terraces group at temperatures between 50 and 65°C and are also found in similar springs in other locations within the United States, Iceland and New Zealand. At lower temperatures, *Chromatium tepidum* inhabits purple-colored anoxygenic mats and *Chlorobium tepidum* inhabits green-colored anoxygenic mats. The laminated nature of GCF mats suggests that, like laminated oxygenic cyanobacterial mats in non-sulfidic hot springs, these anoxygenic mats can be considered modern analogs of stromatolite fossils. Thus, their existence challenges the notion that stromatolites necessarily reflect the presence of microbial mat communities driven by oxygenic phototrophic, a metabolism that oxygenated the Earth. Studies of GCF mats have been focused on whether lipid biomarkers and/or $\delta^{13}C$ signatures might be used to distinguish from oxygenic mats found in alkaline siliceous hot springs, but GCF mats have not been metagenomically analyzed using modern sequencing methods. Here were examine the first metagenomes of New Pit GCF mat in Yellowstone National Park. We assembled and binned 63 metagenomic assembled genomes (MAGs), of which 38 had ≥70 estimated completeness and minimal contamination. The high-quality MAGs represented 15 different phyla including an archaeal lineage and an unknown bacterial phylum. The community consists primarily of *Chloroflexus* as expected, but also contains numerous Thermodesulfobacteriota lineages known for their sulfate-reducing metabolism. In addition, multiple candidate phyla lineages were identified in abundance. Annotated metabolisms consisted of lesser-known carbon fixation pathways, hydrogen oxidation, sulfur oxidation and reduction, and diverse heterotrophic pathways. This is the first known community and metabolic snapshot of an anoxygenic GCF mat, which are likely modern analogs of ancient microbial mats on early Earth.

BBB12 - Perceived Stress and Cortisol Testing in Collegiate Student-Athletes and Non-Athletes

Nicholas Werger

Emory & Henry University, Emory, VA

Everyone in the world experiences stress to some degree, and there are many different ways to define and express it. College students are a specific population of individuals who are exposed to stress quite often with deadlines for classes, clubs and organizations, and for some, athletics. My project sought to determine whether collegiate athletes would be more stressed than collegiate non-athletes at the undergraduate level. The methods were twofold: physiological stress testing was done by obtaining two salivary swabs, one at 9am and another at 4pm, to determine percent change in cortisol over the course of one day, and the other part was a psychological test by means of a survey using the Rotter Locus of Control Scale, Perceived Stress Scale-10, Sport Multidimensional Perfectionism Scale-2, and the Athlete Burnout Questionnaire. The other objective of the study was to look for correlations between high cortisol percent change values and high survey scores.

Two sets of data were collected, one in the Fall of 2023, and the other in the Spring of 2024. The data were analyzed using an Enzyme Linked Immunosorbent Assay (ELISA) kit from Eagle Biosciences. A single sample spectroscopy instrument was used in the Fall, and a plate reader was used in the Spring for data analysis. There was no difference in percent change in cortisol values between athletes and non-athletes (t-test, p=0.121). Non-athletes scored significantly higher on the survey than athletes (t-test, p=0.024).Lastly, high percent change in cortisol values did not correlate with high survey scores. This project highlighted various types of stress and supported the idea that the perception of stress does not correlate with physiological processes in every scenario. Understanding how various factors affect both psychological and physiological stress in different ways can be useful in combating stressors.

BBB13 - Development of Protocol for Determining Soil Bacteria Abundance and Importance to Nutrient Uptake and Crop Yield

Bri Tran, Eric Becraft

University of North Alabama, Florence, AL

Global agriculture faces many challenges in trying to get improved crop yields for food security in countries all around the globe. Soil types, climate, water retention, crop type, soil bacteria, and nutrient availability are all major influences when attempting to grow the maximum yield of a particular crop. Fertilizer companies have been experimenting for decades to determine the best way to deliver primary nutrients such as nitrogen and phosphorous in different soil types. Organo-fertilizers are an optimistic alternative to traditional chemical fertilizers to increase soil nutrient uptake and minimize agricultural run-off. Soil microorganisms have long been known to increase nutrient uptake and improve overall plant health, though it can be difficult to examine soil communities because there are an estimated one-hundred billion bacteria per gram of soil. Only recently has DNA sequencing become cheap enough to analyze the microbes in soil samples in a cost-efficient way. Understanding the role of soil microbiome (defined as the total bacterial community that contributes to the ecosystem) in relation to nutrient uptake and total crop yield could be the next frontier of fertilizer development. Here, in collaboration with the International Fertilizer Development Center (IFDC), we analyzed the microbial diversity and abundance in response to different chemical and organo-fertilizer treatments. Species diversity, evenness, and taxonomic classifications were determined and analyzed relative to the chemical makeup of the fertilizers. We observed an increase in species diversity, evenness, and cell counts for all treatments, with organo-fertilizers having the highest positive impact on the soil microbiome. Additionally, multiple species often arose that are known to be important nitrogen, sulfur and phosphorous cyclers. These preliminary results could ultimacy lead to the establishment of a pipeline to determine the optimum fertilizer / microbiome balance in agricultural soils.

BBB14 - Cross State Dependent Learning using Nicotine & Ethanol with *Caenorhabditis elegans*

Elizabeth Gurshpun

Emory and Henry University, Emory, VA

Caenorhabditis elegans (*C. elegans*) is an excellent model for investigating neural mechanisms of learned behaviors. Here, we investigate state dependent learning (SDL), which occurs when the execution of a learned behavior is more effective when both learning and recall occur in the same internal state. In our SDL assay, we combine the learned behavior of olfactory learning with an altered internal state – ethanol intoxication. In olfactory learning, worms have a reduced response to an attractive odorant cue. When olfactory learning is combined with ethanol intoxication, only worms that are intoxicated during learning and recall show olfactory learning. The worms that learn while exposed to ethanol, but recall without ethanol exposure no longer show olfactory learning. We have characterized ethanol SDL as well as nicotine SDL using *C. elegans*.

We are investigating the possibility of "crossing signals" between neural connections caused by nicotine and ethanol. In this case, we will expose worms to nicotine during olfactory learning, but transfer worms to ethanol exposure during recall. Effectively this will cause cross state dependency, such that worms are learning in one state, but are recalling in another. If enough signals are 'crossed' during nicotine exposure while learning and ethanol exposure during recall, then SDL should occur. If SDL does not occur, then the correct molecular components to cause SDL are not present when switching between nicotine and ethanol in the assay.

Future experiments investigating cross state dependent learning will allow us to find specific neural pathways that may or may not intersect between ethanol and nicotine SDL. This should further determine what mechanistic similarities and differences occur with respect to ethanol and nicotine SDL.

BBB15 - Symbiosis at the Thermal Boundary of Photosynthesis

Alex Tran, Eric Becraft

University of North Alabama, Florence, AL

In the course of decades of studying cyanobacterial mat communities of alkaline siliceous hot springs in Yellowstone National Park scientists have noted the presence of green-colored streamers above the otherwise flat mats formed by Cyanobacteria. These occur in the channels just after the source-pool water begins to flow downstream, where temperatures are on the order of 65-73°C, the upper limit of photosynthesis. Although other three-dimensional structures are formed in cooler downstream effluents by filamentous Cyanobacteria (*Leptolyngbya*), these organisms are not found at temperatures where green streamers occur. Source pools provide energy sources for chemosynthetic streamer forming organisms (*Thermocrinis*) where temperatures are at the temporal limit of photosynthesis in *Synechococcus* Cyanobacteria mats. Hence, there may be ecological niches for both the *Thermocrinis* chemosynthetic streamer organisms and *Synechococcus*, and the green streamers result from the colonization of the former by the

latter organisms. Here were analyze the microbial diversity along effluents of a hot spring in Yellowstone National Park that contains green streamers, including the green streamers themselves. Metagenomes were assembled and binned into representative MAGs (metagenome assembled genomes), and relevant genomes were compared across sample sites. *Synechococcus* that colonize the streamers are evolutionarily divergent from *Synechococcus* in the nearby microbial mat. Additionally, numerous unique genes and potential molecular signatures of symbiosis were identified in the MAGs of the symbiotic organisms. This research is the first molecular analysis of microbial communities within the green streamers in hot spring effluents at the boundaries of photosynthesis.

BBB16 - Investigating the role of FRK in *Danio rerio* development

Ashlyn Kinard, Amaiya McDowell

Lander University, Greenwood, SC

Fyn Related Kinase (FRK), a non-receptor tyrosine-protein kinase, is heavily involved in many functions inside the cell such as cell differentiation, cell signaling, apoptosis, and proliferation. Previous research has shown that while similar to Src Family Kinases (SFK), it is part of a distinct group of Src related tyrosine kinases including SRM and PTK6. Similar to SFKs, FRK has been studied in different cancer cell lines, such as human breast cancer, melanoma, and human hepatoma. FRK has been identified to be a tumor suppressor kinase that can regulate PI3K/AKT signaling activity, through regulation of PTEN. Activity of FRK occurs through phosphorylation of Tyr497 in the C-Term domain. FRK gene expression in adult *Danio rerio* tissues was determined following RNA isolation. It was found that high expression exists in the liver, testis, and gallbladder. This project will investigate the role of FRK in developing *Danio rerio* embryos. FRK Morpholino (FRK MO) was injected into zebrafish embryos, silencing the gene and generating loss of the protein. Preliminary experiments show a decrease in hatching rate following loss of FRK. Future experiments will verify these results and look for any malformations during development. These experiments will provide insight into a potential role for FRK in development under normal conditions.

BBB17 - Describing the monogenean ectoparasites found on freshwater Darter species

Avery Irvin, Jessica Steagall, Jackson Scott

University of North Alabama, Florence, AL

Monogeneans are flatworm ectoparasites that latch onto the gill tissue of many fish species via posterior hooks. They are a highly diverse group with approximately 4,000- 5,000 described species and many more undescribed. Monogeneans can be very specific about which host they choose to inhabit. With a single-host life cycle, they stay on the host they choose for their entire life, which can range from a few days to several years. Monogenean taxa are described based on the fish that they choose as their host. Frequency of monogenean (genus: Aethycteron) inhabitance and survival on freshwater darters (genus: Etheostoma) varies most likely based on seasonality and other factors that are yet to be described. For every observed darter species there appears to be a different species of monogenean that inhabits that host. This poses the question: why are these parasites so host-specific? What do these parasites' differences tell us about their life cycle and infection patterns, and about the ecology and evolutionary history of their hosts? In our research we hope to describe these parasites so that we can lay the foundation for further research regarding both these monogenean parasites and their darter hosts. For each specimen collected, parasites are stained and mounted so that they can then be photographed and measured using a compound microscope. With these measurements and photos, we can provide evidence that these parasites should be classified as their own species due to the vast differences between these and currently described species. This research is critical for understanding this genus of parasites, and the hosts that they inhabit.

BBB18 - Investigating Usage of Non-Canonical Start Codons in *Drosophila melanogaster*

Hannah Griffin

Mercer University, Macon, GA

The fruit fly, *Drosophila melanogaster*, is a model organism whose genes are often used in biological research to gain further understanding of human genes. Typical gene translation begins with ribosome-mediated alignment of a messenger RNA, in which the ribosome uses a methionine amino acid as a starting point for peptide synthesis. The term non-canonical start codon describes a phenomenon where translation begins at a non-methionine amino acid, and it is exceedingly rare in eukaryotes. Through manual gene annotation, I have identified potential non-canonical start codons in two *Drosophila* genes, in one isoform of *widerborst* (*wdb*) and in two isoforms of *shaggy* (*sgg*). I propose to create DNA constructs to investigate the existence and usage of the non-canonical start codons. I will report my progress towards the cloning and western blot analysis to detect the translation of wdb/sgg protein with the non-canonical start codon.

BBB19 - Stress hormone abscisic acid represses shade avoidance response in *Arabidopsis thaliana*

Lydia Uptain, Helena Heiberger

University of North Alabama, Florence, AL

The shade avoidance response in plants includes elongated hypocotyl and petioles, elevated leaf angles, and reduction of photosynthetic pigments. In *Arabidopsis,* phytochrome B (phyB) is primarily responsible for this process. PhyB exists in two isoforms: the inactive P_r form and the active P_{fr} form. P_r and P_{fr} forms are interconvertible by absorbing red and far-red light, respectively. The balance between these two forms will be determined by the ratio of R:FR light in the environment. Normal growth occurs under high R:FR conditions with a higher concentration of P_{fr}, while shade avoidance responses occur under low R:FR conditions with a lower concentration of P_{fr} form. Here, we report that the plant stress hormone abscisic acid (ABA) can also affect the shade avoidance response. A series of computational time-lapse image analyses indicated that the increased leaf elevation angles upon low R:FR treatment were less pronounced when exogenous ABA was applied, whereas the leaf elevation angles under high R:FR conditions were not affected significantly by exogenous ABA. This trend was not limited to two-week-old plants with well-developed petioles but also found in hypocotyls in very young seedlings. These suggest that environmental stress can interfere with plant responses to light conditions.

BBB20 - Developing a multi-omic approach to uncover novel gene-metabolite networks in Human T-cell Leukemia virus (HTLV) carcinogenesis

Samantha Giraldo

Catawba College, Salisbury, NC

Human T-cell Leukemia Virus (HTLV-1) is as human retrovirus that establishes a lifelong infection of host immune cells. In some cases, HTLV infection may develop into a fatal condition known as Adult T-cell Leukemia (ATL). The process by which the virus transforms host cells into a cancerous state is not completely understood, but the HTLV-1 basic leucine zipper factor (HBZ) protein has been shown to play an important role in carcinogenesis. HBZ is a viral transcriptional regulator that influences the expression of both viral and cellular genes. Numerous studies have demonstrated that HBZ alters the gene expression of infected host cells in ways that promote carcinogenesis. However, it remains unclear how these genetic changes result in the metabolic reprogramming that is characteristic of cancer. Through metabolomic analysis, our lab has observed that HBZ modulates several pro-cancer metabolic pathways. Here, we aim to connect HBZ-mediated metabolic reprogramming with the transcriptional reprogramming that is known to occur in infected cells. We will discuss an integrated multi-omic approach to uncover gene-metabolite networks that contribute to HBZ-mediated oncogenesis.

BBB21 - Prevalence rates of *tetB*, *tetA*, and tetM tetracycline resistance genes in environmental *Escherichia coli* isolates from local waterways

Caris Cianelli

Bridgewater College, Bridgewater, VA

The purpose of this study was to determine the prevalence rates of the tetracycline resistance genes tetA, tetB, and tetM in environmental Escherichia coli isolates. Samples were from both an urban and an agricultural waterway were filtered and incubated with Coliscan™ medium to differentiate for fecal coliforms. The resulting colonies were streaked onto EMB and then TSA plates to ensure isolation and presence of E. coli. All media used were supplemented with 10 µg/mL tetracycline in order to maintain selective pressure on the isolates. DNA from the isolates was then extracted and PCR was run using tetA, tetB, and tetM primers to see what genes were present in each isolate, using conditions from a published study. Because multiple non-specific products were observed, we modified the procedure by increasing the annealing temperature from 54°C to 56°C, shortening cycling times, and lowering the concentration of Mg+2. These changes greatly improved specificity with the tetA and tetB, but not the tetM primers. Overall, results tentatively suggested that tetA occurred in isolates from urban and agricultural areas at prevalence rates of 100% and 33.3%, respectively and potentially in a lab strain of E. coli, K12. Results with tetM were too difficult to interpret due to non-specific product formation, but tetB appeared in at least one of the environmental strains and probably in E. coli K12.

BBB22 - Beyond the burn: Investigating the consequences of low-dose UV exposure on DNA damage repair in MCF-7 breast cancer cells

Allison Fredrick, Vraj Patel, Jacy Noble, Erin Witalison

Catawba College, Salisbury, NC

Epithelial cells play a key role in protecting our body from hazardous environmental factors. The most detrimental threat to our cells is the sun because excessive sun exposure can lead to numerous pathologies, as well as sunburn and premature aging. The sun exposes our cells to harmful UV rays, including UVA and UVB rays. Since our skin is our body's first line of defense, epithelial cells are the primary cells affected by sun exposure. This prompted our research to question what is happening on the molecular and genetic level to our cells after exposure to UVA, UVB, and UVC rays. For this project, we are using MCF-7 breast cancer cells cultured under standard, sterile conditions. Our preliminary studies confirmed that >15 second (>25 mJ/cm^2) UVC exposure significantly decreased cell viability, as measured using a Resazurin assay. However, DNA damage, as quantified by a Comet assay, was detected with as little as 5 seconds of UVC exposure. It is well-known that UVC exposure is lethal to cells, but we are interested in determining the molecular effects of low exposure that do not induce a significant decrease in viability. Previous studies indicate that UV exposure induces pyrimidine dimers, which are repaired by nucleotide excision repair (NER), and reactive oxygen species (ROS) production, which can increase genomic instability. To understand the biochemical mechanism of DNA damage and oxidative stress responses to low-dose UVC exposure, we will use reverse transcription-PCR and Western blotting techniques focusing on important DNA repair and oxidative stress pathways. Our results can ultimately help improve our understanding of DNA damage and oxidative stresses caused by UV radiation. Our future studies will compare the effects of UVA and UVB exposure on cancer cell lines and other non-tumorigenic cell lines.

BBB23 - Using Trail Cameras to Explore the Effect of Temperature and Precipitation on Plant Phenophases

Tyler Weiss, Andrew Schwendemann

Lander University, Greenwood, SC

Plants make up the basis of terrestrial ecosystems by providing habitats and photosynthates for other organisms. Since plants are integral to ecosystems, it is important to understand how changing temperatures and precipitation patterns may affect plants. Specifically, plant phenophases such as bud break and leaf senescence have been shown to be affected by droughts and increasing temperatures, and altered plant phenophases may affect synchrony with other species in an ecosystem. For example, many plants rely on pollinators to reproduce, but if the plants begin to flower earlier in spring, the pollinators may not be present to pollinate the plant. Using trail cameras with established archives of pictures, an R package named phenopix can be used to determine the phenophases of forest plants (mainly understory plants) using the green index of an image without specialized equipment. To gather phenophase data, we used a set of thirteen existing trail cameras placed for animal research throughout South Carolina in Greenwood County and Pickens County. We used the phenopix R package to gather vegetative phenophases from 2017-2024. We then used the NOAA Climate Data Online tool to get precipitation and temperature data from the nearest NOAA station to each site. We aim to determine if existing trail cameras used for animal research can be used for plant phenology research without requiring additional specialized equipment while exploring factors that may affect plant phenophases. The data was analyzed to examine the effects of precipitation, temperature, and day of year on the timing of bud break, maximum leaf growth, and senescence phenophases of plants at the trail camera sites.

BBB24 - Examination of *Hamelia patens*

leaf extract potential as T-cell lymphoblastic leukemia therapeutic

Kylie Overstreet

Stetson University, Deland, FL

T-Cell Mediated Lymphoblastic Leukemia (T-ALL) is a rare, aggressive cancer of immature white blood cells. The prognosis of T-ALL has been steadily improving, however there is always a need for treatments with mitigated side effects and improved resolution of the disease. Phytochemicals found in plants have been shown to have anti-tumor effects, and plant-derived compounds have been on the rise as selective and effective treatments for cancer. An alcohol-based crude extract was synthesized from the leaves of the medicinal plant Hamelia patens. The anticancer activity of leaf extract concentrations of 1, 10, 100, and 1000µg/mL were analyzed in vitro utilizing the Jurkat T-ALL cell line at different treatment times of 12, 24, 48, and 72 hours. Trypan Blue cell counts were used to calculate total live cell concentration, dead cell concentration, and cell viability. A Cell Titer Glo assay was used to determine cell metabolic activity, and an Annexin V assay was utilized to examine induction of early and late-stage apoptosis and/or necrosis. Total live cell concentration decreased as leaf extract concentration increased in a time-dependent manner. Jurat cells treated with varying concentrations of the plant the leaf extract caused a statistically significant decrease in cell viability compared to the negative control.

The Cell Titer Glo bioluminescent metabolic assay revealed decreased cell metabolism as plant leaf extract concentration increased. The Annexin V apoptosis assay yielded significant differences in apoptosis between the 100 and 1000µg/mL concentrations and the negative control. Our data suggests that Hamelia patens has potential as a treatment for T-ALL, however the mechanism of action has yet to be discerned. Current studies include examining cell death regulation protein expression changes in treated cells and non-malignant normal cell sensitivity to the leaf extract.

BBB25 - Is the fox afraid of a tiger? Examining responses of meso-predators to native and exotic scents

Ana Price

Catawba College, Salisbury, NC

Due to the loss of apex predators in North America, such as wolves Canis lupus, there is an abundance of meso-predators. The increased population of meso-predators, such as coyotes Canis latrans, can have negative impacts on other carnivores, domestic animals and native prey. This impact is called a trophic cascade and has been widely documented. For instance, the lack of wolves in many parts of North America has freed coyotes from interference competition, allowing their numbers to increase and thereby limiting the abundance of red foxes Vulpes vulpes. Due to the intraguild killing and competition they experience from wolves, coyotes alter their behavior when exposed to scents of wolves. Since animal communication occurs through scents and vocalizations, information can be gathered by individuals of different species (inter-specific) or the same species (intra-specific). Therefore, it has been suggested that humans may be able to manipulate the behavior of meso-predators, for instance, through the use of artificial or fake animal communication 'messages' from apex carnivores. Perhaps certain carnivore scents can be used to fool or trick a meso-predator into believing that an apex predator is present and thereby change the meso-predator's behavior, such as leaving an area where the fake scent has been applied. If successful, this type of artificial animal communication could minimize negative impacts from inflated meso-predator densities. In this project, we will explore how interspecific scent communication within the carnivore guild may change the behavior of meso-predators by observing their reactions on camera traps to a variety of introduced scents. We believe an increase in investigating behaviors and decrease in activity in the area will occur when exposed to scat of varies species across all trophic levels.

BBB26 - Detection of orphan nuclear receptor 4A2 (NR4A2) protein expression and oxidation in human chondrocytes

Madison Roig

Loyola University New Orleans, New Orleans, LA

Osteoarthritis (OA) is a leading cause of joint pain and disability in adults in the United States. OA affects the entire joint and leads to cartilage degradation and bone erosion. This disease is predominantly found in weight bearing joints, like the knees and hips. The orphan nuclear receptor 4A2 (NR4A2) is a constitutively active transcription factor that is expressed at elevated levels in OA cartilage and inflamed tissues. NR4A2 downregulates genes involved in cartilage metabolism and may therefore have a protective function in joints. However, NR4A2 activity may be disrupted by changes in cell signaling pathways and post-translational modifications of the receptor. Oxidative stress conditions are known to increase in joints during OA progression and aging, leading to a number of modifications in target proteins and nucleic acids. We hypothesize that NR4A2 protein is oxidized in response to oxidative stress conditions in chondrocytes and this may decrease transcriptional activity of the receptor. The objectives of this study were to optimize conditions for detection of NR4A2 protein by Western blotting and to establish the kinetics of NR4A2 protein modifications in response to oxidative stress conditions. Initial experiments were conducted in an immortalized human chondrocyte cell line (C28I2) treated with prostaglandin E2 (PGE2) as a positive control. Nuclear and cytoplasmic proteins were extracted from cells and NR4A2 was detected by Western blotting using a monoclonal antibody. Consistent with previous results, NR4A2 protein was potently induced in the nucleus after one hour of PGE2 treatment. In ongoing experiments, C28I2 cells and primary human chondrocytes will be treated with hydrogen peroxide as a model for oxidative stress conditions and NR4A2 will be monitored by Western blotting. Results from this study will provide an experimental framework for defining the specific amino acids of NR4A2 susceptible to oxidative modification in chondrocytes.

BBB27 - Using *eDNA* to Characterize Amphibian Communities in Isolated Wetlands of the Longleaf Pine Ecosystem.

Grayson Dewald, Caleb Yon

The Citadel Military College of South Carolina, Charleston, SC

Environmental DNA (*eDNA*) is the genetic material organisms leave in the environment. In this study, we collected water samples from four isolated wetlands in the Francis Marion National Forest in the winter (January) and spring (March), extracted eDNA, and

used species-specific mitochondrial genes to identify the presence of rare amphibian species. Currently, our target genes are COI (Cytochrome C Oxidase Subunit I) and ND2 (Subunit of NADH dehydrogenase). Our target species is the rare Gopher Frog (*Lithobates capito*), a fossorial species that emerges from upland longleaf pine habitat to breed in isolated temporary ponds after heavy rains. In addition, we are testing for the presence of potentially co-occurring species of the longleaf pine isolated wetlands (*Lithobates sphenocephalus, Anaxyrus terrestris, Pseudacris nigrita, P. crucifer, Acris gryllus,* and *Dryophytes femoralis*). The Gopher frog was present in all four ponds on both sampling dates. *Lithobates sphenocephalus* was present in Sunset Pond in January but present in all four ponds in March. These results may contribute to a better understanding of amphibian phenology in the longleaf pine ecosystem.

BBB28 - Drugs from the dirt: Characterizing antimicrobial production in soil-dwelling bacteria

Nora Ali

Catawba College, Salisbury, NC

In nature, bacteria are in intense competition for resources, which has led many species to evolve molecular "weapons" that kill or inhibit the growth of their rivals. While some of these compounds have been adapted into antibiotic treatments, some strains of pathogenic bacteria are developing resistance to these treatments at an alarming rate. As the crisis of antibiotic resistance worsens, it is crucial to discover new sources of effective antimicrobial compounds. Since many soil-dwelling bacterial species are known producers of these compounds, my project aimed to identify new species or strains of antibiotic-producing soil bacteria collected from the Catawba College Ecological Preserve. This project was performed in cooperation with the Tiny Earth research initiative, a global, student-driven approach to antibiotic discovery.

Soil samples were collected from the Catawba College Stanback Ecological Preserve and cultured in the laboratory and antibiotic production screens were performed using ESKAPE relatives, lab-safe organisms that are genetically similar to commonly antibiotic-resistant bacterial species. Soil isolates found to possess antimicrobial activity were identified using 16s rRNA gene sequencing and genera include *Pseudomonas*, *Prestia*, and *Chromobacterium*. Sequencing results were supported by additional bacterial characterization methods. Antimicrobial compounds of interest will be isolated using an organic extraction method and follow-up experimentation will further confirm their antimicrobial activity.

BBB29 - Longleaf pine native perennial forb seedling recruitment: designing a better seed ball.

Michael DiSilvestro[1], Madeline Schmuck[2,3]

[1]Department of Biology, The Citadel, Charleston, SC, [2]The Citadel Military College of South Carolina, Charleston, SC, [3]Mississippi State University, Biloxi, MS

Reintroducing native plants into restoration and revegetation projects could increase plant species diversity, increase floral resources for pollinators, and positively affect trophic-level interactions in the community. Direct seeding into restoration projects has generally had poor success rates due to biotic and abiotic factors, leading to significant seed wastage of the already insufficient native seed supply. Seed balls (aka. seed aggregates, seed bombs, seed pellets) are a low-cost, low-tech seed enhancement technology where the seeds are encased in a soil and clay matrix, providing good seed-soil contact, controlling seed planting depth, providing nutrients, and protection from seed predators. We conducted a greenhouse and field experiment testing 5.0 g seed ball shape (round vs disk) and cayenne pepper (+/-) on seed germination and seedling recruitment of native perennial understory species of the longleaf pine ecosystem. Repeated measures two-way ANOVA of seedling counts indicate significant species-specific seed ball shape, cayenne pepper, and interactions for the greenhouse and field experiments. Significantly more seedlings were established from disk vs. round seed balls, and considerably fewer seedlings were found in seed balls with cayenne pepper under greenhouse conditions. The field experiments showed significant shape, cayenne pepper, or interactions for seven seed sources, which often differed from greenhouse results. While greenhouse studies are useful for experimentation, field study results likely represent a better estimate of seed enhancement methods on seedling recruitment in the longleaf pine ecosystem.

BBB30 - Microbial Menagerie: Identification and characterization of probiotic species from kombucha

Charity Davies, Erin Witalison

Catawba College, Salisbury, NC

The bacteria found in kombucha can help feed and increase the good bacteria found in your gut. For our project, we wanted to isolate the bacteria found to see the differences between various flavors of kombucha. Our goal is to survey the probiotic species found in commercially available kombucha. We have 6 flavors of kombucha and isolated numerous bacterial colonies with unique colony morphology and characteristics. We will use 16S ribosomal RNA sequencing to identify the isolated bacterial species. We will further characterize the isolated probiotic bacteria based on Gram status and growth on selective and differential media. This work will help

us understand the probiotic variability in commercial probiotic sources.

BBB31 - Environmental predictors of cyanobacteria abundance in freshwater in Upstate South Carolina

Emily Bridgeman, Kimberly Sipanela, Melissa Hayes, Emily Prince

Lander University, Greenwood, SC

Cyanobacteria are photosynthetic bacteria that thrive in stagnant nutrient-rich freshwater. Although they are a major part of the microbial community, some species of cyanobacteria produce toxins that can kill fish and contaminate drinking water supplies. Understanding the environmental conditions that promote cyanobacterial blooms is essential for determining water safety and preserving freshwater ecosystems in Upstate South Carolina. In this study we investigated the relationship between environmental parameters, including nutrients, and the abundance of cyanobacteria in freshwater sites in Upstate South Carolina. We hypothesized that the sites with the highest concentrations of nitrogen and phosphorus would have a greater abundance of cyanobacteria present. We collected water samples from 25 sites in the Upper Saluda Watershed and measured water temperature, conductivity, pH, and the concentrations of ammonia, nitrate, nitrite, phosphate, chlorophyll a, and dissolved oxygen. Nitrate concentrations range from 0 to 4.79 mg/L, nitrite concentrations from 0 to 0.29mg/L, ammonia concentrations from 0 to 0.64mg/L, and phosphate concentrations from 0 to 1.584mg/L. Chlorophyll a concentration was not significantly correlated with any of the nutrients. However, we are still investigating whether nutrient concentrations predict the abundance of cyanobacteria. We have filtered water from each site, extracted DNA, and have sent samples for Illumina MiSeq high-throughput sequencing to identify the bacteria in the community. We will use multiple linear regression to build a model indicating which environmental parameters are important for predicting cyanobacterial abundance in the community. Understanding these relationships could be useful in informing environmental management strategies aimed at controlling harmful algal blooms and promoting healthier aquatic ecosystems.

BBB32 - Optimizing 3D Spheroid Invasion Assays Using the Breast Cancer Model

Anna Keller

Author, SAINT AMANT, LA

The two-dimensional (2D) cell culture models do not fully capture the true in vivo conditions of tumors like loss of diverse phenotypes, unlimited access to nutrients, aberrant cell-cell interactions, and changes in gene expression. A variety of conventional three-dimensional (3D) cell culture methods have been developed to implement tumor models similar to in vivo but they still have limitations of complex and time-consuming cell culture protocol, low experimental reproducibility, and difficulty in use of these models for high throughput settings. We will develop an easy, rapid, reproducible, and standardized 3D tumor spheroid invasion assay using the Incucyte® S3 Live-Cell Analysis.

Optimization of a reproducible 3-D spheroid growth assay. We will seed single-cell suspensions of breast cancer cells on ultra-low attachment plates. A cocktail of growth factors will be used to support proliferation, ensuring uniformity of spheroids. Once formed, we will embed these spheroids of 300–500 µm in Cultrex Reduced Growth Factor Basement Membrane Extract (mimicking the extracellular matrix), and place them in Sartorius Incucyte® Clearview plates with a chemoattractant. Automated image acquisition and analysis will allow for precise, real-time imaging and monitoring of spheroid growth dynamics using the Incucyte® S3. *Comparative analysis.* We will perform a 2D cell versus 3D spheroid comparative analysis of invasion and migration properties and drug response (to doxorubicin) over 72 hours. This will enable us to test that our 3-D spheroid growth assay represents the tumor microenvironment more accurately and offers deeper insights into tumorigenesis and invasion mechanisms.

Future areas of investigation would include performing immunofluorescence staining and confocal microscopy to analyze drug efficacy and changes in drug-target biomarkers using the 3-D spheroid growth assay in a high throughput setting.

BBB33 - The effect of coyote range expansion on foxes in the Southeastern US

Katie Egan, Emily Prince, Lisa McDonald

Lander University, Greenwood, SC

Coyotes (Canis latrans), red foxes (Vulpes vulpes), and gray foxes (Urocyon cinereoargenteus) are canids with similar niches. While foxes have been in South Carolina for hundreds to thousands of years, coyotes have only arrived within the last 50 years. Coyote populations have grown rapidly in South Carolina, but the effect they have on foxes is unknown. Since 2018, we have monitored mammal communities across Upstate South Carolina using a network of trail cameras. We hypothesize that, due to the similarities between the taxa, coyotes are competitively displacing foxes in areas of overlap. We predicted that over the time we have monitored the mammal community, coyote observations have increased, both red and gray fox observations have decreased, and that there is a negative correlation between fox and coyote observations. To test this hypothesis, camera trap data from six different sites (each with 3-4 camera stations) were analyzed for coyote and fox presence. We determined the relative proportion of all mammal observations in each month that were coyotes, red foxes, and gray foxes. We found that over time observations of coyotes have

significantly increased, observations of red foxes have significantly decreased, and observations of gray foxes have not changed significantly. Additionally, we found a significant negative correlation between coyote and red fox observations, but no significant relationship between coyotes and gray foxes. Interestingly, there was a positive correlation between coyote and red fox observations by camera station. This result suggests that coyotes and red foxes occupy a similar habitat. Consequently, coyotes and red foxes compete, and red foxes are being displaced by coyotes as a result.

BBB34 - An Expanded Proteome Analysis of 28 *Borrelia* Species- The Utilization of Transmembrane Domain (TMD) Protein Prediction Programs for distinguishing Lyme-causing and relapsing fever-causing species

Amanda Bullard

Mercer University, Macon, GA

Borrelia is a gram-negative spirochete bacterium implicated in Lyme disease and tick-borne relapsing fever. 14.2-23.4% of the genes in each genome appear to encode transmembrane proteins, located in the membrane of bacterial cells and are involved in signaling, recognition, and transport. Because transmembrane proteins are vital in enabling successful pathogen transmission and bacterial survival, the transmembrane proteins found in *Borrelia* are likely to be a reason that certain species of *Borrelia* cause Lyme disease while others cause relapsing fever. Each protein folds in a specific and unique, yet overall predictable, structure, and the resulting structure is essential for the function of the protein. Wet lab experimental methods can be used to determine protein structure, but it is usually costly, complex, and time-consuming. Thus, highly accurate transmembrane protein prediction programs were used to predict the folding of these proteins and to gather data on the peptide sequences located on the external surface of these cells. Previously, we tested seven protein prediction programs and analyzed them to determine their accuracy, evaluating them based on known three-dimensional structures. After analysis, two programs, CCTOP and TOPCONS, were chosen to analyze the full proteomes of five *Borrelia* species. Here, we add 23 *Borrelia* species and make comparisons between those predictions. The species considered include a total of 15 Lyme disease-causing *Borrelia* species and 13 relapsing fever-causing *Borrelia* species. This study provides further knowledge of transmembrane protein prediction programs and microbiological and genomic features that distinguish Lyme-causing *Borrelia* and relapsing fever *Borrelia*.

BBB35 - Detection of Canine and Human Tick-Borne Pathogens in Northern Kentucky

Faith Piraro

Northern Kentucky University, Highland Heights, KY

Ticks such as Ixodes scapularis (Deer/Black-legged Tick), Amblyomma americanum (Lone Star Tick), Dermacentor variabilis (American Dog Tick), Rhipicephalus sanguineus (Brown Dog Tick), and Amblyomma maculatum (Gulf Coast Tick) are prevalent in Kentucky and may transmit tick-borne pathogens causing Lyme disease, Canine Ehrlichiosis, Rocky Mountain Spotted Fever, Anaplasmosis, and Canine Babesiosis. For this project, ticks were collected at local veterinary clinics in Northern Kentucky. DNA was isolated from the ticks, and analyzed by PCR for the presence of tick-borne pathogens. This project aims to raise awareness among dog owners about the dangers of tick-borne diseases and determine the distribution and prevalence of specific tick-borne pathogens in Northern Kentucky. Initial findings will inform future research endeavors, with the goal of expanding tick collection efforts beyond Northern Kentucky to help establish a more comprehensive surveillance system that monitors both tick populations and the pathogens they carry, ultimately protecting both human and animal health.

BBB36 - Investigating the Mechanistic Effect of Heme in Artemisinin-Induced Ferroptosis Using a Cancer Cell Model

McKenzie Peurifoy, Marit Reckmann

Catawba College, Salisbury, NC

Artemisinin (ART), a novel sesquiterpene lactone endoperoxide-containing molecule, has been studied in recent decades for its potential as an anti-tumor chemotherapeutic drug. The proposed mechanism of action in the tumor cell environment involves dysregulating iron-metabolism and increasing reactive oxygen species (ROS) production and endoplasmic reticulum stress. Heme, an iron-containing porphyrin, has shown to be an effective activator of ART, cleaving the endoperoxide bridge of the ART molecule to produce a carbon-centered radical capable of binding to heme and other molecules. The subsequent production of ROS may in turn trigger ferroptosis, a process that leads to cell death. Research shows that heme serves as a pivotal regulator of chromatin through direct involvement in epigenetic mechanisms. Thus, many cancer cell types increase the production of heme in a process called *heme overdrive*. In general, cells require larger amounts of iron for successful proliferation. Our understanding that cancer cells proliferate abhorrently and shift into heme overdrive, may offer a way to exploit this need to instead induce cellular death. We hypothesize that

increased levels of heme in cancer cells due to heme overdrive cause ART to selectively target cancer cells through a ferroptosis-induction pathway. Using a resazurin-based cell viability assay, this study aims to investigate these potential synergistic growth inhibitory effects on MCF-7 and HELA cancer cell lines by exposing cells to varied concentrations of heme and ART, alone and in combination, for 24, 48 and 72 hours. Here we report our preliminary findings and discuss future research.

BBB37 - Coral Growth Under Varied Light Spectra

Jordan Clark

Northern Kentucky University, Highland Heights, KY

Tropical coral reefs are declining globally due to pollution and other factors. Corals are primary producers in ocean ecosystems that rely on light. These animals use their symbiotic relationship with zooxanthellae to gain energy through photosynthesis. If the light is limited, coral health suffers. In the NKU Coral lab, we have been exploring light levels and the impact it has on coral growth. Corals appear to respond maximally to a prescribed regime of full blue and limited red spectra, but differ in response by species. Our aim is to understand which part of the light spectrum impacts the growth of corals, and so, improve captive rearing efficiency.

BBB38 - Exploring the Interplay of TGF-beta Signaling and the ERG Transcription Factor

Hannah Fitzgibbons, Kaitlyn Eidson

Mercer University, Macon, GA

TGF-β signaling typically regulates apoptosis, suppresses cell growth, and immune responses. However, in cancer, this pathway shifts to promote tumor progression through epithelial-to mesenchymal transition (EMT), metastasis, immune evasion, and angiogenesis, with TGF-β signaling's role changing from tumor-suppressing to tumor-promoting as cancer develops. The ETS related gene, ERG, has previously been implicated with the proliferation, invasion and survival of prostate cancer, leukemia, and Ewing sarcoma. Kaplan-Meier survival analysis shows that high ERG expression is associated with decreased survival in cancers such as bladder, cervical, gastric, and renal cancers. These findings are particularly significant because ERG has not been extensively studied in these contexts. Functional assays demonstrated that ERG knockdown in Hela cells led to a significant decrease in cell migration. The addition of TGF-β to cells with ERG knockdown partially restored migration, suggesting that TGF-β could compensate for the loss of ERG expression. To further investigate whether ERG regulates TGFβ signaling, the effects of galunisertib, a known TGF-β inhibitor, were compared in shERG cells. In normal cells, galunisertib reduces migration, but if it fails to do so in shERG cells, it suggests that ERG and TGF-β are acting through the same pathway. Western blot analysis confirmed the presence of ERG expression in Hela cells and showed that ERG knockdown significantly reduced the expression of TGF-β1. Suggesting that ERG may act upstream of TGF-β, potentially regulating its expression and contributing to cancer cell migration and survival. Targeting ERG could be a potential strategy for modulating TGF-β expression and inhibiting cancer cell migration.

BBB40 - Mechanistic studies of liquid-liquid phase separation by DNA metabolism protein APE1 in genome integrity

Anthony Malone

University of North Carolina at Charlotte, Charlotte, NC

Apurinic/apyrimidinic endonuclease 1 (APE1) is a crucial enzyme that plays a critical role in DNA damage response (DDR) and maintaining genome integrity through its endonuclease and exonuclease activities. Key functions of APE1 include repairing apurinic/apyrimidinic (AP) lesions via its endonuclease activity, participating in nucleotide excision repair (NER), exhibiting 3'-5' exonuclease activity, and contributing to other DNA repair mechanisms. While the involvement of APE1 in DNA repair pathways is well-established, the role and mechanism of APE1 in liquid-liquid phase separation (LLPS) during DDR, particularly in the formation of biomolecular condensates, remain poorly understood. Addressing this knowledge gap could open new avenues for the development of targeted cancer therapies and other potential treatments. This study aims to elucidate the dynamics of APE1 in various DDR pathways and its role in biomolecular condensate formation through LLPS by using fluorescently tagged APE1 proteins. To achieve this, APE1 will be fused with a fluorescent tag, such as eGFP or HALO, along with a Histidine (His) tag via molecular cloning techniques. The recombinant APE1 plasmid will then be amplified in DH5α E. coli cells and used to transform Rosetta (DE3) competent cells for recombinant protein production via IPTG induction. The recombinant proteins will be purified using the His tag and confirmed through Western blotting and Coomassie blue staining. The purified recombinant fluorescently labeled APE1 protein will involve setting up and optimizing in vitro LLPS systems to investigate the dynamics of APE1 in biomolecular condensate formation and its functional role in DDR pathways. In summary, this research seeks to address the existing knowledge gap regarding the dynamic role of APE1 in LLPS and DDR events by employing fluorescent tagging and tracking techniques.

BBB42 - Shelf-life extension of in-house diluent for Hemagglutination Inhibition testing

Makenzie Hester

Research Student, Tifton, GA

Canine parvovirus (CPV) is a DNA non-enveloped virus that targets puppies from six weeks to twenty weeks of age. This range varies, if the canine is not properly vaccinated. CPV is highly infectious and can be easily transmissible in unhygienic environments. CPV can be described as robust, since it's not sensitive to most disinfectants and can live on a surface for years. This virus attacks white blood cells and the gastrointestinal tract in canines, which can be deadly. To lessen the likelihood of this disease, veterinarians immunize using a multivalent vaccine, which contains modified live CPV. This requires an initial vaccination and two follow-up doses with two to four weeks apart to stimulate antibody production against the virus. An annual booster is recommended after the initial vaccination series.

To assess the amount of antibodies produced by the immune system after vaccination, a Hemagglutination Inhibition (HI) test can be conducted. The HI test result allows the veterinarians to know if immunization has been effective and future timing of vaccinations. To conduct this test, swine red blood cells, a canine serum sample, diluent, and the CPV virus are needed. In Georgia, the UGA Tifton Veterinary Diagnostic Laboratory performs this test for local veterinarians and the diluent is produced in-house. This diluent is costly to make and most of the solution is wasted due to the short shelf-life of one month. Experiments were performed with diluents of varying expired duration and controlled samples to evaluate an extension of the shelf-life. Data indicates that the diluent's shelf-life can be extended up to six months.

BBB44 - Analyzing Imported Spices for Heavy Metal Detection Using ICP-MS

Miranda Sellers

Abraham Baldwin Agricultural College, Tifton, GA

Spices are widely used to enhance the flavor and aroma of food dishes. There is widespread concern regarding contamination of these food items with heavy metals. This research will investigate the presence and concentration of heavy metals in various imported [Asian spices] collected from Indian and Nepalese grocery stores located within the United States. These spices are to be analyzed using Inductively Coupled Plasma Mass Spectrometry (ICP-MS). ICP is a highly sensitive machine that detects trace elements, which includes lead (Pb), arsenic (As), and mercury (Hg). These specific metals are of concern due to their potential effects on human health. Consumption of these metals can cause issues such as liver damage, cancer, anemia and reproductive health issues.

The aim of this study will be to assess the levels of contamination and the potential health risks. The results will offer essential information for food safety authorities, emphasizing the importance of enhanced monitoring and quality control to reduce health risks linked to heavy metal exposure from spice consumption.

BBB46 - Don't Sugarcoat it: Xylitol's Inhibitory affects Against *Streptococcus mutans*

Vanessa Ruiz Marin, Francisco Camacho

Catawba College, Salisbury, NC

The human oral microbiome is a complex ecosystem crucial for our systemic health, with *Streptococcus mutans* being an important contributor to dental caries. Xylitol, a natural sugar alcohol, is recognized for its benefits in oral health including the reduction of plaque and bacterial growth. This study hypothesizes that the addition of xylitol will significantly reduce the growth of *S. mutans*, thereby demonstrating its potential as an effective agent in inhibiting the growth of this bacteria. An IRB was submitted to obtain permission to conduct a small-scale clinical trial among a group of college students at Catawba College. The trial was conducted using saliva as our sample medium, the samples were analyzed using a qPCR method and compared using a t-test and a paired t-test to compare the quantity of bacteria found initially in the oral microbiota when using a product with a small concentration of xylitol and compared to a group who received a sugar-based gum and a group who was not introduced to any gum. The group that was treated with a xylitol-based gum resulted in a smaller concentration of *S. mutans* bacteria whereas the group treated with a sugar-based gum showed an increase in quantity of the *S. mutans* bacteria. The consumption of the xylitol-based gum most likely resulted in the decrease of quantity of the *S. mutans* bacteria without changing the overall oral microbiome. The knowledge earned from this research will be used to inform a larger population of the importance of oral health and how they can obtain a healthier oral microbiome, with less frequency of caries by changing a small detail in their daily dietary habits.

Index of Authors

Last Name	First Name	I.	Presentation/Poster Number
Abaturov	Kalina	K	318
Abbott	Alexandria	A	9612
Adams	Joshua	J	73
Adhikari	Utsav	U	280
Aguilar	Dalia	D	307
Ahilon-Calmo	Selina	S	9776
Ahmed Jony	Md Jubair	M	9640
Aiken	Karelle	K	10104
Ake	Jason	J	228, 231, 171
Alexander	Samara	S	283
Ali	Nourhan	N	60
Ali	Nora	N	BBB28
Allen	Taylor	T	271
Alshalabi	Serene	S	30, 246
Alvarez	Alejandro	A	60
Alvarez-Aleman	Anmari	A	9991
Anaya	Christina	D	45
Angalet	Benjamin	B	26
Apprill	Amy	A	121
Arbogast	Brian	B	10407, 10303, 10085, 10174, 10134
Arbour	Jessica	J	9873
Arceo-Gomez	Gerardo	G	10363
Archer	Stephanie	S	80
Ard	Dalton	D	190
Ardón	Marcelo	M	9593
Arjmand	Aurora	A	10466
Armbruster	Jon	J	262
Armstrong	Amanda	A	10081, 10435, 10018
Asselin	Joshua	J	9771
Atar	Odeya	O	41
Atkins	Lilly	L	BBB9
Augustine	Lauren	L	17
Avanzato	Valeria	V	62
Axel	Anne	A	108, 182
Ayala	Angela	A	194
Ayer	Aster	A	312
Bagley	Lila	L	43
Bailey	Joshua	J	305
Bailey	Gillian	G	BBB7
Baker	Logan		BBB10
Bakkegard	Kristin A.	K	287
Balint-Kurti	Jack	J	10228
Ballenger	Julie	J	9964
Bamba	Ninah	N	25

Last Name	First Name	I.	Presentation/Poster Number
Banard-Kubow	Karen	K	61, 49
Barger	Wayne	W	308
Barger	Priscilla	P	216
Barker	Tyler	T	276
Barker	Daniel	D	10363
Barksdale	Madisyn	M	10472
Barnes	Alex	A	180
Barnett	Zanethia C.	Z	10398
Barnett	Kevin	K	10432
Barrett	Nathaniel	N	267
Barshis	Daniel	D	10318
Barthet	Michelle	M	19, 109
Bartholomew	Zak	Z	108, 103
Bartol	Soraya	S	118, 161
Bartol	Ian	I	10047
Bates	Nicholas	N	11
Bates	Sydney	S	272
Battaglia	Loretta	L	10408
Bauer	Ashley	A	10194
Beals	Christopher	C	148
Beatty	Keionna	K	140
Becraft	Eric	E	BBB11, BBB13, BBB15
Bell	Gage	G	134
Bendele	Madison	M	10350
Benedicto Pérez	Julio	J	10247
Bennett	Will	W	306
Bennetzen	Jeffrey	J	153, 9658
Bensel	Kara	K	149
Benton	Ben	B	240
Berry	Desiree	D	109
Bettinger	Jill	J	5
Bhat	Swapna	S	206, 66
Bhattacharjee	Joydeep	J	280
Bhuta	Arvind	A	9733
Bialonska	Dobrusia	D	217
Bickford	Laird	L	139
Bielmyer-Fraser	Gretchen	D	9673
Blackmore	Laurie	L	10457
Blair	Salvatore	S	29
Blanchard	Tom	T	260
Blanton	Hannah	H	10010
Blaschke	Jeremy	J	10375, 10301
Bocchieri	Michael	M	10058
Boddicker	Jennifer	D	45
Bohlen	Samuel	S	54
Bohler	Daniel	D	215
Bolin	Jay	J	225
Bonn	Tiffany	T	197

Last Name	First Name	I.	Presentation/Poster Number
Boodée	Anna	A	267
Borgo Raia	Jennifer	J	185
Bossa	Justina	J	209
Bowers	Keith	E	10164
Bowers	Grant	G	10353
Bowman Cutway	Heather	H	124
Boyd	Chris	C	262
Boyer	Sarah	S	160
Boyet	Logan	L	197
Bozikov	Ada	A	9769
Braddy	Kaylee	K	101
Bradham	Jennifer	J	96, 107
Bradley	Sloan	S	137
Bradley	Keith	K	10026, 9864
Brailey Jones	Phil	P	9658
Brandt	LaRoy	L	10562
Bräuer	Suzanna	S	9593
Brawner	Kyle	K	9771
Brazier	Ashley	A	16
Bresnahan	Philip	P	10361
Brewer	Shannon	S	10284
Brewer	Stephen	S	132
Bridgeman	Emily	E	BBB31
Bring	Zaw	Z	35
Brison	Jordan	J	9897
Brlansky	Ron	R	10242
Brock	Tyler	T	22, 9613
Brockman	Bennett	B	62
Brothers	Sevyn	S	10535, 10231
Brown	Shawn	S	133
Brown	Christopher	C	183, 177
Brown	Ashanti	A	9612
Brown	Tricia	T	10104
Brown	Chelsea	C	221
Browning	Avery	A	9710
Browning	Amelia	A	9598
Bruening	Jamis	J	10081, 10435, 10018
Bryan	Christopher	C	218
Bryan	Madeline	M	BBB3
Bucheli	Sibyl	S	10170, 10168, 10173
Bui	Truc	T	7
Bullard	Amanda	A	BBB34
Bulot	Tyler	T	170
Burba	George	G	276
Burger	JR	J	234
Burger	Joseph	J	254, 172
Burger	Gavriel	G	9744
Burgess	James	J	10283

Last Name	First Name	I.	Presentation/Poster Number
Burkey	Elizabeth	E	228, 231
Burneo	Santiago	S	10174, 10134
Burnett	Valarie	V	10547
Burney	Erin	E	9630
Burns	Michael	M	10027
Burton	Julia	J	10089
Buryak	Anastasiya	A	201
Buscaglia	Maiya	M	154
Busche	Hanna	H	66
Busick	Savanna	S	25, 24, 178
Bussberg	Nicholas	N	9757
Butcher	Loyd	L	228
Byerley Best	Brooke	B	135
Byerly	Lydia	L	58, 211
Byrd	Brian	B	196
Byrnes	Lauren	L	9727
Cabe	Hunter	H	196
Cagle	Maryann	M	145, 154, 133
Camacho	Francisco	F	60, BBB46
Camp	Carlos	C	23, 9613
Campbell	Kaitlin	K	51
Campbell	David	D	9674
Campbell	Timothy	T	9704
Campbell	Foster	F	309, 251, 168
Campbell	Erica	E	295
Camper	Jeff	J	10303, 10174, 10134
Cantrell	Tabitha	T	281
Carmichael	Mary Jane	M	9593, 9594
Carnaggio	Anna	A	9879
Carneiro	Liedson	L	10363
Cashier	Dawson	D	185
Caspary	Melissa	M	138
Cawley	Noel	N	151,
Cecil	Madeline	M	171, 231, 228
Cha	Esprit	E	257
Chambers	David	D	219
Champasouk	Jamie	J	212
Chapman	Harlan	H	126
Charpentier	Corie	C	125, 269
Chartier	Gabrielle	G	10336
Charvat	Robert	R	10102
Chauhan	Maitri	M	198
Chazal	Natalie	N	117
Cheek	Anna	A	95
Cheers	Bryce	B	9714, 9713, 9719
Chen	Daniel Chi-Wen	D	37
Chen	Chi-Wen	C	35, 157
Chen	Feng-Zhi	F	157

Last Name	First Name	I.	Presentation/Poster Number
Chen	Li-An	L	157
Chen	Chi-Wei	C	36
Chu	Kun Yuan	K	9874
Cianelli	Caris	C	BBB21
Cienfuegos	Dylan	D	57
Ciesla	Polly	P	306
Clark	Jordan	J	BBB37
Claude	Gianna	G	243
Cleary	Madison	M	267
Cleland	Corey	C	9943
Cline	Sara	S	201
Cline	Christian	C	10371
Cline	Anna Sophia	A	307
Coffey	Emily	E	10457
Coker	Laci	L	299
Coletti	Juliana	J	80
Collins	Rachel	R	105, 102
Collins	Elizabeth	E	10404
Colvard	Arlo	A	9734
Comer	Barbara	B	143
Contreras	Alex	A	149
Cook	Laura	L	9598
Cook	Kimberly	K	254, 172, 234,
Cooper	Jacob	J	85
Cooper	Mackenzie	M	10375, 10325, 1031
Corder	Katelynn	K	9797
Cornett	Madison	M	136
Cox	Sophia	S	10228
Cox	Lily	L	41
Craig	Maria	M	9727, 9763
Crater	Dinene	D	65, 200
Cresawn	Steven	S	10350
Cronje	Megan	M	BBB5
Crouch	Emma	E	245
Cumberland	Margaret	M	9861
Cunningham	Katalina	K	4
Cunningham	Julia	J	274
Cunningham	Champagne	C	10180
Cunningham	Morgan	M	71
Curry-Lindahl	Kai	K	10174
Curth	Evan	E	294
Cushman	Laary	L	301
Custer	Mackenzie	M	197
Czako	Csilla	C	9864
D'Costa	Allison	A	10075
Dalman	Nancy	N	217, 194
Daniel	Jonathan	J	69
Danielson	Erik	E	10081, 10018

Last Name	First Name	I.	Presentation/Poster Number
Dann	Jeremiah	J	228, 231, 171
Darden	Jamison	J	44
Darrah	Sarah	S	83
Darrow	Elizabeth	E	270, 226, 115
Darst	Sarah	S	79
Davenport	Jon	J	9692, 10137
Davies	Andrew	A	5
Davies	Joel	J	270
Davies	Charity	C	BBB30
Davis	Beka	B	9591
Davis	Rebekah	R	67, 68
Davis	Kathryn	K	9983
Dawes	Rose	R	81, 79, 80
Deason	Jordyn	J	28, BBB6
Debowsky	Peyton	P	108
DeCuir	Tanner	T	10496
DeCuir	Elijah	E	10514
Deeble	Paul	P	9763, 9766
DeLustro	Jenny	J	208
DelViscio	Lexie	L	272
DeMarche	Megan	M	77
DeNeef	Jacob	J	25
Derringer	Dan	D	156
Devereux	Kendra	K	10361
Dewald	Grayson	G	BBB27
Diamond	Alvin	R.A	86
Dias	Luiza	L	36
DiBiagio	Lydia	L	166
Diel	Diane	D	280
DiGeronimo	Peter	P	17
DiMaggio	Lisa	L	81, 114
Diner	Rachel	E.R	10180, 10200, 10248, 10253
Ding	Yi	Y	10075
DiSilvestro	Michael	M	BBB29
DoByne	Raelyn	R	266
Doll	Jason	J	238
Donaubauer	Elyse	E	31
Donmoyer	Jacob	J	99
Donovan	Chelsea	C	10299
Doss	Elizabeth	E	9614
Dovciak	Martin	M	10089
Drace	Kevin	K	214
Draper	Muriel	M	243
Drerup	Ian	I	186
Dubayah	Ralph	R	10081, 10435, 10018
Dugo	Mark	M	314
Dugo	Erika	E	314
Dunagan	Austin	A	2

Last Name	First Name	I.	Presentation/Poster Number
Duncil	Ethan	E	234
Dunkley	Kingsley	K	215
Durden	Lance	L	9747
Durham	Sarah	S	9733
Dykes	Ryley	R	261
Eagle	Lorelei	L	186
Easson	Cole	C	121
Ebersole	Jun	J	10027
Eckert	Ben	B	154
Edinger	Erica	E	129
Edwards	Zack	Z	9714, 9719
Egan	Riley	R	10398
Egan	Katie	K	BBB33
Eggenberger	Savanna	S	212
Eichenberger	Erin	E	236
Eidson	Kaitlyn	K	BBB38
Eisenstat	Jonathan	J	9747
Elliott	Sarah	S	10418
Ellis	Drew	D	295
Elsborg	Mille	M	9808
Ennis	Maegan	M	160
Epling	Claire	C	144
Erbelding	Grant	G	10115, 10114
Eremeeva	Marina	M	9747
Erickson	John Matthew	J	287
Ervin	Gary	G	116
Esquilin	Elik	E	253, 47
Estep	Matt	M	9730, 9726, 9720, 9694
Estes	Paige	P	84
Estifanoes	Nahom	N	10214
Eudy	Alli	A	57
Evans	Jonathan	J	10243
Evans	John	J	10457
Faragher	Sarah	S	197
Farley	Liz	L	10416
Farquhar	Abigail	A	249
Fatunsin	Olufemi	E.O	122
Ferdoush	Jannatul	J	9640
Ferguson	Beth	B	9784
Ferguson	Jake	MJ	10013
Fernandez	Maribel	M	10214
Fernandez-Canela	Josue	J	9658
Ferrari	James	J	283, 239
Ferraro	Cassidy	C	3
Finnerty	Keegan	K	91
Fiore	Cara	C	266, 121
Fiorillo	Riccardo	R	11, 170
Fitzgibbons	Hannah	H	BBB38

Last Name	First Name	I.	Presentation/Poster Number
Fitzpatrick	Benjamin	B	9692, 10175
Flanagan	Erin	E	267
Flanders	Nicholas	N	10318, 10331, 10343, 9922
Flatley	William	W	10305
Fleming	Salem	S	225
Flood	Margi	M	66
Fogelman	Kaelyn	K	10364, 10284, 10336
Foley	Joshua	J	10429
Forrester	Jodi	J	247
Fortino	Kenneth	K	10028
Fortner	Erick	E	23
Foster	Landon	L	10090
Fox	Skyler	S	10243, 9774
Foy	Rebecca	R	9784
Frampton	Arthur	A	9752, 10362, 10395
France	Ellen	E	9874
Francis	Jake	J	242
Francis	Jacob	J	10358
Franzen	David	D	276
Fratini	Gerardo	G	276
Fredericksen	Argo	A	BBB8
Fredrick	Allison	A	BBB22
Fredrickson	Alisha	A	9740
Freundlich	Grace	D	251, 168
Freundlich	Grace	G	10344
Fridley	Jason	J	10089
Friedman	Sofia	S	267, 179
Froberg	Laura	L	253, 47
Frost	Victoria	V	10034, 10195, 10163
Fuller	Teil	T	46
Fuller	Susan	S	10284
Futch	Pearson	P	249
Gagliano	Madeleine	M	311
Gahagen	Ben	B	10333
Galley	Tyler	T	200
Galloway	Laura	L	49
Galves	Jamal	J	9991
Garcia	William	W	215
Garcia Salas	Denise	D	45
Garner	Kathryn	K	107
Garr	Maggie	M	100
Garren	Mary Ann	M	195
Gatens	Lisa	L	10261
Gebhart	Maxwell	M	9782
Geib	Jennifer	J	174
Gemeinhardt	Sydney	S	114
Gentry	Andrew	A	10027
George	Lisa	L	10166

Last Name	First Name	I.	Presentation/Poster Number
George	Haylie	H	185
Gettings	Michael	M	156
Ghate	Deepta	D	316
Ghazali	Elyssa	E	9730
Giammarinaro	Alessio	A	120
Gibbons	Megan	M	10136
Gibson	Brooklyn	B	59
Gibson	Shalise	S	283
Gilbert	Michael	M	189
Giles	David	D	63, 58, 211
Giraldo	Samantha	S	BBB20
Glaves	Celeshia	C	9991
Goad	Ally	A	198
Godwin	Rebecca	R	10, 9
Goebel	Leslie	L	177
Gonzales	Jadon	J	10
Gonzalez	Emilia	E	135
Gonzalez	Jiselle	J	66
Gonzalez	Karen	K	10448
Gonzalez Caquias	Gabriela	G	37
Goode	David	D	55
Goodson	Cody	C	108, 103
Goodwin	Savannah	S	269
Gordon	Zofia	Z	297
Gough	Miranda	M	10102
Goyret	Joaquin	J	2
Graham	Zackary A.	Z	9987, 9626, 10515
Grant	Meredith	M	63, 211
Gray	Austin	A	267
Gray	Lauren	L	9694, 9720
Gray	Elise	E	162, 163
Gray	Jordan	J	10394
Greco	Isabel	I	9884
Green	Nicholas	N	26
Green	Shelby	S	10164
Green	Kate	K	173
Greene	Daniel	D	100
Gregson	Kimberly	K	10027
Gremillion	Sara	S	10104
Griffin	Hannah	H	BBB18
Griscom	Heather	H	106
Grubb	Rindy	R	9
Grubbs	Kunsiri	K	297
Grubbs	Kunsiri Chaw	K	9990
Guerra	Tatiana	T	253, 47
Guerrero	Angelina	A	267
Guglielmetti	John	J	257
Guillaumet	Alban	A	262

Last Name	First Name	I.	Presentation/Poster Number
Gull	Henderson	H	9740
Guo	Edwin	E	40
Gupta	Shipan Das	S	9640
Gurshpun	Elizabeth	E	BBB14
Hagen	Mallory	M	282
Haley	Samantha	S	169
Hall	Katelyn	K	59
Halstead	Emma	E	225
Hamilton	Kandrea	K	121
Hammond	Natallie	N	267
Hammonds-Odie	Latanya	L	10075
Hamrick	Joshua	J	245
Haney	Brandon	B	276
Haney	Mary	M	9728, 9929
Hankins	Kayla	K	135
Hansknecht	Kerry	K	BBB9
Hargrove	Brian	B	9747
Harikumar	Manav	M	62
Harold	Antony	S.A	272
Harris	Stephen	S	301
Harrison	Scott	S	70, 169, 10546, 10313
Harrison Creighton	Joy	J	32
Hartwig	Carmony	C	57
Hasim	Sahar	S	155, 55
Havran	Chris	C	9628
Hawkes	Andrea	A	10361
Hayes	Melissa	M	209, BBB31
Hays	Kim	K	9831
Heiberger	Helena	H	BBB19
Heichelbech	Audrey	A	9857
Helms	Brian	B	10336, 10058, 10364, 10373, 10398, 10379
Helt	Madeline	M	104
Henderson	Carter	C	BBB11
Henning	Jeremiah	J	9777
Hermann	Sydney	S	182
Hernandez	Miguel	M	161
Herndon	Layla	L	210
Hester	Makenzie	M	BBB42
Heydt	Jordan	J	10036, 9968
Hicok	Morgan	M	112
Hightower	Haley	H	278
Hill	Sarah	S	3
Hill	Chris	C	79, 80
Hines	Nora	N	224
Hirani	Rida	R	31
Hodge	Anne-Marie	A	10174, 10134
Hoffman	Kellan	K	220

Last Name	First Name	I.	Presentation/Poster Number
Hofstetter	Jacob	J	10302
Holbert	Hannah	N.H	12
Holder	Mark	M	10414
Holguin	Andrea	A	195
Holierhoek	Kali	K	9914
Holjes	Helaena	H	98
Holloway	John	J	108, 103
Holt	Benjamin	B	304
Holt	Daniel	D	73
Hook	Michael	M	301
Hoover	Mary Catherine	M	267
Hopfensperger	Kristy	K	130
Hopkins	AJ	A	10261, 254
Horn	Charles	C	10545
Horn	Jay	J	10026
Hudgins	Isaiah	I	230
Hughes	Nicole	N	149, 246, 139
Hughes	Indy	I	10542
Hughey	Ethan	E	309, 251, 168
Hunninghake	Abigail	A	10509
Hunt	Nyssa	N	21
Huntley	Rashawna	R	314
Hupp	Jason	J	276
Hurlbert	Jason	J	10242
Hurley	Braeden	B	9712
Hurst-Kennedy	Jennifer	J	188, 44
Hutchison	Courtney	E.C	232
Hyman	Emily	E	10486
Ibsen	Lilly	L	10338
Ingty	Tenzing	T	10472
Irvin	Avery	A	BBB17
Jachowski	David	D	301
Jackson	Paula	P	131
Jackson	Isaac	I	126
Jarrett	Reagan	R	267
Javazon	Elisabeth	E	10476
Jefcoat	Hanna Joy	H	205, 203
Jeffries	Stephanie	S	236, 317, 235, 289
Jessen	Jason	J	32
Jinks	Georgia	G	10375, 10325, 10301
Joesting	Heather	M	78, 271
Johnson	Eric	E	189
Johnson	Paul	P	217
Johnson	Ciera	C	9673
Johnson	Gillian	G	9746
Johnson	William	W	56
Johnson	Jairus	J	60
Johnson	Shonteria	S	160

Last Name	First Name	I.	Presentation/Poster Number
Johnson	Zyra	Z	10173
Johnson	Trinity	T	10261
Jones	Alan	A	19
Jones	Ethan	E	86
Jorge	Malu	M	107
Joy	Mary	M	10364
Juneau	Wanvimol	W	9829
Justus	Kara	K	10086
Kahya	Melike	M	30
Kamasah	Japhet Senyo	J	55
Kamel	Stephanie	S	10407
Kaminsky	Kate	K	301
Karanik	Bee	B	121
Karen	Kasey	K	41
Karriem	Nalah	N	283
Kathilankal	James	J	276
Kaur	Ramneet	R	9964
Kays	Roland	R	10174
KC	Kritika	K	42
Kedar	Gayatri	G	316
Keller	Anna	A	BBB32
Kelly	Lisa	L	51
Kelly	Kevin	K	9964
Kelly	Erin	E	15
Kelly	Josh	J	10143
Kework	Cooper	C	9830, 179
Khambhaita	Deeya	D	273
Khan	Muniza	M	239
Khatiwada	Bal	B	249
Kiefer	Windsor	W	10418
Kinard	Ashlyn	A	BBB16
Kinavey	Peyton	P	19
Kinosian	Sylvia	S	10166
Kluge	Madison	M	225
Knight	Chinyere	C	140
Knowles	Travis	T	10303, 10261, 10085, 10232, 10134, 10174
Knutie	Sarah	S	282, 3
Kobs	Elizabeth	E	86
Koenigstein	Carrie	C	301
Koester	Savanah	S	14
Kohl	Kathryn	K	210
Kohlmeier	Philip	P	9612
Komarnytsky	Slavko	S	9950
Koster	Kaitlin	K	9762
Krakowiak	Alaina	A	10285
Kraus	Lucy	L	267
Krings	Alexander	A	236

Last Name	First Name	I.	Presentation/Poster Number
Kroeger	Matthew	M	9947, 9946, 9961
Krosnick	Shawn	S	10418
Krupa	James	J	10261
Kuhn	Will	W	10301
Kuhn	Alijah	A	245
Kuppinger	Dane	D	257
Kwit	Charles	C	144
La	Andrew	A	56
Laberge	Tammy	T	253, 47
Lal	Archana	A	155
Lamphere	Bradley	B	181
Landress	Chad	C	182
Lane	Serina	S	117
Lane	Ma'Lon	M	110
Laney	Shelton	S	10090
Langley	Danielle	D	237
Lapinska	Julia	J	99
Larcenaire	Craig	C	129
Larsen	Michael	L	259
Latta	Dominick	D	302, 303, 298
Lattus	Elizabeth	E	260
Laughlin	Jared	J	203
Laurencio	David	D	262
Lawrence	Cassidy	C	38
Lawson	Katelyn	M.K	262
Le	Nhien	N	175
Le	Jenny	J	BBB6
Lee	Crystall	C	241, 281
Leege	Lissa	L	248, 101
Lehmann	Jackson	J	293
Lehnert	Matthew	M	9926, 9898, 15
Lester	Miles	M	60
Lewis	Gregory	G	56
Lewis	Ireland	I	106
Lewis	John	J	9598
Lhuillier	Mel	M	10047
Li	Lingyan	L	9898
Liang	En-Ci	E	157
Liao	Min-Ken	M	56
Lichtenstein	Mandi	M	10509
Liljegren	Sarah	S	10110, 187
Lilly	Thomas	T	10476
Lindelof	Kira	K	9718
Lindsay	Jonathan	J	5
Loftis	Layla	L	198
Long	Ben	B	153
López-Camaal	Alfredo	A	49
Lotsis	Luke	L	10392

Last Name	First Name	I.	Presentation/Poster Number
Loucas	Helena	H	10028
Loughman	Zachary	J	231, 186, 17, 12
Loughran	Kate	K	9720
Love	Jason	J	267, 235
Lowe	Holley	H	303, 298
Lowe	Danielle	D	10375, 10325, 10301
Lowry	Shannon	S	51
Lucardi	Rima	R	10542
Lutz	Gretchen	G	9768
Lydeard	Charles	C	9674
Lynch	Arilyn	A	225
Lynch	Molly	M	156
Lynch	Doug	D	276
M Boggess	Laura	L	10285
Madden	Kathleen	K	10148
Magee	Reegan	R	127
Maier	Jessica	J	247
Malloy	Mia	M	10214
Malone	Anthony	A	BBB40
Maloney	Anna	A	135
Mancia	Annalaura	A	9991
Mangan	Scott	S	10542, 10003, 10300
Manish	Bhaswati	B	155
Manor	Brad	B	30
Manuszak	Noah	N	150, 279
Marchetti	Meredith	M	60
Marshall	Parker	P	94
Marsico	Travis	T	10542, 10003
Martens	Christine	C	10048
Marti	Genevieve	G	267
Martin	Victoria	V	10284
Martinez	Melinda	M	9593
Martinez	Emma	E	10027
Martinez	Yireh	Y	193
Martinez	Daniel	D	250
Marvel	Destiny	D	81
Mash	Madison	M	10164
Masika	Christina	C	57
Mathews	Taja	T	223
Mathies	Laura	L	5
Mathieson	Skylar	S	10429
Matthews	Richard	A.R	9894
Matthews	Lillian	L	265
Maus	Ellie	E	76
Maxwell	Stockton	S	10044
May	Paul	P	10081
Mayer	Jacob	J	9752
Mayes	Annabelle	A	78

Last Name	First Name	I.	Presentation/Poster Number
Maze	Jennifer	J	43
Maze	Timothy	T	28
McBane	Emma	E	9797
McCann	Shaugnessy	S	9658
McClure	Collin	C	2
McCoy	Amiyah	A	BBB2
McCoy	John	J	276
McCurdy	Regina	R	10104
McDole	Ellie	E	244
McDonald	Lisa	L	9808, 10014, 10314, 9812, 10308, 9811, 10279, 9809
McDonald	Katherine	K	10291
McDonald	Katie	K	10311
McDowell	Amaiya	A	BBB16
Mchaourab	Hassane	H	27
McKillop	Mackenzie	M	9991
McMahan	Elizabeth	E	BBB7
McMahon	Olivia	O	183
McNeil	Micah	M	236
McNulty	Lili	L	10338, 10283
McQuirter	Marquis	M	81
Meade	Walker	W	25
Mehrotra	Abhi	A	80
Meisel	Casey	C	267, 179
Melrose	Allison	A	9753
Mercer	Amber	A	88, 87
Messick	Robert	R	10330
Michel	J.T.	J	10243
Mignucci-Giannoni	Antonio	A	9991
Miller	Jonathan	J	10364, 10201, 10379, 10336
Miller	Kelly	K	10164
Miller	Mary	M	79, 81, 114, 80
Miller	Jerry	J	267
Miller	Jonathan	J	10381
Mills	Anthony	A	300
Milly	Gemma`	C	10485
Minkara	Maya	M	9640
Minnich	Clara	C	142
Mirabella	Elise	E	9920
Mitchell	Bloo	B	9612
Mitchell	Charlyce	C	82
Mitchell	Blaklie	B	20
Mohammed	Raiz	R	164
Mondor	Ed	E	9747, 9746
Monnier	Nicolette	N	48
Mooradian	Nicole	N	9749
Moore	Jonathan	D	10247
Moore	Jonathan	J	71

Last Name	First Name	I.		Presentation/Poster Number
Morgan	Jessica	J	1	0034
Morgan	Jeanelle	J		206, 66
Morning	July	J		206
Morris	Michael Wayne	M		305, 315
Morris	Jeremy	J		10090
Morris	Ashley	A		48, 311
Morris	Lee	L		229
Morton	Gillian	G		211
Moss	Elizabeth	E		150, 279
Motley	Synclaire	S		175
Murano-Castrejon	Tara	T		143
Murrell	Zack	Z		10371
Musselman	Lytton	L		10318, 10343, 9922
Muthukrishnan	Suresh	S		56
Myers	Kendall	K		9898
Myers	Emily	E		9943
Nagpal	Lekisha	L		10170
Naka	Kozma	K		122
Naman	Erin	E		106
Nansel	Kiley	K		9937
Nedrich	Ellie	E		121
Neff	Abigail	A		222
Nelsen	Naoma	N		14
Nelson	Davis	D		277
Neufeld	Howard	H		67, 68
New	Gabriel	G		128
Newbrey	Jennifer	J		9937
Newbrey	Michael	M		9937
Newman	Molli	M		10364, 10379
Newton	Joseph	J		216
Nibbelink	Megan	M		10414
Nieves	Analuz	A		9647
Nilsson	Jonas	J		10174, 10134
Niraula	Dikshya	D		187
Nitsche	Hope	H		10527
Noble	Jacy	J		BBB22
Noonan	Brice	B		22
Norman	Kerrington	K		75
Novak	Natalie	N		115
Nunn	Colin	C		10398
Nwanagu	Johannamarie	J		309, 251, 168
O'Dell	Lilliane	L		91
O'Neil	Kelly	K		10164
Ocampo	Sariah	S		256
Ojha	Sabnam	S		10110
Olls	Rebeka	R		246
Olson	Julie	J		220
Orewiler	Grace	G		10375, 10301, 10325

Last Name	First Name	I.	Presentation/Poster Number
Orfinger	Alexander	A	8, 7
Orwig	David	D	10018
Osborne	Jessica	J	10076
Ousley	Amelia	A	192
Overstreet	Kylie	K	BBB24
Paccione	Caroline	C	65
Page	Evelyn	E	167
Page	Andrew	A	205
Pai	Ching Hua	C	157
Painting	Tom	T	316
Paiz	Thalía	T	BBB4
Palmquist	Kyle	K	108, 103, 150, 245, 279
Parham	James	J	10027
Parker	Scott	S	19
Parker	Emily	E	252
Parrish	Emily	E	9777
Parrish	Fisher	F	86
Parrish	Tyler	T	305
Parsons	Sarah	S	10228, 10259
Parsons	Adam	A	10551
Partridge	Mark	M	10476
Patel	Vraj	V	BBB22
Pattillo	Katie	K	148
Payne	Elizabeth	E	163
Pederson	Neil	N	10081, 10435, 10018, 9994
Peek	Hettie	H	285
Pell	Rin	R	10164
Penn	Jill	J	10214, 10476, 10466
Penneys	Darin	D	9630
Penwell	William	W	222
Peralta	Lidia	L	10163
Pérez	Jonathan	J	4
Perez	Bella	B	100
Perkins	Geremiah	G	79, 81
Perreault	Andrea	D	10509, 10551, 10518
Perry	Travis	T	95, 94, 85, 84, 83, 134
Petric	Rada	R	10261
Petric	Radmila	R	267
Pettry	Andrew	A	219
Peurifoy	McKenzie	M	BBB36
Pham	Tuyen	T	175
Philip	Emma	E	98
Philips	John	J	82
Phipps	Drew	T	12
Pierce	Cameron	C	307
Pierson	Todd	W	9830, 10526, 9601
Piraro	Faith	F	BBB35
Pitchford	Jonathan	J	132

Last Name	First Name	I.	Presentation/Poster Number
Planck	Marcus	M	266
Plate	Katherin	K	17
Plath	Niklas	N	299, 39
Poindexter	Emily	E	311
Poindexter	Derick	D	10026
Poland	Joshua	J	97
Pold	Alyssa	A	217
Polinski	Allison	A	270, 226, 115
Ponce-Bautista	Giselle	G	89
Poole	Angela	A	192
Poulter	Benjamin	B	10435, 10018
Powell	Mickie	M	10136
Powers	Steven	S	74
Prasifka	Jarrad	J	9784
Preisser	Whitney	W	9833
Price	Ana	A	BBB25
Price	Alexandra	A	9598
Prince	Emily	E	9808, 10016, 10014, 9812, 9811, 9810, 9809
Prins	Julia	J	9711, 10535
Puppo	Pamela	P	9784, 10054, 9599, 9706, 9773
Qian	Jo	J	256
Quaas	Colleen	C	40
Quincy	Kayla	K	10272
Quinn	John	J	6, 288, 293
Quintana	Jack	J	199
Radek	Mikayla	M	9864
Ragland	Ashley	A	259
Ragoobir	Brian	B	255, 204
Rai	David	D	10171
Ramey	Maxwell	M	18
Ramey	Jasmine	J	284
Rana Magar	Santosh	S	10542
Randle	Christopher	C	10173, 10318, 10170, 10168, 9945
Ranger	Christopher	C	9898
Ratnani	Aliza	A	239
Ratta	Ellie	E	255, 204
Raubenolt	Jessi	J	9898
Rayburn	James	J	16, 180
Reckmann	Marit	M	BBB36
Reed	Abbigail	A	105
Reed	Abby	A	10446
Reese	Reagan	R	175
Reeves	Kindle	K	9959, 10281
Reichmuth	Jessica	J	273
Reid	Matthew	M	9712
Reid	Ryan	R	271

Last Name	First Name	I.	Presentation/Poster Number
Reutinger	Bailey	B	9757
Reynolds	Lucas	L	184
Rhodes	Lyndsay	V	9732, 9744, 9756
Rhodes	Travis	T	10168
Rhodes	DeLacy	D	218
Richards	Sophie	S	258
Rickman	Christin	C	198
Ridgell	Lily	L	141
Ridlen	Jenna	J	207
Riggins	Anya	A	188
Riley	Emma	E	143
Rillamas	Marquessa	M	181
Rimkus	Todd	T	10234
Rimkus	Mark	M	10234
Rivera	Erika	E	10342
Rivera-Perez	Carla	C	9991
Roark	Alison	A	69
Roberts	Justin	J	BBB1, BBB6
Robertson	Denice	D	130
Robertson	Chloe	C	244
Robitaille	Isaac	I	138
Robledo	Mario	M	10492
Robles	Zoe	Z	130
Rocha	Claudia	L	40
Rocha	Sabrina	S	88, 87
Rock	Amber	A	10317, 10522
Rodriguez	Matthew	M	225
Rodriguez	Kristine Lynn	K	191
Rodríguez López	Carlos	C	290
Roe	John	J	9983
Rogers	Michael	M	10375
Roig	Madison	M	BBB26
Rokoske	Noah	N	294
Rollins	Hannah	H	207
Rollins	Vanessa	V	61
Rose	Annkatrin	A	306, 294, 104, 295
Rother	Monica	M	252, 278,
Rudock-Bowman	Megan	M	302, 303, 298, 204, 202, 255
Rueda Cediel	Pamela	P	10013
Ruehl	Clifton	C	10171, 10208, 10194
Ruffner	Marvin	M	290
Ruiz	Daniel	D	57
Ruiz	Dulce	D	206
Ruiz Marin	Vanessa	V	BBB46
Runck	Clay	C	10075
Ruschman	Gretchen	G	290
Russell	Gareth	G	10353
Sage	Elijah	E	199

Last Name	First Name	I.	Presentation/Poster Number
Sakaris	Peter	P	11
Saladyga	Thomas	T	59, 136
Salim	Vonny	V	158
Salis	Jade	J	9833
Sanborn	Emma	E	310
Sánchez-Restrepo	Andrés	A	116
Sands	Charles	Q	233
Sato	Olivia	O	72
Sauls	Bailey	B	9692
Saylor	Ryan	R	264, 72, 10338
Schabron	Kathryn	K	262
Schachner	Casey	C	10530
Schafer	Jennifer	J	88, 87, 75
Schafran	Peter	P	9950, 10166, 10366, 10485, 10484
Schaus	Maynar	M	10302
Schiebout	Michael	M	310, 285
Schlueter	Mark	M	9728, 9929, 9655
Schmid	Samuel	S	116
Schmuck	Madeline	M	BBB29, 132
Schneider	Bill	B	10242
Schoppa	Maura	M	197
Schotz	Alfred	A	262
Schroeder	Wanda	W	221
Schumm	Darla	D	156
Schwendemann	Andrew	A	BBB23
Scoffield	Bryson	B	49
Scott	Hannah	H	10090
Scott	Jackson	J	BBB17
Seidita	Elizabeth	E	41
Sellers	Miranda	M	BBB44
Shanks	Ryan	R	194
Shaw	Joey	J	10183, 9952, 9711, 10535, 10231
Shaw	Hunter	H	304
Shelley	Erin	E	261
Shelton	Kerri	K	9964
Shepard	Hannah	H	267
Sheppard	Hunter	H	60
Sherlock	Edie	E	267
Shoemake	Alexander	A	10375, 10301, 10325
Shumaker	Ketia	K	10136
Siefferman	Lynn	L	162, 282, 3, 163
Singh	Shreyash	S	27
Sipanela	Kimberly	K	BBB31
Sir	Sally	S	9981
Skalican Guthrie	Kinsey	T	186
Skinner	Lacy	L	9612

Last Name	First Name	I.	Presentation/Poster Number
Skinner	Katie	K	53
Sloey	Taylor	T	243
Smalls	Jordyn	J	146
Smith	Walter	W	25, 24, 178
Smith	Jean	J	193, 191
Smith	Nicholas	N	144
Smith	Owen	O	56
Smith	Ethan	E	9591, 9751, 9755
Smith	Hunter	H	8
Smith	Harrison	H	118
Smith	Gregory	G	284
Smith	Amber	M	212
Smith	Loraye	L	64
Smith	Kai	K	197
Snodgrass	Logan	L	288
Snyder	Alex	A	176
Sosa	Alejandro	A	116
Soukhamneut	Morgan	M	56
Spann	Cecilia	C	147
Sparks	Eric	E	132
Spence	Katharine	K	10090
Spitler	Connor	C	204, 255
Sriram	Preethi	P	9785
Stalford	Nicholas	N	88, 87, 75
Stan	Kayla	K	9875, 10557
Stanton	Daniel	D	10242
Staples	Lauryn	L	207
Starry	Aiden	A	10375, 10325, 10301
Steagall	Jessica	J	BBB17
Steffen	Morgan	M	10299
Stein	Richard	R	27
Stenger	Cynthia	C	10349, 10405, 10441
Stewart	Zariya	Z	266
Stewart	Catherine	C	107
Stivers	Caleigh	C	6
Stoeckel	James	J	10284
Stout	Matthew	M	93
Stowe	Jules	J	172
Stratman	Maya	M	132
Stuckwisch	Zoe	Z	125
Suddeth	Joseph	J	268
Suissa	Jacob	J	10166, 9696, 10366
Sullivan	Barrie	B	262
Summerrow	Catherine	C	302
Summers	Chenoa	C	240
Sweet	Drew	D	224
Taloumis	Tess	T	74
Tant	Cynthia	C	10136

Last Name	First Name	I.	Presentation/Poster Number
Tarulli	Anthony	A	96
Tasneem	Maisha	M	9640
Taylor	Joseph	J	195
Taylor	Jacob	J	10375, 10301, 10325
Teegarden	Nicholas	N	114
Tessel	Samantha	S	10098
Thiel	Clara	C	141, 296
Thigpen	Robby	R	9606
Thomas	Michelle	M	54, 53
Thompson	Kaitlyn	K	90
Thompson	Jake	J	235
Thorn	Kaila	K	156
Tillman	Ty	T	9712
Timmons	Garrett	G	227
Tipton	Simon	S	123
Tobin	Drew	D	10158
Todd	Carli	C	58
Tolley-Jordan	Lori	L	10148, 10446
Tomba	Abbie	M	173, 112
Tomlin	Gwendolyn	G	297
Toran	Marta	M	9869
Torgesen	Casey	C	50
Torrance	Katherine	K	9987, 10515
Torres	Leigh	L	117
Townsend,Jr.	Victor	V	10302
Tran	Bri	B	BBB13
Tran	Alex	A	BBB15
Trejo	Carolina	C	10543
Trieu	Vien	V	164
Tsai	Kai-En	K	157
Tsangarides	Nicholas	N	9833, 9834
Tseng	Cai-Chieh	C	157
Tu	Taryn	T	194
Tucker	Clay	C	9857
Turgeon	Victoria	V	9884
Turnage	Gray	G	116
Turner	John	J	60
Tyler	Caleb	C	267
Udolisa	Nwanneka	N	313
Umarova	Elmira	E	9612
Underwood	Avery	A	208
Ungberg	Eric	E	10098, 10026
Unger	David	D	9762
Uptain	Lydia	L	BBB19
Vaartjes	Kara	K	255, 204
Vahle	Isabella	I	131
Valiente	Jacqueline	J	9647
van Leeuwen	Siren	S	281, 241

Last Name	First Name	I.	Presentation/Poster Number
Van Skoik	Brogin	B	10187
Vanderhoff	Natasha	N	10303, 10174, 10134, 10085
Vandermast	David	D	9757, 9737
Vanniasinkam	Thiru	T	155
Varadarajan	Sridhar	S	197
Vasco	Alejandra	A	10166
Vasic	Francesca	F	76
Vaughn	Erin	E	10084
Vega	Andrea	A	29
Vera	Jorge	J	279, 150
Vickery	Gracie	G	303, 298, 202
Villanueva	Omar	O	10075
Vincent	Heather	H	9723, 9959, 10281
Vining	Victoria	V	70
Vogenitz	Jack	J	268
Wade	Jessica	J	215
Wadkovsky	Katherine	K	267
Walczak	Ericka	E	10076
Waldron	Jayme	J	182
Walker	Olivia	O	131
Wall	Andy	A	10183
Walters	Eric	E	10318
Wang	Dongfang	D	146
Wang	Xu	X	216
Wang	Haolong	H	216
Ward	Jayla	J	209
Ward	Alleigh	A	223
Wardell	RJ	R	10228
Warfel	Jaycob	J	198
Warfield	Benjamin	B	289
Warner	Morgan	M	238
Warren	Marlena	M	10085
Watersmith	Emma	E	10407
Watkins	Richard	R	223
Watson	Brian	T	12
Weakley	Alan	A	10026
Webb	Madilyn	M	BBB7
Webster	David	D	10261
Weeks	Andrea	A	10354, 10160, 10310, 10404
Weiss	Tyler	T	BBB23
Welch	Shane	S	279, 150
Wenger	Linda	L	9943
Werger	Nicholas	N	BBB12
Wessner	Dave	D	318
West	Sarah	S	9723
Westman	Riley	R	115
Whalen	Brianna	B	92
Whitaker	Melissa	M	10429

Last Name	First Name	I.	Presentation/Poster Number
White	Kristine	N	9912, 9981, 9920, 9914
White	Michelle	M	21
Wickell	David	D	10366
Wickert	Kristen	K	129
Wildman	Dreanna	D	9728, 9929
Wilkins	Dawn	H	233, 232
Willadsen	Peter	P	10228, 10259
Williams	Bryce	B	124
Williams	Shelby	S	192
Williams	Jessica	J	10363, 10307
Williams	Claire	C	263
Williams	Noah	N	275
Williamson	Hailey	H	305
Williamson	Noah	N	9875
Williamson	Sam	S	29
Willis	Annika	A	267
Wilson	Thomas	T	21
Wise	Darla	D	59
Witalison	Erin	E	60, BBB22, BBB30
Wolfe	Dylan	D	9610
Wolff	Robert	R	10554
Wondemu	Blaine	B	264
Woodbridge	Margaret	M	10089
Woods	Natasha	N	89, 92, 99, 98
Wooten	April	A	238
Woriax	Velinda	V	319
Worm	Alexander	A	224
Wright	Douglas	S	9894
Wright	Hannah	H	174
Wright	Michael	M	298, 303
Wright	Tyler	T	100
Wurch	Louie	L	10299
Wyer	Ali	A	231, 171, 228
Wyngaarden	Anna	A	77
Yando	Erik	E	243
Yon	Caleb	C	BBB27
Yoshimura	Kristin	K	10036
Yost	Kerwin	K	195
Youker	Robert	R	267, 195, 196
Young	Rebekah	R	102
Youngsteadt	Elsa	E	126
Ypema	Ari	A	1
Zanin	Kathy	K	40
Zeffiro	Elyse	E	199
Zettler	Jennifer	J	175, 176
Zinnert	Julie	J	89, 99, 92, 98
Zlotea	Victoria	V	BBB7
Zupko	Brianna	B	148

Last Name	First Name	I.	Presentation/Poster Number
Zwiers	Paul	P	164